
ONLINE SEARCH REQUEST FORM
*****USER Sheela Huff SERIAL NUMBER 08/012929
ART UNIT 18010 PHONE 305-78060 DATE 3/11/97

Please give a detailed statement of requirements. Describe as specifically as possible the subject matter to be searched. Define any terms that may have special meaning. Give examples or relevant citations, authors, or keywords, if known.

You may include a copy of the broadest and or relevant claim(s).

Please search SCA ~~1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100~~

~~54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100~~

~~54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100~~

~~1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100~~

→ 2, 4, 11-28, and 53-56.

TXS-

Sheela

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STAFF USE ONLY

COMPLETED 3-19-97
SEARCHER EEF x4391
ONLINE TIME 6 TOTAL TIME 15
(in minutes)
NO. OF DATABASES 46SYSTEMS
11aa CAS ONLINE
13na DARC/QUESTEL
DIALOG
SDC
112 OTHER

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(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:16:58 1997; MasPar time 1.98 Seconds

Tabular output not generated. 57.292 Million cell updates/sec

Title: >US-08-612-929-26

Description: (1-11) from US08612929.pep

Perfect Score: 104

Sequence: 1 RETVFWYVDV 11

Scoring table: PAM 150

Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7

8:part8 9:part9 10:part10 11:part11 12:part12 13:part13

14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 19.055; Variance 73.194; scale 0.260

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	104	100.0	11 13	R70200	MAB 3B9 heavy chain C	3.72e-03
2	104	100.0	140 13	R70190	Mouse MAB 3B9 heavy c	3.72e-03
3	104	100.0	141 13	R70191	Chimeric antibody 3B9	3.72e-03
4	104	100.0	141 13	R70192	Humanized antibody 3B	3.72e-03
5	73	70.2	10 12	R62884	Murine anti-human ath	3.13e+00
6	73	70.2	116 7	R38609	MCPC heavy chain.	3.13e+00
7	73	70.2	126 12	R62880	Murine anti-human ath	3.13e+00
8	73	70.2	126 12	R62879	Murine anti-human ath	3.13e+00
9	66	63.5	106 1	R04937	Sequence of human car	1.33e+01
10	66	63.5	121 18	R88846	Murine antibody 2CE-0	1.33e+01
11	66	63.5	122 16	R79878	Anti-EGFR antibody he	1.33e+01
12	66	63.5	122 1	P91382	Antibody heavy chain	1.33e+01

13	66	63.5	122 18	W02201	CDR switched variable	1.33e+01
14	66	63.5	123 16	R79877	Anti-EGFR antibody he	1.33e+01
15	66	63.5	140 1	P94780	2 H7 VH gene.	1.33e+01
16	66	63.5	140 2	P70627	Sequence encoded by t	1.33e+01
17	66	63.5	147 18	R99687	Monoclonal anti-idiot	1.33e+01
18	66	63.5	147 18	R98411	3H1 heavy chain varia	1.33e+01
19	66	63.5	151 4	P30252	Sequence of the leade	1.33e+01
20	66	63.5	239 12	R64812	ScFv anti-HCG.	1.33e+01
21	65	62.5	556 17	R96737	A. niger Bo-1 carboxy	1.63e+01
22	65	62.5	557 17	R96738	A. niger SFAG 2 carbo	1.63e+01
23	64	61.5	50 2	P70039	Secretory signal sequ	2.00e+01
24	64	61.5	491 9	R48059	Sequence of protease	3.00e+01
25	62	59.6	115 7	R34018	BW 835 VH.	3.00e+01
26	61	58.7	117 2	R07318	VH domain of antibody	3.66e+01
27	61	58.7	118 5	R29701	431/26 VH hum.	3.66e+01
28	61	58.7	119 3	P60335	Immunoglobulin heavy	3.66e+01
29	61	58.7	119 1	P81025	V region of H chain (3.66e+01
30	61	58.7	147 6	R32542	C242 heavy chain vari	3.66e+01
31	61	58.7	148 6	R30455	C242:11 MAB heavy cha	3.66e+01
32	61	58.7	470 2	P70547	Sequence of novel mou	3.66e+01
33	61	58.7	470 3	P60351	Chimeric human-mouse	3.66e+01
34	61	58.7	909 10	R50092	Humanised anti-CEA sF	3.66e+01
35	60	57.7	110 4	R23903	RuBPCase small subuni	4.47e+01
36	60	57.7	4987 3	R10834	Rianodin receptor.	4.47e+01
37	60	57.7	5035 5	R25450	MH mutant porcine rya	4.47e+01
38	60	57.7	5072 2	R11510	Ryanodine receptor de	4.47e+01
39	59	56.7	58 15	R88965	Mutant serine proteas	5.45e+01
40	59	56.7	119 9	R47221	Antibody heavy chain	5.45e+01
41	59	56.7	120 16	R92089	Anti-RSV F glycoprote	5.45e+01
42	59	56.7	120 16	R92088	CDR-grafted anti-RSV	5.45e+01
43	59	56.7	139 12	R62678	CV1748RHA VH region.	5.45e+01
44	59	56.7	139 8	R43693	PB1.3/Humanised heavy	5.45e+01
45	59	56.7	139 8	R43689	PB1.3/Humanised heavy	5.45e+01

ALIGNMENTS

RESULT	1
ID	R70200 standard; Protein; 11 AA.
AC	R70200;
DT	20-SEP-1995 (first entry)
DE	MAB 3B9 heavy chain CDR.
KW	Chimeric antibody; humanized antibody; antibody engineering;
KW	monoclonal antibody; MAB; interleukin-4; IL-4; allergy; CDR;
KW	complementarity determining region.
OS	Mus sp.
PN	W09507301-A.
PD	16-MAR-1995.
PF	07-SEP-1994; U10308.
PR	07-SEP-1993; US-117366.
PR	14-OCT-1993; US-136783.
PA	(SMIK) SMITHKLINE BEECHAM CORP.
PA	(SMIK) SMITHKLINE BEECHAM CORP.
PI	Gross MS, Holmes SD, Sylvester DR;
DR	WPI; 95-123387/16.
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT	from high affinity mAbs - useful in treatment of IL-4-mediated
PT	and IgE-mediated allergic conditions
PS	Disclosure; Page 58; 97pp; English.
CC	Spleen cells from mice immunized with human IL-4 were used to prepare
CC	hybridomas, which were screened for anti-IL-4 MAb secretion. Only
CC	clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC	chains were cloned into pCEM7f+ and transformed into E. coli
CC	DH5-alpha. A heavy chain cDNA clone was sequenced (Q83491) that

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3

CC encoded the protein given in R70190. 3 CDRs (R70198-200) were
CC identified.
SQ Sequence 11 AA;

Query Match 100.0%; Score 104; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.72e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 retvfywyfdv 11
|||||
QY 1 RETVFWYFDV 11

RESULT 2

ID R70190 standard; Protein; 140 AA.
AC R70190;
DT 20-SEP-1995 (first entry)
DE Mouse Mab 3B9 heavy chain.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy.
OS Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Sig_peptide
FT Region 50..56
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 71..86
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 119..129
FT /label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR N-PSDB; Q83491.
PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived
PT from high affinity mabs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.2; 97pp; English.
CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC chains were cloned into pGEM7ft and transformed into E. coli
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for
CC antibody engineering.
SQ Sequence 140 AA;

Query Match 100.0%; Score 104; DB 13; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.72e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 119 retvfywyfdv 129
|||||
QY 1 RETVFWYFDV 11

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4

RESULT 3
ID R70191 standard; Protein; 141 AA.
AC R70191;
DT 20-SEP-1995 (first entry)
DE Chimeric antibody 3B9 heavy chain.
KW Chimeric antibody; antibody engineering; monoclonal antibody;
KW Mab; interleukin-4; IL-4; allergy.
OS Homo sapiens; Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Sig_peptide
FT Region 51..57
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 72..87
FT /label= CDR
FT /note= "complementarity determining region"
FT Peptide 120..130
FT /label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR N-PSDB; Q83492.
PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived
PT from high affinity mabs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.3; 97pp; English.
CC A human/mouse chimeric antibody heavy chain variable region was
CC constructed (given in R70191) that contained the mouse anti-human
CC IL-4 Mab 3B9 variable region including 3 CDRs (R70198-200) and a
CC human antibody signal peptide (R70193). The construct was used
CC for humanized antibody production.
SQ Sequence 141 AA;

Query Match 100.0%; Score 104; DB 13; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.72e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 120 retvfywyfdv 130
|||||
QY 1 RETVFWYFDV 11

RESULT 4

ID R70192 standard; Protein; 141 AA.
AC R70192;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 heavy chain.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW Mab; interleukin-4; IL-4; allergy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Sig_peptide
FT Region 51..57
FT /label= CDR
FT /note= "complementarity determining region"

FT Region 72..87
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 120..130
FT /label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR N-PSDB; Q83493.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.4; 97pp; English.
CC A humanized antibody heavy chain variable region and signal
CC sequence is given in R70192. The signal sequence is also
CC provided in R70193. The CDR sequences of the construct are
CC identical to the native CDRs of mouse anti-human IL-4 mAb
CC 3B9 (R70198-200).
SQ Sequence 141 AA;

Query Match 100.0%; Score 104; DB 13; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.72e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 120 retvfywyfdv 130

QY 1 RETVFWYFDV 11

RESULT 5

ID R62884 standard; peptide; 10 AA.
AC R62884;
DE 18-JUL-1995 (first entry)
DE Murine anti-human atherosclerotic plaque MAb 22D3 VH CDR3.
KW Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;
KW murine monoclonal antibody; heavy chain variable region: CDR3;
KW complementarity determining region; imaging; plaque ablation.
OS Mus musculus.
FH Key Location/Qualifiers
FT Region 1..10
FT /label= CDR3
FN W09425053-A.
PD 10-NOV-1994.
PF 26-APR-1994; U04641.
PR 26-APR-1993; US-053451.
PA (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
PI Calenoff E, Chen FW, Ditlow CC;
DR WPI; 94-357904/44.
DR N-PSDB; Q78738.
PT New antigen comprising hydroxy:steroid and quat. ammonium salt -
PT and related antibodies, useful e.g. for imaging, ablating or
PT treating atherosclerotic plaque, and detecting plaque specific
PT antibodies
PS Claim 199; Page 149; 288pp; English.
CC Mice were immunised with an extract of human atherosclerotic plaque,
CC then spleen cells were fused with SP2/O1-Ag-14 myeloma cells.
CC Hybrids were screened by ELISA for reactivity with the immunogen

CC and clone 22D3 was isolated. The 22D3 antibody reacts specifically
CC with atherosclerotic tissue; it recognises a non-protein antigen
CC containing cholesterol (or similar steroid that is a substrate for
CC cholesterol oxidase) and a quaternary ammonium salt (pref. a
CC phosphatidylcholine or related compound that is a substrate for
CC phospholipase C). The CDR sequences for the heavy and light chains
CC of 22D3 were determined; peptides comprising the CDRs are claimed,
CC including chimeric (CDR-grafted) murine-human antibodies.
SQ Sequence 10 AA;

Query Match 70.2%; Score 73; DB 12; Length 10;
Best Local Similarity 85.7%; Pred. No. 3.13e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 4 yywyfdv 10

QY 5 FYWYFDV 11

RESULT 6

ID R38609 standard; peptide; 116 AA.
AC R38609;
DT 28-OCT-1993 (first entry)
DE MCPC heavy chain.
KW Antibody; variable domain; light; L; heavy; H; consensus;
KW affinity; antigen; immunogenicity; humanisation; framework.
OS Homo sapiens.
PN W09311794-A.
PD 24-JUN-1993.
PF 14-DEC-1992; U10906.
PR 13-DEC-1991; US-808464.
PA (XOMA) XOMA CORP.
PI Fishwild DM, Kohn FR, Little RG, Studnicka GW;
DR WPI; 93-213827/26.
PT Antibodies prepn. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc.
PS Disclosure; Fig 1B; 160pp; English.
CC The amino acid sequences of the light and heavy chains of the
CC variable domains from antibodies HVH [HYHEL-10 Fab-lysosyme complex]
CC (R38601 and R38608, respectively), MCPC [IgA Fab MCP603-phosphocholine
CC complex] (R38602-03 and R38609-10, respectively), NEMM [Ig Fab' NEM
CC (R38604-05 and R38611, respectively) and KOL [IgG1 KOL] (R38606-07 and
CC R38612, respectively) may be used to determine an alignment from which
CC appropriate changes may be made.
CC Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody
CC are not diminished.
SQ Sequence 116 AA;

Query Match 70.2%; Score 73; DB 7; Length 116;
Best Local Similarity 85.7%; Pred. No. 3.13e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 99 yywyfdv 105

QY 5 FYWYFDV 11

RESULT 7

ID R62880 standard; protein; 126 AA.

AC R62880;
 DT 18-JUL-1995 (first entry)
 DE Murine anti-human atherosclerotic plaque MAb 22D3 VH sequence.
 KW Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;
 KW murine monoclonal antibody; heavy chain variable region;
 KW imaging; plaque ablation.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT Misc difference 2
 FT /note= "lys at this position in R62879 and
 FT Gln at this position in R62880; also, the
 FT first 8 amino acids are dictated by the
 FT oligonucleotides used in the PCR and are
 FT not necessarily identical to those of the
 FT murine antibody"
 FT Region 30..34
 FT /label= CDR1
 FT Region 49..65
 FT /label= CDR2
 FT Region 98..107
 FT /label= CDR3
 FT Region 120..126
 FT /label= CH1
 FT /note= "start of constant region"
 PN W09425053-A.
 PD 10-NOV-1994.
 PE 26-APR-1994; U04641.
 PR 26-APR-1993; US-053451.
 PA (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
 PI Calenoff E, Chen FW, Dittlow CC;
 DR WPI; 94-357904/44.
 DR N-PSDB; Q78730.
 PT New antigen comprising hydroxy:steroid and quat. ammonium salt -
 PT and related antibodies, useful e.g. for imaging, ablating or
 PT treating atherosclerotic plaque, and detecting plaque specific
 PT antibodies
 PS Claim 194; Page 145; 288pp; English.
 CC Mice were immunised with an extract of human atherosclerotic plaque,
 CC then spleen cells were fused with SP2/01-Ag-14 myeloma cells.
 CC Hybridomas were screened by ELISA for reactivity with the immunogen
 CC and clone 22D3 was isolated. The 22D3 antibody reacts specifically
 CC with atherosclerotic tissue; it recognises a non-protein antigen
 CC containing cholesterol (or similar steroid that is a substrate for
 CC cholesterol oxidase) and a quaternary ammonium salt (pref. a
 CC phosphatidylcholine or related compound that is a substrate for
 CC phospholipase C).
 SQ Sequence 126 AA;

Query Match 70.2%; Score 73; DB 12; Length 126;
 Best Local Similarity 85.7%; Pred. No. 3.13e+00;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 101 ywyfdiv 107
 :|||||
 Qy 5 FYWYFDV 11

RESULT 8
 ID R62879 standard; protein; 126 AA.
 AC R62879;
 DT 18-JUL-1995 (first entry)
 DE Murine anti-human atherosclerotic plaque MAb 22D3 VH sequence.
 KW Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;
 KW murine monoclonal antibody; heavy chain variable region;

KW imaging; plaque ablation.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT Misc difference 2
 FT /note= "lys at this position in R62879 and
 FT Gln at this position in R62880; also, the
 FT first 8 amino acids are dictated by the
 FT oligonucleotides used in the PCR and are
 FT not necessarily identical to those of the
 FT murine antibody"
 FT Region 30..34
 FT /label= CDR1
 FT Region 49..65
 FT /label= CDR2
 FT Region 98..107
 FT /label= CDR3
 FT Region 120..126
 FT /label= CH1
 FT /note= "start of constant region"
 PN W09425053-A.
 PD 10-NOV-1994.
 PE 26-APR-1994; U04641.
 PR 26-APR-1993; US-053451.
 PA (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
 PI Calenoff E, Chen FW, Dittlow CC;
 DR WPI; 94-357904/44.
 DR N-PSDB; Q78730.
 PT New antigen comprising hydroxy:steroid and quat. ammonium salt -
 PT and related antibodies, useful e.g. for imaging, ablating or
 PT treating atherosclerotic plaque, and detecting plaque specific
 PT antibodies
 PS Claim 194; Page 145; 288pp; English.
 CC Mice were immunised with an extract of human atherosclerotic plaque,
 CC then spleen cells were fused with SP2/01-Ag-14 myeloma cells.
 CC Hybridomas were screened by ELISA for reactivity with the immunogen
 CC and clone 22D3 was isolated. The 22D3 antibody reacts specifically
 CC with atherosclerotic tissue; it recognises a non-protein antigen
 CC containing cholesterol (or similar steroid that is a substrate for
 CC cholesterol oxidase) and a quaternary ammonium salt (pref. a
 CC phosphatidylcholine or related compound that is a substrate for
 CC phospholipase C).
 SQ Sequence 126 AA;

Query Match 70.2%; Score 73; DB 12; Length 126;
 Best Local Similarity 85.7%; Pred. No. 3.13e+00;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 101 ywyfdiv 107
 :|||||
 Qy 5 FYWYFDV 11

RESULT 9
 ID R04937 standard; protein; 106 AA.
 AC R04937;
 DT 10-MAR-1993 (revised)
 DT 28-SEP-1990 (first entry)
 DE Sequence of human carcinoembryonic heavy chain antigen (CEA).
 KW Carcinoembryonic antigen; CEA; Chelate-specific antigen; CHA;
 KW tumor; cancer; serum sickness.
 OS Homo sapiens.
 PN EP-369566-A.
 PD 23-MAY-1990.
 PF 8-MAR-1989; 302313.

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9

PR 17-NOV-1988; US-274105.
 PA (HYBR-) Hybritech Inc.
 PI Johnson NJ, Phelps JL;
 DR WPI; 90-157695/21.
 DR N-PSDB; Q04593.
 PT Bifunctional chimeric antibodies -
 PT having variable regions which recognise different antigens and
 PT metal chelates and human constant regions.
 PS Claim 1; Page 24; 40pp; English.
 CC CEA heavy chain antigen, useful in generating chimeric monoclonal
 CC antibody binding to CEA at a tumour site and a metal chelate bonded
 CC to say a toxin or other drug.
 SQ Sequence 106 AA;

Query Match 63.5%; Score 66; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1.33e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 ywyfdv 94
 |||||
 QY 6 YWYFDV 11

RESULT 10

ID R88846 standard; Protein; 121 AA.
 AC R88846;
 DT 10-OCT-1996 (first entry)
 DE Murine antibody ZCE-025 heavy chain variable region.
 KW Heavy chain; variable region; murine; tumour antigen; antibody;
 KW ZCE-025; construction; CDR switched variable light chain region;
 KW kappa-body fragment; in vitro; in vivo; diagnosis; therapy;
 KW naked antibody; radioimmunotherapy; radioimmunodiagnosis;
 KW radioimmunometric assays; ELISA; immunohistochemical;
 KW complementarity determining region.
 OS Mus musculus.
 PN W09606625-A1.
 PD 07-MAR-1996.
 PF 25-AUG-1995; U10791.
 PR 26-AUG-1994; US-296625.
 PA (ELIL) LILLY & CO ELI.
 PI ILL CR, Ludwig JR, Rathnachalam R;
 DR WPI; 96-160137/16.
 DR N-PSDB; T12813.
 PT Recombinant antibody comprising CDR-switched light chain variable
 PT region - having VL domain framework and VH domain CDRs, useful in
 PT radioimmunotherapy, ELISA assays, etc.
 PS Example 1; Page 61; 162pp; English.
 CC The present sequence is the heavy chain variable (HL) region
 CC of the murine anti-ZCE-025 tumour antigen antibody (Ab). ZCE-025,
 CC which was used in the construction of a CDR switched light chain
 CC variable (VL) region (GSVL) Ab, or kappa-body fragment. A CSVL
 CC comprises at least 1 VL region with 3 CDR, where 1 or more of the
 CC CDR is derived from the corresponding CDR of a VH region of 1
 CC (donor) Ab, and 4 framework (FW) regions where 1 or more of the
 CC regions is derived from the corresponding FW region(s) from the VL
 CC region of the same or different (acceptor) Ab.
 CC The CSVL Ab, or kappa-body fragment can be used in vitro and
 CC in vivo diagnostic and therapeutic applications, including naked Ab
 CC therapy, radioimmunotherapy (i.e. when fused to a chelating peptide
 CC incorporating Yttrium-90 as the therapeutic radioion), in vivo
 CC radioimmunodiagnosis, in vitro radioimmunometric assays, ELISA
 CC and immunohistochemical applications.
 SQ Sequence 121 AA;

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US-08-612-929-26 tag

10

Query Match 63.5%; Score 66; DB 18; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.33e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 105 ywyfdv 110
 |||||
 QY 6 YWYFDV 11

RESULT 11

ID R79878 standard; Protein; 122 AA.
 AC R79878;
 DT 24-MAY-1996 (first entry)
 DE Anti-EGFR antibody heavy chain variable region (Clone L2 8C).
 KW Single chain antibody; antibody; epidermal growth factor receptor;
 KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
 KW assessment; phage antibody library.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT Region 1..30
 FT /label= Framework region 1.
 FT Region 31..35
 FT /label= CDR1.
 FT Region 36..49
 FT /label= Framework region 2.
 FT Region 50..65
 FT /label= CDR2.
 FT Region 66..97
 FT /label= Framework region 3.
 FT Region 98..111
 FT /label= CDR3.
 FT Region 112..122
 FT /label= Framework region 4.
 PN W09525167-A1.
 PD 21-SEP-1995.
 PF 16-MAR-1995; E00978.
 PR 17-MAR-1994; EP-104160.
 PR 02-DEC-1994; EP-118970.
 PA (MERE) MERCK PATENT GMBH.
 PI Adan J, Ansell KH, Bendig MM, Blasco F, Guesow D;
 PI Kettleborough AC, Mitjans F, Piulats J, Rosell E;
 DR WPI; 95-336972/43.
 PT Anti-EGFR antibodies and single chain Fv antibody fragments -
 PT obtained from phage-antibody libraries, useful for diagnosis and
 PT therapy of tumours
 PS Disclosure; Figure 1A; 93pp; English.
 CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies
 CC and antibodies constructed from anti-EGFR antibody fragments can be
 CC used for diagnosis of tumours and assessment of tumour growth in
 CC vitro and in vivo. They may also be used in a pharmaceutical
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
 CC The antibodies and fragments are derived from mice but are humanised
 CC so as to cause minimum reaction against them. They are produced
 CC using the phage antibody library. (See T04011-T04026 and
 CC R79858-R79873)
 SQ Sequence 122 AA;

Query Match 63.5%; Score 66; DB 16; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.33e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 106 ywyfdv 111
 |||||
 QY 6 YWYFDV 11

RESULT 12

ID P91382 standard; protein; 122 AA.
AC P91382;
DT 10-MAR-1993 (revised)
DE Antibody heavy chain variable region against carcinoembryonic antigen.
KW Carcinoembryonic antigen; immunogen; tumour; chimeric antibody.
OS Murine (mouse) hybridoma CEM 231.6.7 (ATCC HB 9620).
PN EP-332424-A.
PD 13-SEP-1989.
PF 08-MAR-1989; 302312.
PR 09-MAR-1988; US-272577.
PA (HYBR) Hybritech Inc.
PI Beidler CB, Johnson MJ, Ludwig JR, Carlo DJ, David GS;
DR WPI; 89-265635/37.
DR N-PSDB; P91382.
PT DNA constructs encoding light or heavy chain variable regions
PT - chimeric monoclonal antibody, specific for human
PT carcinoembryonic antigen, useful for diagnosis, imaging and
PT treatment of tumours.
PS Claim 6; page 18; 32pp; English.
CC This region is encoded in a DNA construct with light chain variable
CC and constant regions, heavy chain constant region, and 2 eukaryotic
CC leader sequences. The chimeric monoclonal antibodies thus formed
CC can be directed against CEA for immunoassay, and imaging and
CC treatment of tumours, eg colorectal or breast carcinoma. The
CC constant regions are human-derived and so are less immunogenic
CC than entirely murine Abs.
SQ Sequence 122 AA;

Query Match

Best Local Similarity 63.5%; Score 66; DB 1; Length 122;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 105 ywyfdv 110

|||||

Qy 6 YWYFDV 11

RESULT 13

ID W02201 standard; Protein; 122 AA.
AC W02201;
DT 10-OCT-1996 (first entry)
DE CDR switched variable light chain region kappa-body fragment.
KW Variable region; murine; human; tumour antigen; plasmacytoma;
KW antibody; ZCE-025; IM9; construction; in vitro; in vivo;
KW CDR switched variable light chain region; kappa-body fragment;
KW diagnosis; therapy; naked antibody; radioimmunotherapy;
KW radioimmunodiagnosics; radioimmunometric assays; ELISA;
KW immunohistochemical; complementarity determining region.
OS Synthetic.
PN W09606625-A1.
PD 07-MAR-1996.
PF 25-AUG-1995; U10791.
PR 26-AUG-1994; US-296625.
PA (ELIL) LILLY & CO ELI.
PI Ili CR, Ludwig JR, Rathnachalam R;
DR WPI; 96-160137/16.
PT Recombinant antibody comprising CDR-switched light chain variable
PT region - having VL domain framework and VH domain CDRs, useful in
PT radioimmunotherapy, ELISA assays, etc.
PS Example 7; Page 92; 162pp; English.

CC The present sequence is a CDR switched light chain variable (VL)
CC region (CSVL) kappa fragment, constructed using the heavy chain
CC variable (VH) region of the murine anti-ZCE-025 tumour antigen
CC antibody (Ab), ZCE-025, and the VL region of the human plasmacytoma
CC cell line IM9 Ab, IM9. A CSVL comprises at least 1 VL region
CC with 3 CDR, where 1 or more of the CDR is derived from the
CC corresponding CDR of a heavy chain variable (VH) region of 1
CC (donor) Ab, and 4 framework (FW) regions where 1 or more of the
CC regions is derived from the corresponding FW region(s) from the VL
CC region of the same or different (acceptor) Ab.
CC The CSVL Ab, or kappa-body fragment can be used in vitro and
CC in vivo diagnostic and therapeutic applications, including naked Ab
CC therapy, radioimmunotherapy (i.e. when fused to a chelating peptide
CC incorporating Yttrium-90 as the therapeutic radionuclide), in vivo
CC radioimmunodiagnosics, in vitro radioimmunometric assays, ELISA
CC and immunohistochemical applications.
SQ Sequence 122 AA;

Query Match 63.5%; Score 66; DB 18; Length 122;

Best Local Similarity 100.0%; Pred. No. 1.33e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 106 ywyfdv 111

|||||

Qy 6 YWYFDV 11

RESULT 14

ID R79877 standard; Protein; 123 AA.

AC R79877;

DT 24-MAY-1996 (first entry)

DE Anti-EGFR antibody heavy chain variable region (Clone L2 1C).

KW Single chain antibody; antibody; epidermal growth factor receptor;

KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;

KW assessment; phage antibody library.

OS Mus musculus.

FH Key Location/Qualifiers

FT Region 1..30

FT /label= Framework region 1.

FT Region 31..35

FT /label= CDR1.

FT Region 36..49

FT /label= Framework region 2.

FT Region 50..66

FT /label= CDR2.

FT Region 67..98

FT /label= Framework region 3.

FT Region 99..112

FT /label= CDR3.

FT Region 113..123

FT /label= Framework region 4.

PN W09525167-A1.

PD 21-SEP-1995.

PF 16-MAR-1995; E00978.

PR 17-MAR-1994; EP-104160.

PR 02-DEC-1994; EP-118970.

PA (MERE) MERCK PATENT GMBH.

PI Adan J, Ansell KH, Bendig MM, Blasco F, Gussow D;

PI Kettleborough AC, Mitjans F, Piulats J, Rosell E;

DR WPI; 95-336972/43.

PT Anti-EGFR antibodies and single chain Fv antibody fragments -

PT obtained from phage-antibody libraries, useful for diagnosis and

PT therapy of tumours

PS Disclosure; Figure 1A; 93pp; English.

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13

CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies
CC and antibodies constructed from anti-EGFR antibody fragments can be
CC used for diagnosis of tumours and assessment of tumour growth in
CC vitro and in vivo. They may also be used in a pharmaceutical
CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
CC The antibodies and fragments are derived from mice but are humanised
CC so as to cause minimum reaction against them. They are produced
CC using the phage antibody library. (See T04011-T04026 and
CC R79858-R79873)
SQ Sequence 123 AA;

Query Match 63.5%; Score 66; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.33e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywyfdv 112
|||||
Qy 6 YWYFDV 11

RESULT 15

ID P94780 standard; protein; 140 AA.
AC P94780;
DT 06-JUL-1990 (first entry)
DE 2 H7 VH gene.
KW Antibodies; passive immunisation; pH3-12a; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label=Leader peptide.
FT Domain 20..49
FT /label=FR1.
FT Domain 50..54
FT /label=CDR1
FT Domain 55..68
FT /label=FR2
FT Domain 69..85
FT /label=CDR2.
FT Domain 86..117
FT /label=FR3.
FT Domain 118..130
FT /label=CDR3.
FT Domain 131..140
FT /label=FR4.
FT Domain 108..123
FT /label=JK2
PN W08900999-A.
PD 9-FEB-1989.
PE 25-JUL-1988; 02514.
PR 24-JUL-1987; US-077528.
PA (ITGE-) Int Genetic Eng Inc.
PI Robinson RR, Liu AY, Horwitz AH, Wall R, Better M;
DR WPI; 89-061144/08.
DR N-PSDB; N91146.
PT Polynucleotide(s) encoding immunoglobulin molecules -
PT used for efficient prodn. of chimeric human or non-human or
PS class switched antibodies.
PS Disclousure; 7pp; English.
CC Sequence carries the variable region of the chimeric immunoglobulin
CC sequence. The antibodies are useful in passive immunisation avoiding
CC negative immune reactions. They are also useful in assaying and in vitro
CC imaging.
SQ Sequence 140 AA;

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14

Query Match 63.5%; Score 66; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.33e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 125 ywyfdv 130
|||||
Qy 6 YWYFDV 11

Search completed: Tue Mar 18 10:17:10 1997
Job time : 12 secs.

W A S E A (TM)

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MPerch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:17:27 1997; MasPar time 1.76 Seconds
Tabular output not generated. 94.634 Million cell updates/sec

Title: >US-08-612-929-28
Description: (1-9) from US08612929.pep
Perfect Score: 60
Sequence: 1 QQSNEPPR 9

Scoring table: PAM 150
Gap 15

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot33
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10

Statistics: Mean 20.411; Variance 22.437; scale 0.910

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	47	78.3	277	5 J11_HCMVA	HYPOTHETICAL PROTEIN	5.76e-01
2	44	73.3	514	5 MP11_MOUSE	M-PHASE INDUCER PHOSP	2.89e+00
3	44	73.3	525	6 NCAP_MEASI	NUCLEOCAPSID PROTEIN.	2.89e+00
4	44	73.3	823	2 CRYW_BACTA	130 KD CRYSTAL PROTEI	2.89e+00
5	44	73.3	1189	2 CRYT_BACTE	134 KD CRYSTAL PROTEI	2.89e+00
6	43	71.7	111	5 KV3M_MOUSE	IG KAPPA CHAIN V-III	4.87e+00
7	43	71.7	111	5 KV3Q_MOUSE	IG KAPPA CHAIN V-III	4.87e+00
8	43	71.7	111	5 KV3H_MOUSE	IG KAPPA CHAIN V-III	4.87e+00
9	43	71.7	111	5 KV3L_MOUSE	IG KAPPA CHAIN V-III	4.87e+00
10	43	71.7	111	5 KV3N_MOUSE	IG KAPPA CHAIN V-III	4.87e+00
11	43	71.7	111	5 KV3O_MOUSE	IG KAPPA CHAIN V-III	4.87e+00
12	43	71.7	132	5 KV3F_MOUSE	IG KAPPA CHAIN PRECUR	4.87e+00
13	42	70.0	194	10 YPE4_NPVLD	HYPOTHETICAL 20.6 KD	8.14e+00

	14	42	70.0	847	10	YAF6_YEAST	HYPOTHETICAL 95.1 KD	8.14e+00
15	41	68.3	268	5	MIND_BACSU	SEPTUM SITE-DETERMINI	1.35e+01	
16	41	68.3	295	6	MYRA_MIGR	MYCINAMICIN-RESISTANC	1.35e+01	
17	40	66.7	111	5	KV3K_MOUSE	IG KAPPA CHAIN V-III	2.21e+01	
18	40	66.7	111	5	KV3J_MOUSE	IG KAPPA CHAIN V-III	2.21e+01	
19	40	66.7	131	5	KV3I_MOUSE	IG KAPPA CHAIN PRECUR	2.21e+01	
20	40	66.7	497	5	LMP2_EBV	GENE TERMINAL PROTEIN	2.21e+01	
21	40	66.7	914	1	AZF1_YEAST	ASPARAGINE-RICH ZINC	2.21e+01	
22	40	66.7	1431	9	TOP2_SCHPO	DNA TOPOISOMERASE II	2.21e+01	
23	39	65.0	109	10	YCKK_HAEIN	HYPOTHETICAL PROTEIN	3.59e+01	
24	39	65.0	207	6	NEF_HVIND	NEGATIVE FACTOR (F-PR	3.59e+01	
25	39	65.0	347	5	MAGP_HUMAN	MELANOMA-ASSOCIATED A	3.59e+01	
26	39	65.0	367	5	IPOU_DROME	INHIBITORY POU PROTEI	3.59e+01	
27	39	65.0	375	3	DEK_HUMAN	DEK PROTEIN.	3.59e+01	
28	39	65.0	414	7	PRS3_CAEEL	PROBABLE 26S PROTEASE	3.59e+01	
29	39	65.0	416	3	FILA_HUMAN	FILAGGRIN PRECURSOR (3.59e+01	
30	39	65.0	446	10	YCAJ_HAEIN	HYPOTHETICAL PROTEIN	3.59e+01	
31	39	65.0	472	5	INI4_HUMAN	INTERFERON-INDUCED 54	3.59e+01	
32	39	65.0	509	10	YB19_YEAST	HYPOTHETICAL 57.1 KD	3.59e+01	
33	39	65.0	581	7	PRIM_ECOLI	DNA PRIMASE (EC 2.7.7	3.59e+01	
34	39	65.0	584	4	GUND_GLOCE	ENDOGALACTINASE D PRECU	3.59e+01	
35	39	65.0	590	9	VG28_HSV11	HYPOTHETICAL GENE 28	3.59e+01	
36	39	65.0	648	1	BGLR_RAT	BETA-GLUCURONIDASE PR	3.59e+01	
37	39	65.0	648	1	BGLR_MOUSE	BETA-GLUCURONIDASE PR	3.59e+01	
38	39	65.0	730	3	ERG7_YEAST	LANOSTEROL SYNTHASE (3.59e+01	
39	39	65.0	1260	6	NEU_RAT	NEU ONCOGENE PRECURSO	3.59e+01	
40	38	63.3	78	6	MULI_NORMO	MAJOR OUTER MEMBRANE	5.78e+01	
41	38	63.3	160	5	MAX_HUMAN	MAX PROTEIN.	5.78e+01	
42	38	63.3	200	10	YM62_CAEEL	HYPOTHETICAL 23.2 KD	5.78e+01	
43	38	63.3	273	4	GVPL_HALSA	GVPL PROTEIN.	5.78e+01	
44	38	63.3	983	5	KHEK_HUMAN	TYROSINE-PROTEIN KINA	5.78e+01	
45	38	63.3	983	5	KEK4_MOUSE	TYROSINE-PROTEIN KINA	5.78e+01	

ALIGNMENTS

RESULT	1	J11_HCMVA	STANDARD;	PRT;	277 AA.
ID	J11_HCMVA	AC	P09711;		
DT	01-MAR-1989 (REL. 10, CREATED)				
DT	01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)				
DT	01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)				
DE	HYPOTHETICAL PROTEIN HKRF (J11).				
OS	HUMAN CYTOMEALOVIRUS (STRAIN AD169).				
OC	VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 87169717.				
RA	WESTON K., BARRELL B.G.;				
RL	J. MOL. BIOL. 192:177-208 (1986).				
RN	[2]				
RP	COMPLETE GENOME.				
RX	MEDLINE; 90269039.				
RA	CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R.,				
RA	HORSNELL T., HUTCHISON C.A. III, KOUZARIDES T., MARTIGNETTI J.A.,				
RA	PREDDIE E., SATCHWELL S.C., TOMLINSON P., WESTON K.M., BARRELL B.G.;				
RL	CURR. TOP. MICROBIOL. IMMUNOL. 154:125-169 (1990).				
DR	EMBL; X17403; -; NOT ANNOTATED_CDS.				
DR	EMBL; X04650; E3275; ALT_SEQ.				
DR	PIR; B26078; Q0BEC2.				
KW	HYPOTHETICAL PROTEIN.				
FT	CARBOHYD 50 50				POTENTIAL.
FT	CARBOHYD 233 233				POTENTIAL.
SQ	SEQUENCE 277 AA; 29115 MW; 1B1F5DCB CRC32;				

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3

Query Match 78.3%; Score 47; DB 5; Length 277;
Best Local Similarity 77.8%; Pred. No. 5.76e-01;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 97 qhsledppr 105
:|:|:|:|:|
Qy 1 QQSNEPPR 9

RESULT 2

ID MP11_MOUSE STANDARD; PRT; 514 AA.
AC P48964;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48).
GN CDC25A OR CDC25M3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE; 95361758.
RA WICKRAMASINGHE D., BECKER S., ERNST M.K., RESNICK J.L.,
RA CANTIANI J.M., TESSAROLLO L., GRABEL L.B., DONOVAN P.J.;
RL DEVELOPMENT 121:2047-2056(1995).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER IN
CC MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR
CC PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE
CC P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
CC PROTEIN TYROSINE + ORTHOPHOSPHATE.
CC -!- SIMILARITY: STRONG, TO OTHER SPECIES M-PHASE INDUCER PHOSPHATASE
CC AND IN GENERAL TO PROTEIN-TYROSINE PHOSPHATASES.
DR EMBL; U73233; G862992; -.
KW CELL DIVISION; MITOSIS; HYDROLASE; MULTIGENE FAMILY.
FT ACT SITE 421 421 BY SIMILARITY.
SQ SEQUENCE 514 AA; 57758 MW; EDECB85C CRC32;

Query Match 73.3%; Score 44; DB 5; Length 514;
Best Local Similarity 55.6%; Pred. No. 2.89e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 269 drsheeppr 277
:|:|:|:|:|
Qy 1 QQSNEPPR 9

RESULT 3

ID NCAP_MEASI STANDARD; PRT; 525 AA.
AC P26029;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE NUCLEOCAPSID PROTEIN.
GN NP OR N.
OS MEASLES VIRUS (STRAIN IP-3-CA) (SUBACUTE SCLEROSE PANENCEPHALITIS
OS VIRUS).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; PARAMYXOVIRIDAE;
OC MORBILLIVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92263801.

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RA SCHMID A., SPIELHOFER P., CATTANEO R., BACZKO K., TER MEULEN V.,
RA BILLETTER M.A.;
RL VIROLOGY 188:910-915(1992).
CC -!- FUNCTION: MOST ABUNDANT PROTEIN IN THE VIRION AND AN IMPORTANT
CC ELEMENT CONFERRING HELICAL SYMMETRY ON THE NUCLEOPROTEIN CORE AS
CC WELL AS INTERACTING WITH M PROTEIN DURING VIRION FORMATION.
CC -!- SIMILARITY: TO OTHER PARAMYXOVIRUSES NUCLEOCAPSID PROTEINS.
DR EMBL; X16566; G60539; -.
KW NUCLEOCAPSID.
SQ SEQUENCE 525 AA; 58206 MW; 80A2FA0D CRC32;

Query Match 73.3%; Score 44; DB 6; Length 525;
Best Local Similarity 55.6%; Pred. No. 2.89e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 423 dgseneppr 431
:|:|:|:|:|
Qy 1 QQSNEPPR 9

RESULT 4

ID CRYW_BACTA STANDARD; PRT; 823 AA.
AC P10327;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
DE 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL
DE PROTOXIN) (FRAGMENT).
OS BACILLUS THURINGIENSIS (SUBSP. AIZAWAI).
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=7-29;
RX MEDLINE; 89343627.
RA SANCHIS V., LERECHUS D., MENOUE M., CHAUFAX J., GUO S., LECADET M.M.;
RL MOL. MICROBIOL. 3:229-238(1989).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS.
CC -!- TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
DR EMBL; X13620; G40356; -.
DR PIR; S04181; S04181.
DR HSSP; P07130; IDLC.
KW TOXIN; SPORE FORMATION.
FT NON TER 823 823
SQ SEQUENCE 823 AA; 92854 MW; B17D932D CRC32;

Query Match 73.3%; Score 44; DB 2; Length 823;
Best Local Similarity 44.4%; Pred. No. 2.89e+00;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 344 reangeppr 352
:|:|:|:|:|
Qy 1 QQSNEPPR 9

RESULT 5

ID CRYT_BACTE STANDARD; PRT; 1189 AA.
AC P05518;
DT 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT 01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)

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DE 134 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL
DE PROTOXIN).
OS BACILLUS THURINGIENSIS (SUBSP. ENTOMOCIDUS).
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=60.5;
RX MEDLINE; 88289380.
RA HONEE G., VAN DER SALT T.P.M., VISSER B.;
RL NUCLEIC ACIDS RES. 16:6240-6240(1988).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF SPIDOPTERA SPECIES.
CC -!- TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
DR EMBL; X07518; G40294; -.
DR PIR; S00944; S00944.
DR HSP; P07130; IDIC.
KW TOXIN; SPORULATION.
SQ SEQUENCE 1189 AA; 134836 MW; 30C5D51C CRC32;

Query Match 73.3%; Score 44; DB 2; Length 1189;
Best Local Similarity 44.4%; Pred. No. 2.89e+00;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 344 reanqppr 352
QY :::::||||
1 QQSNEPDR 9

RESULT 6
ID KV3M MOUSE STANDARD; PRT; 111 AA.

AC P01655;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7043).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; A01937; KWS43.
DR HSP; P01679; ICGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; ADC728CA CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.87e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 93 qgsnedp 99
|||||||
QY 1 QQSNEPDR 7

RESULT 7
ID KV3Q MOUSE STANDARD; PRT; 111 AA.
AC P01659;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7769).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; E01937; KWS69.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 9CB705B9 CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.87e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsnedp 99
|||||||
QY 1 QQSNEPDR 7

RESULT 8
ID KV3H MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 3741 AND TEPC 111).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RA PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
CC -!- THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.

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DR PIR; A01934; KVM537.
DR HSP; P01679; ICGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; 7650289 CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.87e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsndp 99
|||||||
Qy 1 QQSNDP 7

RESULT 9
ID KV3L MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (CBPC 101).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
CC -I- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVM5C1.
DR HSP; P01679; ICGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; A2AC84CT CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.87e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsndp 99
|||||||
Qy 1 QQSNDP 7

RESULT 10
ID KV3N_MOUSE STANDARD; PRT; 111 AA.

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AC P01666;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7183).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; B01937; KVM583.
DR HSP; P01679; ICGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 041902B8 CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.87e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsndp 99
|||||||
Qy 1 QQSNDP 7

RESULT 11
ID KV3O MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 6308).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; C01937; KVM508.
DR HSP; P01679; ICGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; F7865271 CRC32;

Query Match 71.7%; Score 43; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 4.87e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsnedp 99
 |||||||
 Qy 1 QQSNEDP 7

RESULT 12
 ID KV3F MOUSE STANDARD; PRT; 132 AA.
 AC P01658;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 321).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE OF 1-37.
 RX MEDLINE; 78235887.
 RA BURSTEIN Y., SCHECHTER I.;
 RL BIOCHEMISTRY 17:2392-2400(1978).
 RN [2]
 RP SEQUENCE OF 21-132.
 RX MEDLINE; 73140224.
 RA MCKEAN D.J., POTTER M., HOOD L.E.;
 RL BIOCHEMISTRY 12:749-759(1973).
 CC -/- THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN
 CC WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE
 CC MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.
 DR PIR; A01933; KVM632.
 DR HSP; P01679; IGB.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 132 IG KAPPA CHAIN V-III REGION (MOPC 321).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 59 73 FRAMEWORK 2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 81 112 FRAMEWORK 3.
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 122 131 FRAMEWORK 4.
 FT DISULFID 43 112 BY SIMILARITY.
 FT NON TER 132 132
 SQ SEQUENCE 132 AA; E57F824 CRC32;

Query Match 71.7%; Score 43; DB 5; Length 132;
 Best Local Similarity 28.6%; Pred. No. 4.87e+00;
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 113 zzebzbp 119
 ::::::|
 Qy 1 QQSNEDP 7

RESULT 13
 ID YPE4_NPVID STANDARD; PRT; 194 AA.
 AC P36866;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)

DE HYPOTHETICAL 20.6 KD PROTEIN IN PE 3' REGION (ORF 4).
 OS LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYHEDROSIS VIRUS (LDMNPV).
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE; EUBACULOVIRINAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92300345.
 RA BJORNSSON R.M., ROHRMANN G.F.;
 RL J. GEN. VIROL. 73:1499-1504(1992).
 DR EMBL; D10836; E55473; -.
 DR PIR; JQ1560; JQ1560.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 194 AA; 20578 MW; F21E7B9A CRC32;

Query Match 70.0%; Score 42; DB 10; Length 194;
 Best Local Similarity 50.0%; Pred. No. 8.14e+00;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 172 qgrdeppr 179
 |: ::|||
 Qy 2 QSNEDPPR 9

RESULT 14
 ID YAF6 YEAST STANDARD; PRT; 847 AA.
 AC P39717; P39716;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 95.1 KD PROTEIN IN CNEL-ACSI INTERGENIC REGION.
 GN YAL056W.
 OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RX MEDLINE; 95249563.
 RA BUSSEY H., KABACK D.B., ZHONG W., VO D.T., CLARK M.W., FORTIN N.,
 RA HALL J., OUELLETTE B.F.F., KENG T., BARTON A.B., SU Y., DAVIES C.K.,
 RA STORMS R.K.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 92:3809-3813(1995).
 DR EMBL; U12980; G623256; -.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 847 AA; 95108 MW; 666443E9 CRC32;

Query Match 70.0%; Score 42; DB 10; Length 847;
 Best Local Similarity 37.5%; Pred. No. 8.14e+00;
 Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 772 enddeppr 779
 ::::::|
 Qy 2 QSNEDPPR 9

RESULT 15
 ID MIND_BACSU STANDARD; PRT; 268 AA.
 AC Q01464;
 DT 01-JUL-1993 (REL. 26, CREATED)
 DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE SEPTUM SITE-DETERMINING PROTEIN MIND.
 GN MIND OR DIVIVB.
 OS BACILLUS SUBTILIS.
 OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE; 93015732.
 RA VARLEY A.W., STEWART G.C.;
 RL J. BACTERIOL. 174:6729-6742(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE; 93211302.
 RA LEE S., PRICE C.W.;
 RL MOL. MICROBIOL. 7:601-610(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93015731.
 RA LEVIN P.A., MARGOLIS P.S., SETLOW P., LOSICK R., SUN D.;
 RL J. BACTERIOL. 174:6717-6728(1992).
 CC -!- FUNCTION: MEMBRANE ATPASE REQUIRED FOR THE CORRECT PLACEMENT
 CC OF THE DIVISION SITE. CELL DIVISION INHIBITORS MINC AND MIND ACT
 CC IN CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF
 CC THE CELL DIVISION SEPTUM AT ALL POTENTIAL SITES. FTSZ SEEMS TO BE
 CC THE TARGET OF MINCD. MIND PLAYS AN ACCESSORY ROLE, ENHANCING THE
 CC INHIBITORY EFFECT OF MINC AND ALLOWING INTERACTION WITH MINE.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
 DR EMBL; M95582; G143216; -.
 DR EMBL; Z15113; G580893; -.
 DR EMBL; M96343; G142859; -.
 DR PIR; S31205; S31205.
 DR PIR; G45239; G45239.
 DR PIR; F45240; F45240.
 DR SUBTILIST; BG10330; MIND.
 KW CELL DIVISION; SEPTATION; ATP-BINDING; MEMBRANE.
 FT NP BIND 10 17 ATP (POTENTIAL).
 SQ SEQUENCE 268 AA; 29407 MW; 122E55F1 CRC32;

Query Match 68.3%; Score 41; DB 5; Length 268;
 Best Local Similarity 55.6%; Pred.No. 1.35e+01;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 162 qeenleppr 170
 I: I :|||
 Qy 1 QQSNEPPR 9

Search completed: Tue Mar 18 10:17:36 1997
 Job time : 9 secs.

WATERMAN

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPerch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:17:54 1997; MasPar time 3.14 Seconds

Tabular output not generated. 73.712 Million cell updates/sec

Title: >US-08-612-929-28

Description: (1-9) from US08612929, pep

Perfect Score: 60

Sequence: 1 QQSNEPPR 9

Scoring table: PAM 150

Gap 15

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: pir48

1:unl1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
14:unrev

Statistics: Mean 19.758; Variance 27.311; scale 0.723

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	49	81.7	209	6	JQ2347	hypothetical 23.6K p	1.53e+00
2	47	78.3	112	5	S19971	Ig kappa chain V reg	3.83e+00
3	47	78.3	131	5	PH1226	Ig kappa chain precu	3.83e+00
4	47	78.3	277	3	QQBEC2	HKGRFX protein - huma	3.83e+00
5	44	73.3	643	12	A43423	dyein 74K chain, cy	1.45e+01
6	44	73.3	823	6	S04181	parasporal crystal p	1.45e+01
7	44	73.3	1176	6	A48970	insecticidal crystal	1.45e+01
8	44	73.3	1189	6	S00944	parasporal crystal p	1.45e+01
9	43	71.7	65	12	C38601	Ig kappa chain V reg	2.24e+01
10	43	71.7	81	12	S42193	Ig kappa chain V reg	2.24e+01
11	43	71.7	85	12	S42189	Ig kappa chain V reg	2.24e+01
12	43	71.7	87	12	S42190	Ig kappa chain V reg	2.24e+01

13	43	71.7	88	12	S42194	Ig kappa chain V reg	2.24e+01
14	43	71.7	90	12	S42187	Ig kappa chain V reg	2.24e+01
15	43	71.7	96	12	B49442	Ig light chain V reg	2.24e+01
16	43	71.7	107	5	S26344	Ig kappa chain V reg	2.24e+01
17	43	71.7	107	5	S26344	Ig kappa chain V reg	2.24e+01
18	43	71.7	111	2	KVMS31	Ig kappa chain V reg	2.24e+01
19	43	71.7	111	5	S09966	Ig kappa chain V-J r	2.24e+01
20	43	71.7	111	2	KVMS08	Ig kappa chain V reg	2.24e+01
21	43	71.7	111	2	KVMS83	Ig kappa chain V reg	2.24e+01
22	43	71.7	111	5	A33936	Ig kappa chain V reg	2.24e+01
23	43	71.7	111	2	KVMS43	Ig kappa chain V reg	2.24e+01
24	43	71.7	111	2	KVMS37	Ig kappa chain V reg	2.24e+01
25	43	71.7	111	2	KVMS69	Ig kappa chain V reg	2.24e+01
26	43	71.7	132	2	KVMS32	Ig kappa chain precu	2.24e+01
27	42	70.0	67	5	PH1081	Ig light chain V reg	3.43e+01
28	42	70.0	194	6	JQ1560	hypothetical 20.6K p	3.43e+01
29	42	70.0	303	12	A40807	membrane glycoprotein	3.43e+01
30	42	70.0	847	9	S51965	hypothetical protein	3.43e+01
31	41	68.3	268	8	G45239	septum placement det	5.21e+01
32	41	68.3	306	12	S59863	polyA binding protei	5.21e+01
33	40	66.7	65	12	B38601	Ig kappa chain V reg	7.87e+01
34	40	66.7	93	12	A38601	Ig kappa chain V reg	7.87e+01
35	40	66.7	102	5	PH1078	Ig light chain V reg	7.87e+01
36	40	66.7	111	12	D45722	anti-glycoprotein H	7.87e+01
37	40	66.7	131	2	KVMSW6	Ig kappa chain precu	7.87e+01
38	40	66.7	497	3	WMBELM	membrane protein IMP	7.87e+01
39	40	66.7	715	12	A53209	adseverin - bovine	7.87e+01
40	40	66.7	914	14	S61671	hypothetical protein	7.87e+01
41	40	66.7	914	9	S46593	asparagine-rich zinc	7.87e+01
42	40	66.7	1431	1	ISZPT2	DNA topoisomerase (A	7.87e+01
43	39	65.0	509	10	S45413	probable membrane pr	1.18e+02
44	39	65.0	648	4	A32576	beta-glucuronidase (1.18e+02
45	39	65.0	731	10	A57741	lanosterol synthase	1.18e+02

ALIGNMENTS

RESULT 1
ENTRY JQ2347 #type complete
TITLE hypothetical 23.6K protein - turkey herpesvirus
ALTERNATE_NAMES ORF2 protein
ORGANISM #formal name turkey herpesvirus
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Aug-1994
ACCESSION JQ2347
REFERENCE JQ2346
#authors Zelnik, V.; Dartell, R.; Audonnet, J.C.; Smith, G.D.; Riviere, M.; Pastorek, J.; Ross, L.J.N.
#journal J. Gen. Virol. (1993) 74:2151-2162
#title The complete sequence and gene organization of the short unique region of herpesvirus of turkeys.
#accession JQ2347
##molecule type DNA
##residues 1-209 ##label ZEL
##cross-references EMBL:X68653
##experimental source strain FC126
SUMMARY #length 209 #molecular-weight 23610 #checksum 68

Query Match 81.7%; Score 49; DB 6; Length 209;
Best Local Similarity 75.0%; Pred. No. 1.53e+00;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 112 qnceppr 119
|:|:|:|

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3

QY 2 QQSNEPP 9

RESULT 2
ENTRY
TITLE Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-1995
ACCESSIONS S19971; S19973
REFERENCE S19963
#authors Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
#submission submitted to the EMBL Data Library, March 1992
#description Structural characterization of CD4 mAb.
#accession S19971
##molecule_type mRNA
##residues 1-112 #label WEI
##cross-references EMBL:X65091
##experimental_source clone M-T310
#accession S19973
##molecule_type mRNA
##residues 1-112 #label WEW
##cross-references EMBL:X65092
##experimental_source M-T404
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 112 #checksum 4782

Query Match 78.3%; Score 47; DB 5; Length 112;
Best Local Similarity 87.5%; Pred. No. 3.83e+00;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 93 qqsedpp 100
!!!:!!!
QY 1 QQSNEPP 8

RESULT 3
ENTRY
TITLE Ig kappa chain precursor V region (M-T310) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 30-Apr-1995
ACCESSIONS PH1226
REFERENCE PH1224
#authors Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz, H.; Weiss, E.H.; Rieber, E.P.; Riethmuller, G.; Weidle, U.H.
#journal Gene (1992) 121:271-278
#title Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the human interleukin-2 receptor.
#accession PH1226
##molecule_type mRNA
##residues 1-131 #label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE 1-20
21-131 #domain signal sequence #status predicted #label SIG
#product Ig light chain V region #status predicted
#label MAT
#length 131 #checksum 4648

Query Match 78.3%; Score 47; DB 5; Length 131;

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Best Local Similarity 87.5%; Pred. No. 3.83e+00;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 113 qqsedpp 120
!!!:!!!
QY 1 QQSNEPP 8

RESULT 4
ENTRY
TITLE QQBE2 #type complete
ORGANISM HKRFX protein - human cytomegalovirus (strain AD169)
DATE 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 08-Apr-1994
ACCESSIONS B26078
REFERENCE A92935
#authors Weston, K.; Barrell, B.G.
#journal J. Mol. Biol. (1986) 192:177-208
#title Sequence of the short unique region, short repeats, and part of the long repeats of human cytomegalovirus.
#cross-references MUID:87169717
#accession B26078
##molecule_type DNA
##residues 1-277 #label WES

COMMENT The DNA sequence was obtained from EMBL, release 13.
GENETICS
#gene HKRFX
CLASSIFICATION #superfamily cytomegalovirus HKRFX protein
SUMMARY #length 277 #molecular-weight 29115 #checksum 4671

Query Match 78.3%; Score 47; DB 3; Length 277;
Best Local Similarity 77.8%; Pred. No. 3.83e+00;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 97 qhsedpp 105
!!!:!!!
QY 1 QQSNEPP 9

RESULT 5
ENTRY
TITLE A43423 #type complete
ORGANISM dynein 74K chain, cytosolic - rat
DATE 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 19-Oct-1995
ACCESSIONS A43423; S26608
REFERENCE A43423
#authors Paschal, B.M.; Mikami, A.; Pfister, K.K.; Vallee, R.B.
#journal J. Cell Biol. (1992) 118:1133-1143
#title Homology of the 74-kD cytoplasmic dynein subunit with a flagellar dynein polypeptide suggests an intracellular targeting function.
#cross-references MUID:92381100
#accession A43423
##status preliminary
##molecule_type mRNA
##residues 1-643 #label PAS
##cross-references NCBI:111952; NCBI:111953
##experimental_source brain
##note sequence extracted from NCBI backbone
REFERENCE S26608
#authors Paschal, B.M.; Mikami, A.; Pfister, K.K.; Vallee, R.B.
#submission submitted to the EMBL Data Library, June 1992
#description Molecular cloning of a cytoplasmic dynein subunit: homology

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with a flagellar dynein polypeptide.

#accession S26608
#status preliminary
#molecule_type mRNA
#residues 1-643 #label PAS2
#cross-references EMBL:X66845
SUMMARY
#length 643 #molecular-weight 72754 #checksum 8108

Query Match 73.3%; Score 44; DB 12; Length 643;
Best Local Similarity 55.6%; Pred. No. 1.45e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 204 qetkeappr 212
:::|||||
QY 1 QQSNEPPR 9

RESULT 6
ENTRY
TITLE
ALTERNATE_NAMES S04181 #type fragment
ENTRY parasporal crystal protein - Bacillus thuringiensis (strain
TITLE aizawai 7.29) (fragment)
ORGANISM delta-endotoxin
#formal_name Bacillus thuringiensis
DATE 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
30-Sep-1993

ACCESSIONS S04181
REFERENCE S04181
#authors Sanchis, V.; Lereclus, D.; Menou, G.; Chaufaux, J.; Guo, S.;
Lecadet, M.M.
#journal Mol. Microbiol. (1989) 3:229-238
#title Nucleotide sequence and analysis of the N-terminal coding
region of the Spodoptera-active delta-endotoxin gene of
Bacillus thuringiensis aizawai 7.29.

#cross-references MUID:89343627

#accession S04181
#molecule_type DNA
#residues 1-823 #label SAN
#cross-references EMBL:X13620

GENETICS bta
#gene #superfamily parasporal crystal protein
SUMMARY #length 823 #checksum 803

Query Match 73.3%; Score 44; DB 6; Length 823;
Best Local Similarity 44.4%; Pred. No. 1.45e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 344 reangeppr 352
:::|||||
QY 1 QQSNEPPR 9

RESULT 7
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title

A48970 #type complete
insecticidal crystal toxin CryIC(b) - Bacillus thuringiensis
#formal_name Bacillus thuringiensis
19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
12-Apr-1995
A48970
A48970
Kalman, S.; Kiehne, K.L.; Libs, J.L.; Yamamoto, T.
Appl. Environ. Microbiol. (1993) 59:1131-1137
Cloning of a novel cryIC-type gene from a strain of Bacillus
thuringiensis subsp. galleriae.

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#cross-references MUID:93236401
#accession A48970
#status preliminary
#molecule_type nucleic acid
#residues 1-1176 #label KAL
#cross-references NCBI:129672; NCBI:129675
#experimental_source subsp. galleriae HD29
#note #sequence extracted from NCBI backbone
CLASSIFICATION #superfamily parasporal crystal protein
SUMMARY #length 1176 #molecular-weight 132867 #checksum 6817

Query Match 73.3%; Score 44; DB 6; Length 1176;
Best Local Similarity 44.4%; Pred. No. 1.45e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 344 reangeppr 352
:::|||||
QY 1 QQSNEPPR 9

RESULT 8
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title

S00944 #type complete
parasporal crystal protein - Bacillus thuringiensis (strain
entomocidus 60.5)
#formal_name Bacillus thuringiensis
31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change
18-Nov-1994
S00944
S00944
Honee, G.; van der Salm, T.; Visser, B.
Nucleic Acids Res. (1988) 16:6240
Nucleotide sequence of crystal protein gene isolated from B.
thuringiensis subspecies entomocidus 60.5 coding for a
toxin highly active against Spodoptera species.

#cross-references MUID:88289380

#accession S00944
#molecule_type DNA
#residues 1-1189 #label HON
#cross-references EMBL:X07518

#note translation of nucleotide sequence not given
CLASSIFICATION #superfamily parasporal crystal protein
SUMMARY #length 1189 #molecular-weight 134836 #checksum 5153

Query Match 73.3%; Score 44; DB 6; Length 1189;
Best Local Similarity 44.4%; Pred. No. 1.45e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 344 reangeppr 352
:::|||||
QY 1 QQSNEPPR 9

RESULT 9
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title

C38601 #type fragment
Ig kappa chain V region (2B5) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change
23-Mar-1993
C38601
A38601
Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. (1991) 266:2134-2142
Common structural features among monoclonal antibodies
binding the same antigenic region of cytochrome c.

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```

#cross-references MUID:91115823
#accession C38601
#status preliminary
#molecule_type mRNA
#residues 1-65 #label GOS
#cross-references CB:457980
SUMMARY #length 65 #checksum 8125

Query Match 71.7%; Score 43; DB 12; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.24e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 46 qgsndp 52
|||||
Qy 1 QQSNDP 7

RESULT 10
ENTRY #type fragment
TITLE Ig kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 07-Oct-1994 #sequence_revision 26-May-1995 #text_change
26-May-1995
ACCESSIONS S42193
REFERENCE S42176
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal Eur. J. Immunol. (1993) 23:2503-2510
#title Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
#accession S42193
#status preliminary
#molecule_type DNA
#residues 1-81 #label MOJ
#cross-references EMBL:Z25456
#note the authors translated the codon GTT for residue 36 as
Ala
SUMMARY #length 81 #checksum 9746

Query Match 71.7%; Score 43; DB 12; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.24e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 75 qgsndp 81
|||||
Qy 1 QQSNDP 7

RESULT 11
ENTRY #type fragment
TITLE Ig kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995
ACCESSIONS S42189
REFERENCE S42176
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal Eur. J. Immunol. (1993) 23:2503-2510
#title Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
#accession S42189
#status preliminary
#molecule_type DNA

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```

#residues 1-85 #label MOJ
#cross-references EMBL:Z25448
SUMMARY #length 85 #checksum 7866

Query Match 71.7%; Score 43; DB 12; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.24e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 79 qgsndp 85
|||||
Qy 1 QQSNDP 7

RESULT 12
ENTRY #type fragment
TITLE Ig kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
13-Jan-1995
ACCESSIONS S42190
REFERENCE S42176
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal Eur. J. Immunol. (1993) 23:2503-2510
#title Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
#accession S42190
#status preliminary
#molecule_type DNA
#residues 1-87 #label MOJ
#cross-references EMBL:Z25450
SUMMARY #length 87 #checksum 2354

Query Match 71.7%; Score 43; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.24e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 81 qgsndp 87
|||||
Qy 1 QQSNDP 7

RESULT 13
ENTRY #type fragment
TITLE Ig kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995
ACCESSIONS S42194
REFERENCE S42176
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal Eur. J. Immunol. (1993) 23:2503-2510
#title Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
#accession S42194
#status preliminary
#molecule_type DNA
#residues 1-88 #label MOJ
#cross-references EMBL:Z25458
SUMMARY #length 88 #checksum 4364

Query Match 71.7%; Score 43; DB 12; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.24e+01;

```


Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 82 qgsnedp 88
|||||||
Qy 1 QQSNEDP 7

RESULT 14

ENTRY S42187 #type fragment
TITLE Ig kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995
ACCESSIONS S42187
REFERENCE S42176
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal Eur. J. Immunol. (1993) 23:2503-2510
#title Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
#accession S42187
##status preliminary
##molecule_type DNA
##residues 1-90 #label MOJ
##cross-references EMBL:Z25444
SUMMARY #length 90 #checksum 9303

Query Match 71.7%; Score 43; DB 12; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.24e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 84 qgsnedp 90
|||||||
Qy 1 QQSNEDP 7

RESULT 15

ENTRY B49442 #type fragment
TITLE Ig light chain V region (50.1) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995
ACCESSIONS B49442
REFERENCE A49442
#authors Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.;
Roguska, M.; Hincapie, L.M.; Simmerman, H.K.B.; Profy,
A.T.; Wilson, I.A.
#journal Proteins (1992) 14:499-508
#title Crystallization, sequence, and preliminary crystallographic
data for an antipeptide Fab 50.1 and peptide complexes with
the principal neutralizing determinant of HIV-1 gp120.
#accession B49442
##status preliminary; not compared with conceptual translation
##molecule_type DNA
##residues 1-96 #label STU
SUMMARY #length 96 #checksum 7322

Query Match 71.7%; Score 43; DB 12; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.24e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 85 qgsnedp 91
|||||||
Qy 1 QQSNEDP 7

Search completed: Tue Mar 18 10:18:13 1997
Job time : 19 secs.

WQ5REH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPerch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:18:30 1997; MasPar time 2.12 Seconds
43.783 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-28

Description: (1-9) from US08612929.pep

Perfect Score: 60

Sequence: 1 QQSNEPPR 9

Scoring table: PAM 150

Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 14.223; Variance 40.970; scale 0.347

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	60	100.0	9	13 R70201	Humanized antibody 3B	6.85e-01
2	60	100.0	131	13 R75355	Humanized antibody 3B	6.85e-01
3	51	85.0	9	13 R70197	MAB 3B9 light chain C	8.52e+00
4	51	85.0	131	13 R70202	Humanized antibody 3B	8.52e+00
5	51	85.0	131	6 R29008	p64-k4 protein produc	8.52e+00
6	51	85.0	132	13 R70189	Mouse MAB 3B9 light c	8.52e+00
7	49	81.7	209	2 R12300	ORF-2 of Herpes Virus	1.47e+01
8	47	78.3	131	6 R32123	Anti-CD4 antibody MT	2.53e+01
9	45	75.0	132	7 R37716	Mouse 4C10 anti-idiot	4.32e+01
10	44	73.3	17	12 R66145	CD-4 antibody variabl	5.63e+01
11	44	73.3	103	9 R47933	Light chain region of	5.63e+01
12	44	73.3	111	9 R47935	Humanised light chain	5.63e+01

13	44	73.3	115	1	R04134	Anti-leu 3a light cha	5.63e+01
14	44	73.3	131	1	R04132	Anti-leu 3a light cha	5.63e+01
15	44	73.3	823	1	P81502	delta-endotoxin again	5.63e+01
16	44	73.3	823	1	P80972	Sequence encoded by 3	5.63e+01
17	44	73.3	1163	14	R85147	CryIC/CryIA(B) chim	5.63e+01
18	44	73.3	1189	8	R39757	Delta endotoxin.	5.63e+01
19	44	73.3	1189	3	R10193	Insecticidal crystal	5.63e+01
20	44	73.3	1189	13	R71463	Crystall protein encod	5.63e+01
21	44	73.3	1189	2	R10130	Lepidopteran-active t	5.63e+01
22	44	73.3	1190	14	R85150	CryIC/CryIA(B) altern	5.63e+01
23	43	71.7	9	14	R75477	Mouse antibody light	7.32e+01
24	43	71.7	9	14	R75478	Mouse antibody light	7.32e+01
25	43	71.7	106	6	R33309	MaE15 light chain.	7.32e+01
26	43	71.7	111	11	R60306	Chimeric anti HIV ant	7.32e+01
27	43	71.7	111	9	R47494	Murine anti-CD18 Ab 6	7.32e+01
28	43	71.7	111	11	R60302	Anti HIV antibody lig	7.32e+01
29	43	71.7	111	10	R55127	Mouse-human chimeric	7.32e+01
30	43	71.7	111	10	R55123	Mouse anti-HIV mu5.5	7.32e+01
31	43	71.7	111	9	R47492	Humanised anti-CD18 A	7.32e+01
32	43	71.7	111	1	P90541	Immunoglobulin L chai	7.32e+01
33	43	71.7	112	3	R13089	Murine 1B4 light chai	7.32e+01
34	43	71.7	112	5	R24575	Human x mouse modifie	7.32e+01
35	43	71.7	131	1	P90543	Amino acids sequence	7.32e+01
36	42	70.0	175	1	P91482	Translation product o	9.51e+01
37	42	70.0	1434	17	R94380	Mouse patched protein	9.51e+01
38	42	70.0	1447	17	R75375	Human patched protein	9.51e+01
39	41	68.3	132	3	R10920	kappa light chain var	1.23e+02
40	41	68.3	146	11	R58877	Rat-413 cadherin part	1.23e+02
41	41	68.3	146	17	R87119	Protocadherin clone R	1.23e+02
42	40	66.7	110	10	R60810	Light chain variable	1.60e+02
43	40	66.7	111	9	R48622	Sequence of the human	1.60e+02
44	40	66.7	112	14	R79158	Human IgE receptor-bi	1.60e+02
45	40	66.7	715	15	R80482	Recombinant bovine ad	1.60e+02

ALIGNMENTS

RESULT 1
ID R70201 standard; Protein; 9 AA.
AC R70201;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain CDR.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW MAb; interleukin-4; IL-4; allergy; CDR;
KW complementarity determining region.
OS Homo sapiens.
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PI (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Page 28; 97pp; English.
CC A humanized antibody light chain variable region and signal
CC sequence is given in R75355. The signal sequence is also
CC provided in R70194. The sequences of the first 2 CDRs
CC are identical to mouse anti-human IL-4 MAb 3B9 light chain
CC CDRs (given in R70195-96), but the third (R70201) differs

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CC by a single amino acid from the native mouse CDR (R70197).
SQ Sequence 9 AA;

Query Match 100.0%; Score 60; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.85e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qgsnedppr 9
| | | | | | | | | |
Qy 1 QQSNEPPR 9

RESULT 2

ID R75355 standard; Protein; 131 AA.
AC R75355;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW Mab; interleukin-4; IL-4; allergy.
OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..20

FT /label= Sig_peptide

FT Region 43..57

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 73..79

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 112..120

FT /label= CDR

FT /note= "complementarity determining region"

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

DR N-PSDB; Q73986.

PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived
PT from high affinity mabs - useful in treatment of IL-4-mediated

PS Disclosure; Fig.5; 97pp; English.

CC A humanized antibody light chain variable region and signal
CC sequence is given in R75355. The signal sequence is also

CC provided in R70194. The sequences of the first 2 CDRs

CC are identical to mouse anti-human IL-4 Mab 3B9 light chain

CC CDRs (given in R70195-96), but the third (R70201) differs

CC by a single amino acid from the native mouse CDR (R70197).

SQ Sequence 131 AA;

Query Match 100.0%; Score 60; DB 13; Length 131;
Best Local Similarity 100.0%; Pred. No. 6.85e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 112 qgsnedppr 120

| | | | | | | | | |

Qy 1 QQSNEPPR 9

RESULT 3

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4

ID R70197 standard; Protein; 9 AA.

AC R70197;

DT 20-SEP-1995 (first entry)

DE MAB 3B9 light chain CDR.

KW Chimeric antibody; humanized antibody; antibody engineering;

KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; CDR;

KW complementarity determining region.

OS Mus sp.

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived
PT from high affinity mabs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Page 56; 97pp; English.

CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only

CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy

CC chains were cloned into pCEV7f+ and transformed into E. coli

CC DH5-alpha. A light chain cDNA clone was sequenced (Q83490) that

CC encoded the protein given in R70189. 3 CDRs (R70195-97) were

CC identified.

SQ Sequence 9 AA;

Query Match 85.0%; Score 51; DB 13; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.52e+00;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qgsnedppr 8

| | | | | | | |

Qy 1 QQSNEPPR 8

RESULT 4

ID R70202 standard; Protein; 131 AA.

AC R70202;

DT 20-SEP-1995 (first entry)

DE Humanized antibody 3B9 light chain.

KW Humanized antibody; antibody engineering; monoclonal antibody;

KW Mab; interleukin-4; IL-4; allergy.

OS Homo sapiens.

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

DR N-PSDB; Q83520.

PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived
PT from high affinity mabs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Page 71-72; 97pp; English.

CC A humanized antibody light chain variable region and signal

CC sequence is given in R75355. The signal sequence is also

CC provided in R70194. The sequences of the 3 CDRs

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CC are identical to mouse anti-human IL-4 Mab 3B9 light chain
CC CDRs (given in R70195-97).
SQ Sequence 131 AA;

Query Match 85.0%; Score 51; DB 13; Length 131;
Best Local Similarity 100.0%; Pred. No. 8.52e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 112 qgsnedpp 119
|||||||
QY 1 QQSNEDEPP 8

RESULT 5
ID R29008 standard; Protein; 131 AA.

AC R29008;
DT 30-MAR-1993 (first entry)
DE p64-k4 protein product.
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
KW plasmid; p64-k4; p64-h2.
OS Synthetic.

FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "Signal peptide"
FT Protein 21..131
FT /note= "Mature peptide"
PN W09219759-A.
PD 12-NOV-1992.
PE 24-APR-1992; J00544.
PR 25-APR-1991; JP-095476.
PR 19-FEB-1992; JP-032084.
PA (CHUS) CHUGAI SEIYAKU KK.
PI Bendig MW, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WPI; 92-398882/48.

DR N-PSDB; Q30757.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PS Disclosure; Page 124-125; 207pp; Japanese.
CC The sequences given in R29008-09 were encoded by plasmids which were
CC used in example to illustrate the production of a human antibody which
CC recognises human interleukin-6 receptor (IL-6R). The antibody
CC comprises light (L) chain and heavy (H) chain variable regions which
CC were derived from a mouse monoclonal antibody produced from the
CC hybridoma AUK64-7 which contained the plasmids p64-k4 and p64-h2.
SQ Sequence 131 AA;

Query Match 85.0%; Score 51; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 8.52e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 113 qgsnedpp 120
|||||||
QY 1 QQSNEDEPP 8

RESULT 6
ID R70189 standard; Protein; 132 AA.

AC R70189;
DT 20-SEP-1995 (first entry)
DE Mouse Mab 3B9 light chain.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy.

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OS Mus sp. Location/Qualifiers
FH Key 1..20
FT Peptide /label= Sig_peptide
FT Region 44..58
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 74..80
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 113..121
FT /label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvestre DR;
DR WPI; 95-123387/16.
DR N-PSDB; Q83490.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.1; 97pp; English.
CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC chains were cloned into pCEM7f+ and transformed into E. coli
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for
CC antibody engineering.
SQ Sequence 132 AA;

Query Match 85.0%; Score 51; DB 13; Length 132;
Best Local Similarity 100.0%; Pred. No. 8.52e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 113 qgsnedpp 120
|||||||
QY 1 QQSNEDEPP 8

RESULT 7
ID R12300 standard; Protein; 209 AA.

AC R12300;
DT 13-AUG-1991 (first entry)
DE ORF-2 of Herpes Virus of turkeys genome insertion region.
KW HVT; vaccine.
OS Synthetic.
PN EP-431668-A.
PD 12-JUN-1991.
PF 21-NOV-1990; 203076.
PR 04-DEC-1989; EP-203071.
PR 21-NOV-1990; EP-203076.
PA (ALKU) AKZO NV.
PI Sondermeijer PJA, Claessens JAJ, Mockett APA;
DR WPI; 91-172965/24.
PT Recombinant HVT contg. heterologous gene - the gene is situated
PT in defined insert region in genome, recombinant HVT can be used
PT to produce vector vaccine.
PS Claim 1; Page 14; 30pp; English.
CC The sequence (SEQ ID NO:2) is encoded by ORF-2 of the HVT genome.

CC The DNA contains a BgIII site into which DNA encoding an epitope
 CC can be inserted for the prodn. of a viral vaccine. Sequences en-
 CC coding, for example, Newcastle Disease Virus or Marek's disease
 CC antigens can be inserted for vaccines for poultry.
 CC See also R12301-R12303.
 SQ Sequence 209 AA;

Query Match 81.7%; Score 49; DB 2; Length 209;
 Best Local Similarity 75.0%; Pred. No. 1.47e+01;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 112 qnneppr 119
 |:|:|:|
 Qy 2 QSNEDPPR 9

RESULT 8
 ID R32123 standard; Protein; 131 AA.
 AC R32123;
 DT 02-JUN-1993 (first entry)
 DE Anti-CD4 antibody MT 3.10 light chain variable region.
 KW immunosuppression; tissue transplantation; graft; L chain; V region;
 KW T-helper cell inhibition; transplant rejection; MAb;
 KW interleukin-2 receptor.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= signal
 FT Region 21..120
 FT /label= Variable
 FT Region 121..131
 FT /label= J1
 PN DE4143214-A.
 PD 28-JAN-1993.
 PF 30-DEC-1991; 143214.
 PR 25-JUL-1991; DE-124759.
 PR 30-DEC-1991; DE-143214.
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 PI Kalura B, Riethmuller G, Scheuer W, Weidle U;
 DR WPI; 93-037582/05.
 DR N-PSDB; Q36609.
 PT Synergistic antibody compen. for use as immunosuppressant -
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
 PT alpha- or anti-IL2R beta antibodies
 PS Claim 5; Page 11; 18pp; German.
 CC This sequence is the light chain variable region of a preferred
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic
 CC composition. MAb MT 3.10 is deposited as clone 3.101/8B10 (ECACC
 CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R
 CC alpha or beta antibody. Individually the antibodies are strongly
 CC inhibiting and when used together their immunosuppressive properties
 CC are improved; they synergistically inhibit T-helper cell
 CC proliferation to effectively inhibit transplant rejection at low
 CC doses without significantly reducing the general immune response.
 CC See also Q36608-Q36616.
 SQ Sequence 131 AA;

Query Match 78.3%; Score 47; DB 6; Length 131;
 Best Local Similarity 87.5%; Pred. No. 2.53e+01;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 113 qgsedpp 120
 |:|:|:|
 Qy 1 QQSNEDPP 8

RESULT 9
 ID R37716 standard; Protein; 132 AA.
 AC R37716;
 DT 30-SEP-1993 (first entry)
 DE Mouse 4C10 anti-idiotypic Ab light chain V region.
 KW MAIA; monoclonal antibody; hybridoma; organ transplant rejection;
 KW immuno-modulator; cancer; treatment; diagnosis; melanoma;
 KW anti-cancer immunity; enhancement; suppression.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT Misc_difference 31
 FT /note= "Thr -> Ser, from PCR substituted gene"
 PN W09310221-A.
 PD 27-MAY-1993.
 PF 12-NOV-1992; U10166.
 PR 13-NOV-1991; US-791934.
 PA (REGC) UNIV CALIFORNIA.
 PI Hastings A, Irie RF, Morrison SL.
 DR WPI; 93-182538/22.
 PT Chimeric murine-human anti-idiotypic monoclonal antibodies -
 PT useful as immuno-modulators for treating and diagnosing cancers,
 PT and for suppressing organ transplant rejection and auto-immune
 PT diseases
 PS Disclosure; Page 30-31; 46pp; English.
 CC The sequence is that of the 4C10 anti-idiotypic Ab light chain V region
 CC which was used in the construction of a murine/human monoclonal
 CC anti-idiotypic antibody (MAIA). The MAIA elicits an anti-ganglioside
 CC response and produces antibodies which induce cytotoxic destruction
 CC of cancer cells bearing the gangliosides. It can be used for treating
 CC cancers partic. melanomas. It can also be used as an immunomodulator to
 CC enhance anti-cancer immunity, suppress organ transplant rejection and
 CC suppress autoimmune disease. The MAIA can also be used in the diagnosis
 CC of cancers.
 SQ Sequence 132 AA;

Query Match 75.0%; Score 45; DB 7; Length 132;
 Best Local Similarity 77.8%; Pred. No. 4.32e+01;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 113 qgsedptw 121
 |:|:|:|:|
 Qy 1 QQSNEDPPR 9

RESULT 10
 ID R66145 standard; peptide; 17 AA.
 AC R66145;
 DT 12-JUL-1995 (first entry)
 DE CD-4 antibody variable region complementary peptide.
 KW CD-4 antibody variable region; complementary peptide;
 KW extra-corporeal blood circulation; cell filter material.
 OS Synthetic.
 PN J06296663-A.
 PD 27-SEP-1994.
 PF 17-MAR-1993; JP-057206.
 PR (TOYM) TOYOBO KK.
 DR WPI; 94-346316/43.
 PT Material for collecting cells positive for CD-4 antibody -
 PT comprises nonwoven fabric having keto-alkyl halide functional gp
 PS Example 3; Page 8; 9pp; Japanese.
 CC R66140-R66146 are peptides complementary to the variable region
 CC of the CD-4 antibody, these peptides are fixed onto a claimed

CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with
 CC keto-alkyl halide functional groups. This material can be used
 CC as a filter for CD-4 positive cells in a medical treatment
 CC involving the extra-corporeal circulation of blood.
 SQ Sequence 17 AA;

Query Match 73.3%; Score 44; DB 12; Length 17;

Best Local Similarity 87.5%; Pred. No. 5.63e+01;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 9 gqsvdpp 16

|||||

QY 1 QQSNEDPP 8

RESULT 11

ID R47933 standard; Protein; 103 AA.

AC R47933;

DT 24-JUL-1994 (first entry)

DE Light chain region of 23F2G.

KW Amplification; 23F2G; humanised antibody; heavy chain; light chain;

KW hybridoma; inflammation; CD18; human leukocyte integrins; mAb 60.3;

KW monoclonal antibody; LFA-1; adhesion; migration; multiple

KW sclerosis; MS.

PN W09402175-A.

PD 03-FEB-1994.

PF 16-JUL-1993; U06734.

PR 16-JUL-1992; US-915068.

PR 10-MAY-1993; US-060699.

PA (ICOS-) ICOS CORP.

PA (UNIW) UNIV WASHINGTON.

PI Rose LM;

DR WPI; 94-048551/06.

DR N-PSDB; Q55917.

PT Antibodies immunologically reactive with the CD18 of human

PT leukocyte integrins and/or competing with mAb 60.3 for binding to

PT human LFA-1 - for alleviating symptoms associated with

PT inflammatory disease states

PS Example 6; Page 43; 58pp; English.

CC Total RNA was isolated from the hybridoma cell line 23F2G and first

CC strand cDNA was synthesised using the total RNA as a template. The

CC first strand cDNA was used as a template for PCR to obtain double

CC stranded DNA fragments encoding the variable regions of both the

CC heavy and light chains of monoclonal antibody 23F2G. The sequence

CC shown is that of the light chain variable region of MAb 23F2G

CC The humanised form of MAb 23F2G may be administered to

CC alleviate symptoms associated with inflammatory disease states, esp.

CC for the inhibition of inflammatory processes associated with

CC multiple sclerosis. The MAb blocks leukocyte adhesion and

CC migration to inflammatory sites. The MAb is an anti-CD18 integrin

CC antibody which competes with MAb 60.3 for binding to LFA-1.

CC See also R47931-6.

SQ Sequence 103 AA;

Query Match 73.3%; Score 44; DB 9; Length 103;

Best Local Similarity 75.0%; Pred. No. 5.63e+01;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 85 hqndedpp 92

:| |||||

QY 1 QQSNEDPP 8

RESULT 12

ID R47935 standard; Protein; 111 AA.

AC R47935;

DT 24-JUL-1994 (first entry)

DE Humanised light chain region of 23F2G.

KW Amplification; 23F2G; humanised antibody; heavy chain; light chain;

KW hybridoma; inflammation; CD18; human leukocyte integrins; mAb 60.3;

KW monoclonal antibody; LFA-1; adhesion; migration; multiple

KW sclerosis; MS.

PN W09402175-A.

PD 03-FEB-1994.

PF 16-JUL-1993; U06734.

PR 16-JUL-1992; US-915068.

PR 10-MAY-1993; US-060699.

PA (ICOS-) ICOS CORP.

PA (UNIW) UNIV WASHINGTON.

PI Rose LM;

DR WPI; 94-048551/06.

DR N-PSDB; Q55917.

PT Antibodies immunologically reactive with the CD18 of human

PT leukocyte integrins and/or competing with mAb 60.3 for binding to

PT human LFA-1 - for alleviating symptoms associated with

PT inflammatory disease states

PS Example 6; Page 45; 58pp; English.

CC Total RNA was isolated from the hybridoma cell line 23F2G and first

CC strand cDNA was synthesised using the total RNA as a template. The

CC first strand cDNA was used as a template for PCR to obtain double

CC stranded DNA fragments encoding the variable regions of both the

CC heavy and light chains of monoclonal antibody 23F2G. The sequence

CC shown is a humanised form of the light chain variable region of MAb

CC 23F2G. The humanised form of MAb 23F2G may be administered to

CC alleviate symptoms associated with inflammatory disease states, esp.

CC for the inhibition of inflammatory processes associated with

CC multiple sclerosis. The MAb blocks leukocyte adhesion and

CC migration to inflammatory sites. The MAb is an anti-CD18 integrin

CC antibody which competes with MAb 60.3 for binding to LFA-1.

CC See also R47931-6.

SQ Sequence 111 AA;

Query Match 73.3%; Score 44; DB 9; Length 111;

Best Local Similarity 75.0%; Pred. No. 5.63e+01;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 93 hqndedpp 100

:| |||||

QY 1 QQSNEDPP 8

RESULT 13

ID R04134 standard; protein; 115 AA.

AC R04134;

DT 06-SEP-1990 (first entry)

DE Anti-Leu 3a light chain variable region gene product, KOL/206 V1.

KW HIV; AIDS; anti-Leu3a; vaccine; ds.

OS Mus musculus.

PN EP-365209-A.

PD 25-APR-1990.

PF 11-OCT-1989; 010415.

PR 17-OCT-1988; US-260558.

PA (BECT) Becton Dickinson Co.

PI Hinton R, Oi VT;

DR WPI; 90-126329/17.

DR N-PSDB; Q04041.

PT New chimeric variants of murine antibody anti-leucine -

PT contg. human antibody regions, and DNA encoding sequences.

PS Claim 4; Fig 4; 12pp; English.

CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be

CC used to form chimeric mouse-variable, human-constant region Abs

CC suggested as being useful as a vaccine to HIV.

SQ Sequence 115 AA;

Query Match 73.3%; Score 44; DB 1; Length 115;

Best Local Similarity 87.5%; Pred. No. 5.63e+01;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 96 qgsyedpp 103

|||||

Qy 1 QQSNEPPP 8

RESULT 14

ID R04132 standard; protein; 131 AA.

AC R04132;

DT 06-SEP-1990 (first entry)

DE Anti-Leu 3a light chain variable region gene product, 206 Vx.

KW HIV; AIDS; anti-Leu3A; vaccine; ds.

OS Mus musculus.

PN EP-365209-A.

PD 25-APR-1990.

PF 11-OCT-1989; 010415.

PR 17-OCT-1988; US-260558.

PA (BECT) Becton Dickinson Co.

PI Hinton R. Oi VT;

DR WPI; 90-126329/17.

DR N-PSDB; Q04039.

PT New chimeric variants of murine antibody anti-leucine -

PT contg. human antibody regions, and DNA encoding sequences.

PS Claim 1; Fig 2; 12pp; English.

CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be

CC used to form chimeric mouse-variable, human-constant region Abs

CC suggested as being useful as a vaccine to HIV.

SQ Sequence 131 AA;

Query Match 73.3%; Score 44; DB 1; Length 131;

Best Local Similarity 87.5%; Pred. No. 5.63e+01;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 113 qgsyedpp 120

|||||

Qy 1 QQSNEPPP 8

RESULT 15

ID P81502 standard; protein; 823 AA.

AC P81502;

DT 23-OCT-1990 (first entry)

DE delta-endotoxin against Lepidoptera larvae

KW Lepidoptera larvae; insecticide; Bacillus thuringiensis;

KW Spodoptera littoralis; delta endotoxin; ss.

OS synthetic.

FH Key Location/Qualifiers

FT Region 1..620

FT /label=N-terminal half

ET /note="responsible for toxicity"

PN W08809812-A.

PD 15-DEC-1988.

PF 09-JUN-1988; F00292.

PR 12-JUN-1987; DK-002990.

PA (NOVO) Novo Industri A/S.

PI Sanchis V, Lereclus D, Menou G;

DR WPI; 88-368626/51.

DR N-PSDB; N91949.

PT New nucleotide sequences encoding new polypeptide -

PT with selective action against lepidopteran larvae esp Spodoptera

PT littoralis

PS Claim 14; Page 52; 65pp; French.

CC Polypeptide is encoded by a 3kb HindIII-PstI fragment of

CC Bacillus thuringiensis. Recombinant sequences can also be

CC constructed from 2 diff strains of B.thuringiensis. The sequence

CC between bases 50 to 985 is claimed separately as this encodes "at

CC least a part of the N-terminal region of an insecticidal

CC polypeptide". There is a variable amino acid at posn 124 which is

CC Ala in the sequence given here but which is Glu in the shorter

CC sequence.

SQ Sequence 823 AA;

Query Match 73.3%; Score 44; DB 1; Length 823;

Best Local Similarity 44.4%; Pred. No. 5.63e+01;

Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 344 reangeppr 352

|||||

Qy 1 QQSNEPPP 9

Search completed: Tue Mar 18 10:18:41 1997

Job time : 11 secs.

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:09:20 1997; MasPar time 2.23 Seconds
124.694 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-16
Description: (1-15) from US08612929.pep
Perfect Score: 102
Sequence: 1 KASQSDVDYDGDGYM 15

Scoring table: PAM 150
Gap 15

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot33
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10

Statistics: Mean 26.187; Variance 34.386; scale 0.762

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	102	100.0	111	5	KV30_MOUSE IG KAPPA CHAIN V-III	7.90e-11
2	102	100.0	111	5	KV3N_MOUSE IG KAPPA CHAIN V-III	7.90e-11
3	102	100.0	111	5	KV3M_MOUSE IG KAPPA CHAIN V-III	7.90e-11
4	102	100.0	111	5	KV3Q_MOUSE IG KAPPA CHAIN V-III	7.90e-11
5	96	94.1	110	5	KV3P_MOUSE IG KAPPA CHAIN V-III	2.46e-09
6	94	92.2	111	5	KV3L_MOUSE IG KAPPA CHAIN V-III	7.64e-09
7	60	58.8	111	5	KV3C_MOUSE IG KAPPA CHAIN V-III	3.36e-01
8	60	58.8	112	5	KV3C_MOUSE IG KAPPA CHAIN V-III	3.36e-01
9	58	56.9	679	6	PB2_STRN PENICILLIN-BINDING PR	8.29e-01
10	57	55.9	113	5	KV2B_HUMAN IG KAPPA CHAIN V-II R	1.29e+00
11	56	54.9	108	5	KV3V_MOUSE IG KAPPA CHAIN V-III	2.00e+00
12	56	54.9	111	5	KV3H_MOUSE IG KAPPA CHAIN V-III	2.00e+00
13	56	54.9	111	5	KV3J_MOUSE IG KAPPA CHAIN V-III	2.00e+00

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14	56	54.9	111	5	KV3K_MOUSE IG KAPPA CHAIN V-III	2.00e+00
15	56	54.9	131	5	KV3I_MOUSE IG KAPPA CHAIN V-III	2.00e+00
16	56	54.9	459	2	CCMH_HAEIN CYTOCHROME C-TYPE BIO	2.00e+00
17	56	54.9	512	9	VC02_VACCC PROTEIN C2.	2.00e+00
18	56	54.9	512	9	VC02_VACCC PROTEIN C2.	2.00e+00
19	55	53.9	272	9	TYPH_MYCHO THYMIDINE PHOSPHORYLA	3.09e+00
20	54	52.9	57	6	NG4_DROME NEM-GLUE PROTEIN 4 PR	4.74e+00
21	54	52.9	111	5	KV3A_MOUSE IG KAPPA CHAIN V-III	4.74e+00
22	54	52.9	112	5	KV3B_MOUSE IG KAPPA CHAIN V-III	4.74e+00
23	54	52.9	133	5	KV2F_HUMAN IG KAPPA CHAIN PRECUR	4.74e+00
24	54	52.9	452	9	VE2_HPV17 E2 PROTEIN.	4.74e+00
25	54	52.9	501	9	VGLC_HSVMD SECRETORY GLYCOPROTEI	4.74e+00
26	54	52.9	501	9	VGLC_HSVMB SECRETORY GLYCOPROTEI	4.74e+00
27	54	52.9	501	9	VGLC_HSVMB SECRETORY GLYCOPROTEI	4.74e+00
28	54	52.9	505	9	VGLC_HSVMB SECRETORY GLYCOPROTEI	4.74e+00
29	54	52.9	716	5	KIF2_MOUSE KINESIN-LIKE PROTEIN	4.74e+00
30	54	52.9	1955	1	AGRI_CHICK AGRIN PRECURSOR.	4.74e+00
31	54	52.9	3951	9	VGF1_IBVB F1 PROTEIN.	4.74e+00
32	53	52.0	83	4	IBB3_SOYBN BOWMAN-BIRK TYPE PROT	7.22e+00
33	53	52.0	416	10	YRM6_CAEEL HYPOTHETICAL 46.4 KD	7.22e+00
34	53	52.0	591	9	VR2_SALCH 65 KD VIRULENCE PROTE	7.22e+00
35	53	52.0	593	9	VR2_SALDU 65 KD VIRULENCE PROTE	7.22e+00
36	52	51.0	269	9	TRQA_HAEIN PSEUDOURIDYLATE SYNTH	1.09e+01
37	52	51.0	270	9	TRQA_ECOLI PSEUDOURIDYLATE SYNTH	1.09e+01
38	52	51.0	319	10	YK5_CAEEL PROBABLE G PROTEIN-CO	1.09e+01
39	52	51.0	334	9	VE2_BPVA E2 PROTEIN.	1.09e+01
40	52	51.0	396	8	SOX-11 CHICK SOX-11 PROTEIN.	1.09e+01
41	52	51.0	638	3	ER72_MOUSE PROTEIN DISULFIDE ISO	1.09e+01
42	52	51.0	643	3	ER72_RAT PROTEIN DISULFIDE ISO	1.09e+01
43	52	51.0	855	9	VGLH_HSVF4 GLYCOPROTEIN H PRECUR	1.09e+01
44	52	51.0	2291	8	RREP_BEV RNA-DIRECTED RNA POLY	1.09e+01
45	51	50.0	323	10	YAMB_THETU HYPOTHETICAL 35.6 KD	1.65e+01

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	111 AA.
ID	KV30_MOUSE			
AC	P01667;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DE	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN V-III REGION (PC 6308).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE; 79073152.			
RA	WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;			
RL	NATURE 276:785-790(1978).			
DR	PIR; C01937; KVM508.			
DR	HSSP; P01679; IGG8.			
KW	IMMUNOGLOBULIN V REGION.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 38			
FT	DOMAIN 39 53			
FT	DOMAIN 54 60			
FT	DOMAIN 61 92			
FT	DOMAIN 93 101			
FT	DOMAIN 102 111			
FT	DISULFID 23 92			
FT	NON_TER 111 111			
SQ	SEQUENCE 111 AA; 12071 MW; F7865271 CRC32;			

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DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7210).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; D01937; KWS10.
DR HSP; P01679; IGGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 100
FT DOMAIN 101 110
FT DISULFID 23 92
FT NON TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; BF45B542 CRC32;

Query Match 94.1%; Score 96; DB 5; Length 110;
Best Local Similarity 93.3%; Pred. No. 2.46e-09;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqvdydgsym 38
|||||:|||||
Qy 1 KASQVDYDGSYMN 15

RESULT 6
ID KV3L MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (CBPC 101).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
CC -1- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KWS1.
DR HSP; P01679; IGGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; AZAC84C7 CRC32;

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Query Match 92.2%; Score 94; DB 5; Length 111;
Best Local Similarity 86.7%; Pred. No. 7.64e-09;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 24 kasqvdydgsym 38
|||||:|||||
Qy 1 KASQVDYDGSYMN 15

RESULT 7
ID KV3C MOUSE STANDARD; PRT; 111 AA.
AC P01656;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (MOPC 70).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 67056897.
RA GRAY W.R., DREYER W.J., HOOD L.E.;
RL SCIENCE 155:465-467(1967).
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01930; KWS80.
DR HSP; P01679; IGGB.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11904 MW; 76BA04CC CRC32;

Query Match 58.8%; Score 60; DB 5; Length 111;
Best Local Similarity 60.0%; Pred. No. 3.36e-01;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 24 rasesvdngisfmm 38
:|||||:|||||
Qy 1 KASQVDYDGSYMN 15

RESULT 8
ID KV3G MOUSE STANDARD; PRT; 112 AA.
AC P01659;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (TEPC 124).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 73140225.
RA MCKEAN D.J., POTTER M., HOOD L.E.;
RL BIOCHEMISTRY 12:760-771(1973).
DR PIR; A01933; KWS32.

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DR HSP; P01679; IGB.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 29 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 112 112
 SQ SEQUENCE 112 AA; 12339 MW; 4504DDOE CRC32;
 Query Match 58.8%; Score 60; DB 5; Length 112;
 Best Local Similarity 46.7%; Pred. No. 3.36e-01;
 Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 24 raszsvnwygnsmz 38
 QY 1 KASQSDYDGDSTYN 15
 RESULT 9
 ID PBP2 STRPN STANDARD; PRT; 679 AA.
 AC P10524;
 DT 01-JUL-1989 (REL. 11, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
 DE PENICILLIN-BINDING PROTEIN 2B.
 GN PENA.
 OS STREPTOCOCCUS PNEUMONIAE.
 OC PROKARYOTA; FIRMICUTES; COCCI; STREPTOCOCCACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R6;
 RX MEDLINE; 90016914.
 RA DOWSON C.G., HUTCHISON A., SPRATT B.G.;
 RL NUCLEIC ACIDS RES. 17:7518-7518(1989).
 RN [2]
 RP SEQUENCE OF 194-679 FROM N.A.
 RC STRAIN=64147, AND R6;
 RX MEDLINE; 89237905.
 RA DOWSON C.G., HUTCHISON A., SPRATT B.G.;
 RL MOL. MICROBIOL. 3:95-102(1989).
 CC -1- SIMILARITY: ONLY SMALL REGIONS OF SIMILARITY (AROUND THE ACTIVE SITE SERINE) TO OTHER PENICILLIN-RECOGNIZING ENZYMES.
 DR EMBL; X13137; G47400; -.
 DR EMBL; X16022; G984233; -.
 DR EMBL; X13136; G47398; -.
 DR PIR; S06000; S06000.
 KW CELL WALL; PEPTIDOGLYCAN SYNTHESIS; ANTIBIOTIC RESISTANCE.
 FT VARIANT 332 332
 FT VARIANT 425 431
 FT VARIANT 445 445
 FT VARIANT 475 475
 FT VARIANT 488 488
 FT VARIANT 511 511
 FT VARIANT 537 537
 FT VARIANT 596 596
 FT VARIANT 673 675
 SQ SEQUENCE 679 AA; 73722 MW; 85F09C45 CRC32;

Query Match 56.9%; Score 58; DB 6; Length 679;
 Best Local Similarity 38.5%; Pred. No. 8.29e-01;

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Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 Db 435 avqaleysntym 447
 QY 2 ASQSDYDGDSTYN 14
 RESULT 10
 ID KV2B HUMAN STANDARD; PRT; 113 AA.
 AC P01615;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (FR).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 76253627.
 RA RIESEN W.F., JATON J.-C.;
 RL BIOCHEMISTRY 15:3829-3833(1976).
 CC -1- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
 DR PIR; A01886; K2HUFR.
 DR HSP; P01607; IJEL.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT DOMAIN 40 54
 FT DOMAIN 55 61
 FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON TER 113 113
 SQ SEQUENCE 113 AA; 12660 MW; 53CADDDE CRC32;

Query Match 55.9%; Score 57; DB 5; Length 113;
 Best Local Similarity 37.5%; Pred. No. 1.29e+00;
 Matches 6; Conservative 8; Mismatches 1; Indels 1; Gaps 1;
 Db 24 rasqslvyrbqbylb 39
 QY 1 KASQSDYDGDSTYN 15
 RESULT 11
 ID KV3V MOUSE STANDARD; PRT; 108 AA.
 AC P01674;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (PC 2154).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 DR PIR; A01940; KMS54.
 DR HSP; P01679; IACY.

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KW IMMUNOGLOBULIN V REGION.

FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 108
 FT DISULFID 23 92
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11699 MW; E28989GCC CRC32;

Query Match 54.9%; Score 56; DB 5; Length 108;
 Best Local Similarity 60.0%; Pred. No. 2.00e+00;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 24 rasevsvdsgnsmf 38
 :||||| i|||:
 Qy 1 KASQSDVDGDSYMN 15

RESULT 12

ID KV3H MOUSE STANDARD; PRT; 111 AA.
 AC P01660;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (PC 3741 AND TEPC 111).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE (PC 3741).
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 [2]
 RP SEQUENCE (TEPC 111).
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).

Query Match 54.9%; Score 56; DB 5; Length 111;
 Best Local Similarity 53.3%; Pred. No. 2.00e+00;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 24 rasevsvdsgnsmf 38
 :||||| i|||:
 Qy 1 KASQSDVDGDSYMN 15

KW IMMUNOGLOBULIN V REGION.

FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12099 MW; 76502E89 CRC32;

Query Match 54.9%; Score 56; DB 5; Length 111;
 Best Local Similarity 53.3%; Pred. No. 2.00e+00;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 24 rasevsvdsgnsmf 38
 :||||| i|||:
 Qy 1 KASQSDVDGDSYMN 15

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RESULT 13
 ID KV3J MOUSE STANDARD; PRT; 111 AA.
 AC P01662;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (ABPC 22 AND PC 9245).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE (ABPC 22).
 RX MEDLINE; 79012520.
 RA MCKEAN D.J., BELL M., POTTER M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
 [2]
 RP SEQUENCE (PC 9245).
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 CC -!- THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.

DR PIR; A01935; KVM56.
 DR HSP; P01679; IAC.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12041 MW; 711C554A CRC32;

Query Match 54.9%; Score 56; DB 5; Length 111;
 Best Local Similarity 53.3%; Pred. No. 2.00e+00;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 24 rasevsvdsgnsmf 38
 :||||| i|||:
 Qy 1 KASQSDVDGDSYMN 15

RESULT 14

ID KV3K MOUSE STANDARD; PRT; 111 AA.
 AC P01663;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (PC 4050).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 DR PIR; A01935; KVM56.
 DR HSP; P01679; IAC.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12041 MW; 711C554A CRC32;

Query Match 54.9%; Score 56; DB 5; Length 111;
 Best Local Similarity 53.3%; Pred. No. 2.00e+00;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 24 rasevsvdsgnsmf 38
 :||||| i|||:
 Qy 1 KASQSDVDGDSYMN 15

RESULT 14
 ID KV3K MOUSE STANDARD; PRT; 111 AA.
 AC P01663;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (PC 4050).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 DR PIR; A01935; KVM56.
 DR HSP; P01679; IAC.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12041 MW; 711C554A CRC32;

Query Match 54.9%; Score 56; DB 5; Length 111;
 Best Local Similarity 53.3%; Pred. No. 2.00e+00;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 24 rasevsvdsgnsmf 38
 :||||| i|||:
 Qy 1 KASQSDVDGDSYMN 15

FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 39 53 FRAMEWORK 2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 61 92 FRAMEWORK 3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 111 FRAMEWORK 4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12005 MW; 5EBF3264 CRC32;

Query Match 54.9%; Score 56; DB 5; Length 111;
 Best Local Similarity 53.3%; Pred. No. 2.00e+00;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 24 rasesvdsygnsfmh 38
 :||:|||| |:|:|:
 QY 1 KASQSVYDGD SYMN 15

RESULT 15
 ID KV31 MOUSE STANDARD; PRT; 131 AA.
 AC P01661;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 63).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE OF 1-35.
 RX MEDLINE; 78235887.
 RA BURSTEIN Y., SCHECHTER I.;
 RL BIOCHEMISTRY 17:2392-2400(1978).
 RN [2]
 RP SEQUENCE OF 21-131.
 RX MEDLINE; 73140225.
 RA MCKEAN D.J., POTTER M., HOOD L.E.;
 RL BIOCHEMISTRY 12:760-771(1973).
 RN [3]
 RP REVISIONS.
 RX MEDLINE; 79012520.
 RA MCKEAN D.J., BELL M., POTTER M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
 DR PIR; A01935; KVM5M6.
 DR HSP; P01679; IACY.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION (MOPC 63).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 59 73 FRAMEWORK 2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 81 112 FRAMEWORK 3.
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 122 131 FRAMEWORK 4.
 FT DISULFID 43 112 BY SIMILARITY.
 FT NON TER 131 131
 SQ SEQUENCE 131 AA; 14291 MW; 9D55A06B CRC32;

Query Match 54.9%; Score 56; DB 5; Length 131;
 Best Local Similarity 53.3%; Pred. No. 2.00e+00;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 44 rasesvdsygnsfmh 38
 :||:|||| |:|:|:
 QY 1 KASQSVYDGD SYMN 15

Search completed: Tue Mar 18 10:09:29 1997
 Job time : 9 secs.

Result No.	Query			Description			Pred. No.
	Score	Match	Length	ID	DB		
1	102	100.0	81	12	S42193	Ig kappa chain V reg	2.14e-08
2	102	100.0	85	12	S42199	Ig kappa chain V reg	2.14e-08
3	102	100.0	87	12	S42190	Ig kappa chain V reg	2.14e-08
4	102	100.0	88	12	S42194	Ig kappa chain V reg	2.14e-08
5	102	100.0	90	12	S42187	Ig kappa chain V reg	2.14e-08
6	102	100.0	93	12	A38601	Ig kappa chain V reg	2.14e-08
7	102	100.0	111	2	KWMS43	Ig kappa chain V reg	2.14e-08
8	102	100.0	111	2	KWMS93	Ig kappa chain V reg	2.14e-08
9	102	100.0	111	2	KWMS08	Ig kappa chain V reg	2.14e-08
10	102	100.0	111	2	KWMS69	Ig kappa chain V reg	2.14e-08
11	96	94.1	110	2	KWMS10	Ig kappa chain V reg	3.65e-07
12	96	94.1	112	5	S19971	Ig kappa chain V reg	3.65e-07

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QY 1 KASQSVYDGDGYM 15

RESULT 2

ENTRY S42189 #type fragment

TITLE Ig kappa chain V region - mouse (fragment)

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change

21-Jul-1995

ACCESSIONS S42189

REFERENCE S42176

#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.

#journal Eur. J. Immunol. (1993) 23:2503-2510

#title Variable region gene selection of immunoglobulin G-expressing

B cells with specificity for a defined epitope on type II

#accession S42189

#status preliminary

#molecule_type DNA

#residues 1-85 #label MOJ

#cross-references EMBL:225448

SUMMARY #length 85 #checksum 7866

Query Match

Best Local Similarity 100.0%; Score 102; DB 12; Length 85;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 kasqvdydgsym 24

QY 1 KASQSVYDGDGYM 15

RESULT 3

ENTRY S42190 #type fragment

TITLE Ig kappa chain V region - mouse (fragment)

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change

13-Jan-1995

ACCESSIONS S42190

REFERENCE S42176

#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.

#journal Eur. J. Immunol. (1993) 23:2503-2510

#title Variable region gene selection of immunoglobulin G-expressing

B cells with specificity for a defined epitope on type II

#accession S42190

#status preliminary

#molecule_type DNA

#residues 1-87 #label MOJ

#cross-references EMBL:225450

SUMMARY #length 87 #checksum 2354

Query Match

Best Local Similarity 100.0%; Score 102; DB 12; Length 87;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 kasqvdydgsym 26

QY 1 KASQSVYDGDGYM 15

RESULT 4

ENTRY S42194 #type fragment

TITLE

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change

21-Jul-1995

ACCESSIONS S42194

REFERENCE S42176

#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.

#journal Eur. J. Immunol. (1993) 23:2503-2510

#title Variable region gene selection of immunoglobulin G-expressing

B cells with specificity for a defined epitope on type II

#accession S42194

#status preliminary

#molecule_type DNA

#residues 1-88 #label MOJ

#cross-references EMBL:225458

SUMMARY #length 88 #checksum 4364

Query Match

Best Local Similarity 100.0%; Score 102; DB 12; Length 88;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 kasqvdydgsym 27

QY 1 KASQSVYDGDGYM 15

RESULT 5

ENTRY S42187 #type fragment

TITLE Ig kappa chain V region - mouse (fragment)

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change

21-Jul-1995

ACCESSIONS S42187

REFERENCE S42176

#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.

#journal Eur. J. Immunol. (1993) 23:2503-2510

#title Variable region gene selection of immunoglobulin G-expressing

B cells with specificity for a defined epitope on type II

#accession S42187

#status preliminary

#molecule_type DNA

#residues 1-90 #label MOJ

#cross-references EMBL:225444

SUMMARY #length 90 #checksum 9303

Query Match

Best Local Similarity 100.0%; Score 102; DB 12; Length 90;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 kasqvdydgsym 29

QY 1 KASQSVYDGDGYM 15

RESULT 6

ENTRY A38601 #type fragment

TITLE Ig kappa chain V region (IG3) - mouse (fragment)

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change

23-Mar-1993

ACCESSIONS A38601

REFERENCE A38601

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##authors Goshorn, S.C.; Retzel, E.; Jermerson, R.
##journal J. Biol. Chem. (1991) 266:2134-2142
##title Common structural features among monoclonal antibodies
binding the same antigenic region of cytochrome c.
##cross-references MUID:91115823
##accession A38601
##status preliminary
##molecule_type mRNA
##residues 1-93 ##label GOS
##cross-references GB:M57978
SUMMARY
#length 93 #checksum 6635

Query Match 100.0%; Score 102; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.14e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 kasqsvdydgsymn 19
|||||
Qy 1 KASQSVDYDGD SYMN 15

RESULT 7
ENTRY KWS43 #type complete
TITLE Ig kappa chain V region (PC7043) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
05-Apr-1995
ACCESSIONS A01937
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce
immunoglobulin diversity.
#cross-references MUID:79073152
#accession A01937
##molecule_type protein
##residues 1-111 ##label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
23-92 #disulfide_bonds #status predicted
SUMMARY #length 111 #molecular_weight 12002 #checksum 438

Query Match 100.0%; Score 102; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.14e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsymn 38
|||||
Qy 1 KASQSVDYDGD SYMN 15

RESULT 8
ENTRY KWS83 #type complete
TITLE Ig kappa chain V region (PC7183) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
30-Sep-1993
ACCESSIONS B01937; A01937
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce
immunoglobulin diversity.
#cross-references MUID:79073152

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##accession B01937
##molecule_type protein
##residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
23-92 #disulfide_bonds #status predicted
SUMMARY #length 111 #molecular_weight 11952 #checksum 9

Query Match 100.0%; Score 102; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.14e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsymn 38
|||||
Qy 1 KASQSVDYDGD SYMN 15

RESULT 9
ENTRY KWS08 #type complete
TITLE Ig kappa chain V region (PC6308) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
30-Sep-1993
ACCESSIONS C01937; A01937
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce
immunoglobulin diversity.
#cross-references MUID:79073152
#accession C01937
##molecule_type protein
##residues 1-111 ##label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
23-92 #disulfide_bonds #status predicted
SUMMARY #length 111 #molecular_weight 12071 #checksum 2195

Query Match 100.0%; Score 102; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.14e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsymn 38
|||||
Qy 1 KASQSVDYDGD SYMN 15

RESULT 10
ENTRY KWS69 #type complete
TITLE Ig kappa chain V region (PC7769) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
30-Sep-1993
ACCESSIONS E01937; A01937
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce
immunoglobulin diversity.
#cross-references MUID:79073152
#accession E01937
##molecule_type protein

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##residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
23-92 #disulfide bonds #status predicted
SUMMARY #length 111 #molecular-weight 12011 #checksum 562

Query Match 100.0%; Score 102; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.14e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqslvdgdsym 38
|||||:|||||
Qy 1 KASQSVYDGD SYM 15

RESULT 11
ENTRY KWMS10 #type complete
TITLE Ig kappa chain V region (PC7210) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 30-Sep-1993
ACCESSIONS D01937; A01937
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce immunoglobulin diversity.

#cross-references M01D:79073152
#accession D01937
##molecule_type protein
##residues 1-110 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
23-92 #disulfide bonds #status predicted
SUMMARY #length 110 #molecular-weight 11950 #checksum 6378

Query Match 94.1%; Score 96; DB 2; Length 110;
Best Local Similarity 93.3%; Pred. No. 3.65e-07;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqslvdgdsym 38
|||||:|||||
Qy 1 KASQSVYDGD SYM 15

RESULT 12
ENTRY S19971 #type fragment
TITLE Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-1995
ACCESSIONS S19971; S19973
REFERENCE S19963
#authors Weissenhorn, W.; Riethmüller, G.; Weiss, E.M.; Rieber, E.P.
#submission submitted to the EMBL Data Library, March 1992
#description Structural characterization of CD4 mAb.

#accession S19971
##molecule_type mRNA
##residues 1-112 ##label WEI
#cross-references EMBL:X65091
#experimental_source clone M-T310

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#accession S19973
##molecule_type mRNA
##residues 1-112 ##label WEI
#cross-references EMBL:X65092
#experimental_source M-T404
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 112 #checksum 4782

Query Match 94.1%; Score 96; DB 5; Length 112;
Best Local Similarity 93.3%; Pred. No. 3.65e-07;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqslvdgdsym 38
|||||:|||||
Qy 1 KASQSVYDGD SYM 15

RESULT 13
ENTRY PHI226 #type fragment
TITLE Ig kappa chain precursor V region (M-T310) - human (fragment)
ORGANISM #formal name Homo sapiens #common name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 30-Apr-1995
ACCESSIONS PHI226
REFERENCE PHI224
#authors Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz, H.; Weiss, E.H.; Rieber, E.P.; Riethmüller, G.; Weidle, U.H.

#journal Gene (1992) 121:271-278
#title Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the human interleukin-2 receptor.
#accession PHI226
##molecule_type mRNA
##residues 1-131 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
1-20 #domain signal sequence #status predicted #label SIG\
21-131 #product Ig light chain V region #status predicted #label MAT
SUMMARY #length 131 #checksum 4648

Query Match 94.1%; Score 96; DB 5; Length 131;
Best Local Similarity 93.3%; Pred. No. 3.65e-07;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 44 kasqslvdgdsym 58
|||||:|||||
Qy 1 KASQSVYDGD SYM 15

RESULT 14
ENTRY S09966 #type fragment
TITLE Ig kappa chain V-J region (IE10) - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 30-Sep-1993
ACCESSIONS S09966
REFERENCE S09955
#authors Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.

#journal Eur. J. Immunol. (1990) 20:771-777
#title Variable region sequences of pathogenic anti-mouse red blood

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cell autoantibodies from autoimmune NZB mice.

#cross-references MUID:90269328
#accession S09966
##molecule type mRNA
##residues 1-111 ##label REI
##cross-references EMEL:X51854
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 111 #checksum 3572

Query Match 93.1%; Score 95; DB 5; Length 111;
Best Local Similarity 93.3%; Pred. No. 5.82e-07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 24 kasxsvdydgdysmn 38
|||||
Qy 1 KASQSVDYDGDYSMN 15

RESULT 15
ENTRY KVMSC1 #type complete
TITLE Ig kappa chain V region (CBPC 101) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 05-Apr-1995
ACCESSIONS A01936
REFERENCE A93822
#authors McKean, D.J.; Bell, M.; Potter, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1978) 75:3913-3917
#title Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.
#cross-references MUID:79012520
#accession A01936

##molecule type protein
##residues 1-111 ##label MCK
COMMENT This chain was isolated from a myeloma protein.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE 23-92
SUMMARY #length 111 #molecular-weight 11964 #checksum 1507

Query Match 92.2%; Score 94; DB 2; Length 111;
Best Local Similarity 86.7%; Pred. No. 9.27e-07;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 24 kasqsvdytqesymn 38
|||||
Qy 1 KASQSVDYDGDYSMN 15

Search completed: Tue Mar 18 10:09:56 1997
Job time : 11 secs.

W P S R E F
***** (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 15:53:20 1997; MafPar time 1.91 Seconds
80.791 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-16
Description: (1-15) from US08612929.pep
Perfect Score: 102
Sequence: 1 KASQSDYDCSYMN 15

Scoring table: PAM 150
Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 18.026; Variance 58.782; scale 0.307

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	102	100.0	15	13	R70195	Mab 3B9 light chain C
2	102	100.0	19	12	R66143	CD-4 antibody variabl
3	102	100.0	106	6	R33309	MAE15 light chain.
4	102	100.0	111	11	R60302	Anti HIV antibody lig
5	102	100.0	111	6	R33305	MAE11 light chain.
6	102	100.0	111	11	R60306	Chimeric anti HIV ant
7	102	100.0	111	10	R55127	Mouse-human chimeric
8	102	100.0	111	10	R55123	Mouse anti-HIV mu5.5
9	102	100.0	111	1	P90541	Immunoglobulin L chai
10	102	100.0	112	5	R24575	Human x mouse modifie
11	102	100.0	115	1	R04134	Anti-Leu 3a light cha
12	102	100.0	120	9	R48618	Sequence of the monoc

13	102	100.0	131	13	R75355	Humanized antibody 3B
14	102	100.0	131	1	P90543	Amino acids sequence
15	102	100.0	131	1	R04132	Anti-Leu 3a light cha
16	102	100.0	131	13	R70202	Humanized antibody 3B
17	102	100.0	132	13	R70189	Mouse MAb 3B9 light c
18	99	97.1	218	6	R33312	Humanised MAE11 Versi
19	98	96.1	239	16	R79866	Anti-EGFR single chai
20	96	94.1	131	6	R32123	Anti-CD4 antibody MT
21	83	81.4	209	12	R63117	Light chain of anti-H
22	70	68.6	11	12	R66140	CD-4 antibody variabl
23	63	61.8	131	1	R05089	Light chain variable
24	60	58.8	259	18	R98901	Penicillin-resistant
25	56	54.9	108	8	R42633	Light chain variable
26	56	54.9	108	15	R80942	Antibody MK2-CH(gamma
27	56	54.9	111	9	R47494	Murine anti-CD18 Ab 6
28	56	54.9	111	13	R65174	Region producing huma
29	56	54.9	111	13	R65172	Murine NM-01 variable
30	56	54.9	111	9	R48622	Sequence of the human
31	56	54.9	111	9	R48623	Sequence of the human
32	56	54.9	111	9	R47492	Humanised anti-CD18 A
33	56	54.9	112	14	R79158	Human IgE receptor-bi
34	56	54.9	112	3	R13089	Murine 1B4 light chai
35	56	54.9	112	2	R10539	Chimeric MAb 9.2.27 1
36	56	54.9	112	15	R79156	Human IgE receptor-bi
37	56	54.9	121	9	R48615	Sequence of the monoc
38	56	54.9	131	6	R29008	p64-k4 protein produc
39	55	53.9	111	15	R85236	Murine 206 antibody v
40	55	53.9	111	15	R85242	Humanised antibody va
41	55	53.9	113	16	R79892	Anti-EGFR antibody li
42	55	53.9	113	16	R79891	Anti-EGFR antibody li
43	55	53.9	113	16	R79882	Anti-EGFR antibody li
44	55	53.9	131	6	R30881	Antibody 4A2 light ch
45	54	52.9	111	5	R25725	Humanised VI. region o

ALIGNMENTS

RESULT 1
ID R70195 standard; Protein; 15 AA.
AC R70195;
DT 20-SEP-1995 (first entry)
DE MAb 3B9 light chain CDR.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
PI WPI; 95-123387/16.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Page 54; 97pp; English.
CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC chains were cloned into pGEM7f+ and transformed into E. coli
CC DH5-alpha. A light chain cDNA clone was sequenced (083490) that

CC encoded the protein given in R70189. 3 CDRs (R70195-97) were
 CC identified.
 SQ Sequence 15 AA;

Query Match 100.0%; Score 102; DB 13; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.86e-04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 kasqsvdydgdsgym 15
 |||||
 Qy 1 KASQSVYDGDGYM 15

RESULT 2

ID R66143 standard; peptide; 19 AA.
 AC R66143;
 DT 12-JUL-1995 (first entry)
 DE CD-4 antibody variable region complementary peptide.
 KW CD-4 antibody variable region; complementary peptide;
 KW extra-corporeal blood circulation; cell filter material.
 OS Synthetic.
 PN J06269663-A.
 PD 27-SEP-1994.
 PF 17-MAR-1993; 057206.
 PR 17-MAR-1993; JP-057206.
 PA (TOYM) TOY080 KK.
 DR WPI; 94-346316/43.
 PT Material for collecting cells positive for CD-4 antibody -
 PT comprises nonwoven fabric having keto-alkyl halide functional gp
 PS Example 1; Page 6; 9pp; Japanese.
 CC R66140-R66146 are peptides complementary to the variable region
 CC of the CD-4 antibody, these peptides are fixed onto a claimed
 CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with
 CC keto-alkyl halide functional groups. This material can be used
 CC as a filter for CD-4 positive cells in a medical treatment
 CC involving the extra-corporeal circulation of blood.
 SQ Sequence 19 AA;

Query Match 100.0%; Score 102; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.86e-04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 kasqsvdydgdsgym 19
 |||||
 Qy 1 KASQSVYDGDGYM 15

RESULT 3

ID R33309 standard; Protein; 106 AA.
 AC R33309;
 DT 05-JUL-1993 (first entry)
 DE Mae15 light chain.
 KW Antibody; high affinity; FCEH; low affinity; FCEH;
 KW IgE receptor; histamine; mast cell; basophil; Kabat;
 KW CDR; murine; MAE11; MAE13; MAE15; MAE17.
 OS Synthetic.
 PN W09304173-A.
 PD 04-MAR-1993.
 PF 14-AUG-1992; U06860.
 PR 14-AUG-1991; US-744768.
 PR 07-MAY-1992; US-879495.
 PA (GETH) GENENTECH INC.
 PI Jardieu PM, Presta LG;
 DR WPI; 93-094004/11.

PT Polypeptide(s) binding to specific Fc epsilon receptors - act as
 PT IgE antagonists; useful for treating and preventing IgE-mediated
 PT disorders e.g. allergies
 PS Disclosure; Fig 2; 113pp; English.
 CC Antibodies capable of binding FCEH-bound IgE but which are
 CC substantially incapable of binding FCEH-bound IgE or inducing
 CC histamine release from mast cells or basophils, comprise a human
 CC Kabat CDR domain into which has been substituted a positionally
 CC analogous residue from a Kabat CDR domain of the murine anti-huIgE
 CC antibodies MAE11, MAE13, MAE15 or MAE17.
 SQ Sequence 106 AA;

Query Match 100.0%; Score 102; DB 6; Length 106;
 Best Local Similarity 100.0%; Pred. No. 2.86e-04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgdsgym 38
 |||||
 Qy 1 KASQSVYDGDGYM 15

RESULT 4

ID R60302 standard; Protein; 111 AA.
 AC R60302;
 DT 09-MAR-1995 (first entry)
 DE Anti HIV antibody light chain variable region.
 KW Antibody; heavy chain; light chain; human immunodeficiency virus;
 KW HIV; acquired immune deficiency syndrome; AIDS: treatment;
 KW prophylaxis; Mus musculus; Homo sapiens.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT Region 1..23
 FT /label= Framework region 1.
 FT Region 24..38
 FT /label= CDR1.
 FT Region 39..53
 FT /label= Framework region 2.
 FT Region 54..60
 FT /label= CDR2.
 FT Region 61..92
 FT /label= Framework region 3.
 FT Region 93..101
 FT /label= CDR3.
 FT Region 102..111
 FT /label= Framework region 4.
 PN W09415969-A.
 PD 21-JUL-1994.
 PF 14-JAN-1993; J00039.
 PR 14-JAN-1993; AD-032671.
 PR 14-JAN-1993; WO-J00039.
 PA (KAGA) CEMO SERO THERAPEUTIC RES INST.
 PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
 PI Tokiyoshi S;
 DR WPI; 94-249145/30.
 DR N-PSDB; Q70372.
 PT Recombinant chimeric anti HIV antibody - useful for the treatment
 PT and prevention of HIV
 PS Claim 15; Figure 4; 51pp; Japanese.
 CC The recombinant antibody light chain has neutralising activity
 CC against HIV. Chimeric antibodies comprising both mouse and human
 CC sequences are useful in the treatment/prevention of AIDS caused by
 CC HIV.
 SQ Sequence 111 AA;

Query Match 100.0%; Score 102; DB 11; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38
|||||
Qy 1 KASQSVDYDGSYMN 15

RESULT 5

ID R33305 standard; protein; 111 AA.
AC R33305;
DT 05-JUL-1993 (first entry)
DE Maell light chain.
KW Antibody; high affinity; FCEH; low affinity; FCEL;
KW IgE receptor; histamine; mast cell; basophil; Kabat;
KW CDR; murine; MAE11; MAE13; MAE15; MAE17.
OS Synthetic.
PN W09304173-A.
PD 04-MAR-1993.
PF 14-AUG-1992; 006860.
PR 14-AUG-1991; US-744768.
PR 07-MAY-1992; US-879495.
PA (GETH) GENENTECH INC.
PI Jardieu PM, Presta LG;
DR WPI; 93-094004/11.
DT Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
PT disorders e.g. allergies
PS Disclosure; Fig 2; 113pp; English.
CC Antibodies capable of binding FCEL-bound IgE but which are
CC substantially incapable of binding FCEH-bound IgE or inducing
CC histamine release from mast cells or basophils, comprise a human
CC Kabat CDR domain into which has been substituted a positionally
CC analogous residue from a Kabat CDR domain of the murine anti-huIgE
CC antibodies MAE11, MAE13, MAE15 or MAE17.
SQ Sequence 111 AA;

Query Match 100.0%; Score 102; DB 6; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38
|||||
Qy 1 KASQSVDYDGSYMN 15

RESULT 6

ID R60306 standard; Protein; 111 AA.
AC R60306;
DT 13-MAR-1995 (first entry)
DE Chimeric anti HIV antibody light chain variable region.
KW Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS: treatment;
KW prophylaxis; Mus musculus; Homo sapiens.
OS Chimeric Homo sapiens
OS Chimeric Mus musculus.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= Framework region 1.
FT Region 24..38
FT /label= CDR1.
FT /note= "Mouse derived amino acid sequence."
FT Region 39..53

FT /label= Framework region 2.
FT Region 54..60
FT /label= CDR2.
FT /note= "Mouse derived amino acid sequence."
FT Region 61..92
FT /label= Framework region 3.
FT Region 93..101
FT /label= CDR3.
FT /note= "Mouse derived amino acid sequence."
FT Region 102..111
FT /label= Framework region 4.
PN W09415969-A.
PD 21-JUL-1994.
PF 14-JAN-1993; J00039.
PR 14-JAN-1993; AU-032671.
PR 14-JAN-1993; WO-J00039.
PA (KAGA) CEMO SERO THERAPEUTIC RES INST.
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiozaki K;
PI Tokiyoshi S;
DR WPI; 94-249145/30.
DR N-PSDB; R60306.
PT Recombinant chimeric anti HIV antibody - useful for the treatment
PT and prevention of HIV
PS Claim 14; Figure 12; 51pp; Japanese.
CC The recombinant antibody light chain has neutralising activity
CC against HIV. Chimeric antibodies comprising both mouse and human
CC sequences are useful in the treatment/prevention of AIDS caused by
CC HIV.
SQ Sequence 111 AA;

Query Match 100.0%; Score 102; DB 11; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38
|||||
Qy 1 KASQSVDYDGSYMN 15

RESULT 7

ID R55127 standard; Protein; 111 AA.
AC R55127;
DT 30-JAN-1995 (first entry)
DE Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.
KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
KW human immunodeficiency virus; variable region; VL chain; murine;
KW chimeric; humanised.
OS Chimeric Mus musculus.
OS Chimeric Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT /note= "human"
FT Region 24..38
FT /label= CDR1
FT /note= "murine"
FT Region 39..53
FT /label= FR2
FT Region 54..60
FT /label= CDR2
FT /note= "murine"
FT Region 61..92
FT /label= FR3
FT /note= "human"

FT Region 93..101
/label= CDR3
FT /note= "murine"
FT Region 102..111
FT /label= FR4
FT /note= "human"
PN J06125783-A.
PD 10-MAY-1994.
PE 28-DEC-1991; 359808.
PR 28-DEC-1991; JP-359808.
PA (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
DR WPI: 94-187942/23.
DR N-PSDB; Q65558.
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
and recombinant antibody consisting of the H- and L-chains,
useful in AIDS therapy
PS Claim 5; Fig 12; 22pp; Japanese.
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (R55120-R55123). The murine anti-HIV CDRs were
CC introduced into human framework regions to construct chimeric
CC antibodies (R55124-R55127).
SQ Sequence 111 AA;

Query Match 100.0%; Score 102; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38
|||||
Qy 1 KASQSVDYDGSYMN 15

RESULT 8

ID R55123 standard; Protein; 111 AA.
AC R55123;
DT 27-JAN-1995 (first entry)
DE Mouse anti-HIV mu5.5 light chain variable region.
KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
human immunodeficiency virus; variable region; VH chain; murine.
OS Mus musculus.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT Region 24..38
FT /label= CDR1
FT Region 39..53
FT /label= FR2
FT Region 54..60
FT /label= CDR2
FT Region 61..92
FT /label= FR3
FT Region 93..101
FT /label= CDR3
FT Region 102..111
FT /label= FR4
PN J06125783-A.
PD 10-MAY-1994.
PE 28-DEC-1991; 359808.
PR 28-DEC-1991; JP-359808.
PA (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
DR WPI: 94-187942/23.
DR N-PSDB; Q65554.
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -

PT and recombinant antibody consisting of the H- and L-chains,
useful in AIDS therapy
PS Example 3; Fig 4; 22pp; Japanese.
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (R55120-R55123). The murine anti-HIV CDRs were
CC introduced into human framework regions to construct chimeric
CC antibodies (R55124-R55127).
SQ Sequence 111 AA;

Query Match 100.0%; Score 102; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38
|||||
Qy 1 KASQSVDYDGSYMN 15

RESULT 9

ID P90541 standard; protein; 111 AA.
AC P90541;
DT 20-OCT-1989 (first entry)
DE Immunoglobulin L chain variable region.
KW Immunoglobulin; L chain variable region; HIV.
OS Mus musculus
PN EP-327000-A.
PD 09-AUG-1989.
PF 30-JAN-1989; 101583.
PR 30-JAN-1988; JP-20255.
PR 08-JUL-1988; JP-171385.
PA (****) The Chemo-Sero-Therapeutic Research Institute.
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,
PI Takatsuki K;
DR WPI: 89-229050/32.
DR N-PSDB; N90491, N90492, N90493.
PT Chimeric anti-human immune virus antibodies - contg. mouse variable
PT regions and human constant regions for diagnosis, treatment and
PT prevention of AIDS
PS Claim 5; page 15; 33pp; English.
CC The sequence is an L chain variable region from an immunoglobulin with
CC anti-HIV neutralising activity. See N90491-3, and N90495.
SQ Sequence 111 AA;

Query Match 100.0%; Score 102; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38
|||||
Qy 1 KASQSVDYDGSYMN 15

RESULT 10

ID R24575 standard; Protein; 112 AA.
AC R24575;
DT 08-DEC-1992 (first entry)
DE Human x mouse modified anti-HIV antibody Light chain RL0.5beta.
KW Heavy; light; CDR; HIV; AIDS; REI; 0.5beta.
OS Synthetic.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT Region 24..38

FT /label= CDR1 39..53
FT Region
FT /label= FR2 54..60
FT Region
FT /label= CDR2 61..92
FT Region
FT /label= FR3 93..101
FT Region
FT /label= CDR3 102..112
FT Region
FT /label= FR4
PN J04141095-A.
PD 14-MAY-1992.
PF 02-OCT-1990; 266091.
PR 02-OCT-1990; JP-266091.
PA (KAGA) KAGAKU OYOBI KESSEI RYOH.
DR WPI; 92-212765/26.
PT New recombinant modified anti-HIV antibodies - comprise human x
PT mouse modified antibody H and L chains
PS Disclosure; Fig 2; 15pp; Japanese.
CC The framework regions (FR) are derived from the human antibody
CC REL. The CDRs are mouse monoclonal antibody 0.5beta derived
CC sequences. The anti-HIV modified antibody can be used for the
CC prophylaxis and treatment of AIDS.
CC Specific examples of the H chain are given in R24556-58 and
CC R24560-62. A specific example of the L chain is given in R24575.
SQ Sequence 112 AA;

Query Match 100.0%; Score 102; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38
|||||
Qy 1 KASQSVDYDGD SYMN 15

RESULT 11
ID R04134 standard; protein; 115 AA.
AC R04134;
DT 06-SEP-1990 (first entry)
DE Anti-leu 3a light chain variable region gene product, KOL/206 V1.
KW HIV; AIDS; anti-leu3a; vaccine; ds.
OS Mus musculus.
PN EP-365209-A.
PD 25-APR-1990.
PF 11-OCT-1989; 010415.
PR 17-OCT-1988; US-260558.
PA (BECT) Becton Dickinson Co.
PI Hinton R, Oi VT;
DR WPI; 90-126329/17.
DR N-PSDB; Q04041.
PT New chimeric variants of murine antibody anti-leucine -
PT contg. human antibody regions, and DNA encoding sequences.
PS Claim 4; Fig 4; 12pp; English.
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
CC used to form chimeric mouse-variable, human-constant region Abs
CC suggested as being useful as a vaccine to HIV.
SQ Sequence 115 AA;

Query Match 100.0%; Score 102; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 kasqsvdydgsym 41
|||||
Qy 1 KASQSVDYDGD SYMN 15

RESULT 12
ID R48618 standard; Protein; 120 AA.
AC R48618;
DT 03-SEP-1994 (first entry)
DE Sequence of the monoclonal antibody BAT123 light chain
DE variable region.
KW Epitope; monoclonal antibody; BAT123; variable light.
OS Synthetic.
PN W09404574-A.
PD 03-MAR-1994.
PF 24-AUG-1993; U07967.
PR 24-AUG-1992; W0-007111.
PR 22-APR-1993; US-039457.
PA (NISP) NISSIN SHOKUHIN KAISHA LTD.
PI Onno T;
DR WPI; 94-083117/10.
PT New humanised antibody specific for epitope on HIV-1 gp 120 -
PT able to neutralise infection of HG cells, also nucleic acid
PT encoding it, useful for passive immunisation to treat or prevent
PT HIV-1 infection
PS Example; Page 47; 91pp; English.
CC GPCR is a portion of HIV-1 gp120 or gp160 protein. Monoclonal
CC antibodies (MAbs) that react with this and which have the capacity
CC to neutralise the infection of H9 cells in culture by live HIV-1
CC strains MN and 11IB are claimed. Specifically illustrating the
CC invention are the murine MAb (designated NM-01) produced by
CC hybridoma cell line HB 10726 which is deposited under ATCC No. HB
CC 10726. The DNA sequences of the variable regions of the heavy and
CC light chains of MAB NM-01 were cloned by PCR using cDNA generated
CC from hybridoma HB 10726 cytoplasmic RNA as template. The DNA was
CC then sequenced. The DNA and deduced AA sequences are given in
CC Q56685/R48613; Q56686/R48615. Resequencing the variable regions
CC of MAB NM-01 resulted in the sequences set out in Q56687/R48614
CC and Q56688/R48616. The heavy chain variable region of NM-01
CC differs from that of the MAB BA123, as reported in Liou et al.,
CC by 46 AAs out of a total of 120. The light chain variable regions
CC of these two Abs differ by 23 AAs. Significantly, the three CDRs
CC in the heavy chain (V-H) of the NM-01 molecule are about 41 to 90%
CC different in sequence from those of BAT123, while the sequences of
CC the three CDRs in the light chain (V-L) vary by about 29-47%
CC compared to NM-01.
SQ Sequence 120 AA;

Query Match 100.0%; Score 102; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 kasqsvdydgsym 38
|||||
Qy 1 KASQSVDYDGD SYMN 15

RESULT 13
ID R75355 standard; Protein; 131 AA.
AC R75355;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW MAb; interleukin-4; IL-4; allergy.

OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Sig_peptide
FT Region 43..57
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 73..79
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 112..120
FT /label= CDR
FT /note= "complementarity determining region"
PN WO9507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross M5, Holmes SD, Sylvester DR;
DR WPI: 95-123387/16.
DR N-PSDB; Q73986.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions
PS Disclosure; Fig.5; 97pp; English.
CC A humanized antibody light chain variable region and signal sequence is given in R75355. The signal sequence is also provided in R70194. The sequences of the first 2 CDRs are identical to mouse anti-human IL-4 MAb 3B9 light chain CDRs (given in R70195-96), but the third (R70201) differs by a single amino acid from the native mouse CDR (R70197).
SQ Sequence 131 AA;
Query Match 100.0%; Score 102; DB 13; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 43 kasqsvdydgsym 57
QY 1 KASQSVDYDGD SYNM 15
RESULT 14
ID P90543 standard; protein; 131 AA.
AC P90543;
DT 20-OCT-1989 (first entry)
DE Amino acids sequence of a V chi region gene.
KW V cji region; immunoglobulin; L chain variable region; HIV.
OS Mus musculus
PN EP-327000-A.
PD 09-AUG-1989.
PF 30-JAN-1989; 101583.
PR 30-JAN-1988; JP-20255.
PR 08-JUL-1988; JP-171385.
PA The Chemo-Sero-Therapeutic Research Institute.
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T, Takatsuki K;
DR WPI: 89-229050/32.
DR N-PSDB; N90495.
PT Chimeric anti-human immune virus antibodies - contg. mouse variable regions and human constant regions for diagnosis, treatment and prevention of AIDS

PS Disclosure; Fig 8; 33pp; English.
CC The sequence is encoded by a V chi region gene (see N90495).
CC The sequence from Asp 21 encodes the L chain variable region.
SQ Sequence 131 AA;
Query Match 100.0%; Score 102; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 44 kasqsvdydgsym 58
QY 1 KASQSVDYDGD SYNM 15
RESULT 15
ID R04132 standard; protein; 131 AA.
AC R04132;
DT 06-SEP-1990 (first entry)
DE Anti-Leu 3a light chain variable region gene product, 206 Vx.
KW HIV; AIDS; anti-Leu3A; vaccine; ds.
OS Mus musculus.
PN EP-365209-A.
PD 23-APR-1990.
PF 11-OCT-1989; 010415.
PR 17-OCT-1988; US-260558.
PA (BECT) Becton Dickinson Co.
PI Hinton R, Oi VT;
DR WPI: 90-126329/17.
DR N-PSDB; Q04039.
PT New chimeric variants of murine antibody anti-leucine - PT contg. human antibody regions, and DNA encoding sequences.
PS Claim 1; Fig 2; 12pp; English.
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be CC used to form chimeric mouse-variable, human-constant region Abs CC suggested as being useful as a vaccine to HIV.
SQ Sequence 131 AA;
Query Match 100.0%; Score 102; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 44 kasqsvdydgsym 58
QY 1 KASQSVDYDGD SYNM 15
RESULT 16
ID R70202 standard; Protein; 131 AA.
AC R70202;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain.
KW Humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy.
OS Homo sapiens.
PN WO9507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross M5, Holmes SD, Sylvester DR;
DR WPI: 95-123387/16.
DR N-PSDB; Q83520.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Page 71-72; 97pp; English.
CC A humanized antibody light chain variable region and signal
CC sequence is given in R75355. The signal sequence is also
CC provided in R70194. The sequences of the 3 CDRs
CC are identical to mouse anti-human IL-4 Mab 389 light chain
CC CDRs (given in R70195-97).
SQ Sequence 131 AA;

Query Match 100.0%; Score 102; DB 13; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 kasqsvdydgsymn 57
|||||
Qy 1 KASQSVDYDGD SYMN 15

RESULT 17
ID R70189 standard; Protein; 132 AA.
AC R70189;
DT 20-SEP-1995 (first entry)
DE Mouse Mab 389 light chain.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy.
OS Mus sp.

FH Key Location/Qualifiers

FT Peptide 1..20
FT /Label= Sig_peptide
FT Region 44..58
FT /Label= CDR
FT /note= "complementarity determining region"
FT Region 74..80
FT /Label= CDR
FT /note= "complementarity determining region"
FT Region 113..121

FT /Label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.
PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

DR N-PSDB; Q83490.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.1; 97pp; English.

CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC chains were cloned into pCEW7f+ and transformed into E. coli
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for
CC antibody engineering.

SQ Sequence 132 AA;

Query Match 100.0%; Score 102; DB 13; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.86e-04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 44 kasqsvdydgsymn 58
|||||
Qy 1 KASQSVDYDGD SYMN 15

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Job time : 15 secs.

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3

Query Match 100.0%; Score 35; DB 5; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.92e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60
Qy 1 AASLES 7

RESULT 2

ID KV3Q MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7169).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]

RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; E01937; KWS69.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 9CB705B9 CRC32;

Query Match 100.0%; Score 35; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.92e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60
Qy 1 AASLES 7

RESULT 3

ID KV3N MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7183).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]

RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; B01937; KWS83.

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4

DR HSP; P01679; IGGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 041902B8 CRC32;

Query Match 100.0%; Score 35; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.92e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60
Qy 1 AASLES 7

RESULT 4

ID KV3M MOUSE STANDARD; PRT; 111 AA.
AC P01655;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7043).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]

RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; A01937; KWS43.
DR HSP; P01679; IGGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; ADC728CA CRC32;

Query Match 100.0%; Score 35; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.92e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60
Qy 1 AASLES 7

RESULT 5

ID KV3L MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IC KAPPA CHAIN V-III REGION (CBPC 101).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KWSCL.
DR HSP; P01679; IGBB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; A2AC84C7 CRC32;

Query Match 100.0%; Score 35; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.92e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60
|||||||
Qy 1 AASNL5 7

RESULT 6
ID YIEO HAEIN STANDARD; PRT; 463 AA.
AC P44903;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL PROTEIN H10852.
GN H10852.
OS HAEMOPHILUS INFLUENZAE.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20;
RX MEDLINE; 95350630.
RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA KERIYAGE A.R., BUIT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GECHAGEN N.S.M.,
RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
RA VENTER J.C.;
RL SCIENCE 269:496-512(1995).

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
(PROBABLE).
CC -!- SIMILARITY: STRONG, TO E.COLI YIEO.
CC -!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN

CC AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
DR EMBL; L45490; G1005907; -.
DR EMBL; U32766; G925898; -.
KW HYPOTHETICAL PROTEIN; TRANSPORT; TRANSMEMBRANE; INNER MEMBRANE.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 49 69 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 107 127 POTENTIAL.
FT TRANSMEM 139 159 POTENTIAL.
FT TRANSMEM 165 185 POTENTIAL.
FT TRANSMEM 197 217 POTENTIAL.
FT TRANSMEM 225 245 POTENTIAL.
FT TRANSMEM 267 287 POTENTIAL.
FT TRANSMEM 298 318 POTENTIAL.
FT TRANSMEM 328 348 POTENTIAL.
FT TRANSMEM 354 374 POTENTIAL.
FT TRANSMEM 393 413 POTENTIAL.
FT TRANSMEM 429 449 POTENTIAL.
SQ SEQUENCE 463 AA; 50002 MW; 5CAE40A0 CRC32;

Query Match 100.0%; Score 35; DB 10; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.92e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 94 aasles 100
|||||||
Qy 1 AASNL5 7

RESULT 7
ID VP9 WTVNU STANDARD; PRT; 313 AA.
AC P31611;
DT 01-JUL-1993 (REL. 26, CREATED)
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE STRUCTURAL PROTEIN P9 (CAPSOMERE PROTEIN P9) (PROTEIN P9S11).
OS WOUND TUMOR VIRUS (STRAIN NJ) (WTV).
OC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; PHYTOREOVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92074261.
RA HILLMAN B.I., ANZOILA J.V., HALPERN B.T., CAVILEER T.D., NUSS D.L.;
RL VIROLOGY 185:896-900(1991).
CC -!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.
DR EMBL; M77020; G336173; -.
DR PIR; C41705; QMXRW.
KW NONSTRUCTURAL PROTEIN.
SQ SEQUENCE 313 AA; 35551 MW; D42189CE CRC32;

Query Match 97.1%; Score 34; DB 9; Length 313;
Best Local Similarity 85.7%; Pred. No. 4.16e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 294 aasles 300
|||||||
Qy 1 AASNL5 7

RESULT 8
ID VP9 WTV STANDARD; PRT; 313 AA.
AC P12326;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)

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DE STRUCTURAL PROTEIN P9 (CAPSOMERE PROTEIN P9) (PROTEIN P9S11).
 GN S11.
 OS ROUND TUMOR VIRUS (HTV).
 OC VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; PHYTOREOVIRUSES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89263810.
 RA DALL D.J., ANZOLA J.V., XU Z., NUSS D.L.;
 RL NUCLEIC ACIDS RES. 17:3599-3599(1989).
 CC -!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.
 DR EMBL; X14219; G62265; -.
 DR PIR; S04139; OMXRT.
 SQ SEQUENCE 313 AA; 35606 MW; 85FB39FC CRC32;

Query Match 97.1%; Score 34; DB 9; Length 313;
 Best Local Similarity 85.7%; Pred. No. 4.16e+00;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 294 aasnlde 300
 |||||
 Qy 1 AASNLES 7

RESULT 9
 ID KL68 DROME STANDARD; PRT; 784 AA.
 AC P46867;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE KINESIN-LIKE PROTEIN KLP68D.
 GN KLP68D OR KLP5.
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95050960.
 RA PESAVENTO P.A., STEWART R.J., GOLDSTEIN L.S.B.;
 RL J. CELL BIOL. 127:1041-1048(1994).
 RN [2]
 RP SEQUENCE OF 220-342 FROM N.A.
 RX MEDLINE; 92020874.
 RA STEWART R.J., PESAVENTO P.A., MOERPEL D.N., GOLDSTEIN L.S.B.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 88:8470-8474(1991).
 CC -!- FUNCTION: PLUS-END DIRECTED MICROTUBULE MOTOR THAT MAY BE USED FOR
 CC ANTEROGRADE AXONAL TRANSPORT AND COULD CONCEIVABLY MOVE CARGOES IN
 CC FLY NEURONS DIFFERENT THAN THOSE MOVED BY KINESIN HEAVY CHAIN OR
 CC OTHER PLUS-END DIRECTED MOTORS.
 CC -!- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CENTRAL NERVOUS
 CC SYSTEM AND IN A SUBSET OF THE PERIPHERAL NERVOUS SYSTEM DURING
 CC EMBRYOGENESIS.
 CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
 CC II SUBFAMILY.
 DR EMBL; U15974; G565090; -.
 DR EMBL; M74431; G157792; -.
 DR FLYBASE; FBGN0004381; KLP68D.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN.
 KW MOTOR PROTEIN; MICROTUBULES; ATP-BINDING; COILED COIL.
 FT NP BIND 106 113 ATP (POTENTIAL).
 FT CONFLICT 220 221 SS -> TC (IN REF. 2).
 FT CONFLICT 338 342 GSPAK -> VRQV (IN REF. 2).
 SQ SEQUENCE 784 AA; 88193 MW; D705B2F2 CRC32;

Query Match 97.1%; Score 34; DB 5; Length 784;
 Best Local Similarity 85.7%; Pred. No. 4.16e+00;

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Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 751 aasnlde 757
 |||||
 Qy 1 AASNLES 7

RESULT 10
 ID KV30 MOUSE STANDARD; PRT; 111 AA.
 AC P01667;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IC KAPPA CHAIN V-III REGION (PC 6308).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 DR PIR; C01937; KVM508.
 DR HSP; P01679; IGGB.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12071 MW; F7865271 CRC32;

Query Match 94.3%; Score 33; DB 5; Length 111;
 Best Local Similarity 85.7%; Pred. No. 8.83e+00;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 54 tasnlde 60
 :|||||
 Qy 1 AASNLES 7

RESULT 11
 ID KICH HUMAN STANDARD; PRT; 456 AA.
 AC P35790;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE CHOLINE KINASE (EC 2.7.1.32).
 GN CHK OR CKI.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92316236.
 RA HOSKA K., TANAKA S., NIKAWA J.I., YAMASHITA S.;
 RL FEBS LETT. 304:229-232(1992).
 CC -!- FUNCTION: MAY HAVE A REGULATORY ROLE IN PHOSPHATIDYLCHOLINE
 CC SYNTHESIS.
 CC -!- CATALYTIC ACTIVITY: ATP + CHOLINE = ADP + O-PHOSPHOCHOLINE.

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CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- PATHWAY: INITIAL STEP OF THE CDP-CHOLINE AND CDP-ETHANOLAMINE
CC PATHWAYS.
CC -!- SIMILARITY: TO OTHER CHOLINE KINASES.
DR EMBL; D10704; G219541; -.
DR PIR; S23104; S23104.
DR MIM; 118491; 11TH EDITION.
KW TRANSFERASE; KINASE.
FT ACT SITE 303 303 BY SIMILARITY.
SQ SEQUENCE 456 AA; 52065 MW; BE4AB383 CRC32;

Query Match 94.3%; Score 33; DB 5; Length 456;
Best Local Similarity 85.7%; Pred. No. 8.83e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 39 asadles 45
|||||
QY 1 AASNLES 7

RESULT 12
ID KV1C HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (GAL).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 75059122.
RA LAURE C.J., WATANABE S., HILSCHMANN N.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 354:1503-1504 (1973).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
DR PIR; A01867; K1HUG1.
DR HSP; P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; CCAEAD2 CRC32;

Query Match 91.4%; Score 32; DB 5; Length 108;
Best Local Similarity 85.7%; Pred. No. 1.84e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 50 asadles 56
|||||
QY 1 AASNLES 7

RESULT 13
ID HMC3 MESAU STANDARD; PRT; 313 AA.
AC Q04649;
DT 01-JUN-1994 (REL. 29, CREATED)

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DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HOMEOBOX PROTEIN CDX-3.
GN CDX-3.
OS MESOCRITETUS AURATUS (GOLDEN HAMSTER).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93051335.
RA GERMAN M.S., WANG J., CHADWICK R.B., RUTTER W.J.;
RL GENES DEV. 6:2165-2176 (1992).
CC -!- FUNCTION: ACTS AS A TRANSCRIPTIONAL ACTIVATOR BY BINDING TO THE
CC FLAT ELEMENT WHICH IS A BETA-CELL-SPECIFIC TRANSCRIPTIONAL
CC ENHANCER FOUND IN THE INSULIN GENE.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: WITH OTHER "CAUDAL-TYPE" HOMEOBOX DOMAINS.
DR EMBL; X81404; G587458; -.
DR PIR; A46233; A46233.
DR HSP; P02833; ISAN.
DR PROSITE; PS00027; HOMEOBOX.
KW HOMEOBOX; DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN;
KW TRANSCRIPTION REGULATION; ACTIVATOR.
FT DOMAIN 46 53 POLY-ALA.
FT DNA_BIND 185 244 HOMEOBOX (BY SIMILARITY).
FT DOMAIN 113 124 HIS-RICH.
FT DOMAIN 249 259 POLY-GLN.
SQ SEQUENCE 313 AA; 33559 MW; 875299E1 CRC32;

Query Match 91.4%; Score 32; DB 4; Length 313;
Best Local Similarity 71.4%; Pred. No. 1.84e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 51 asadles 57
|||||
QY 1 AASNLES 7

RESULT 14
ID KV1B HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (AU).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 72189444.
RA SCHIEGL H., HILSCHMANN N.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 353:345-370 (1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE; 77022433.
RA FEHLHAMMER H., SCHIFFER M., EPP O., COLMAN P.M., LATTMAN E.E.,
RA SCHWAGER P., STEIGEMANN W., SCHRAMM H.J.;
RL BIOPHYS. STRUCT. MECH. 1:139-146 (1975).
CC -!- THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR
CC REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF
CC THE KAPPA CHAIN REI.
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS IS A BENCE-JONES PROTEIN.

DR PIR; A01862; K1HDAU.
 DR HSP; P01607; I1GM.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; B455AF00 CRC32;

Query Match 88.6%; Score 31; DB 5; Length 108;
 Best Local Similarity 100.0%; Pred. No. 3.73e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 51 asnles 56
 |||||
 Qy 2 ASNLES 7

RESULT 15
 ID KV3V MOUSE STANDARD; PRT; 108 AA.
 AC P01674;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (PC 2154).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 DR PIR; A01940; KWS54.
 DR HSP; P01679; IACY.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 39 53 FRAMEWORK 2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 61 92 FRAMEWORK 3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 108 FRAMEWORK 4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11699 MW; E28999CC CRC32;

Query Match 88.6%; Score 31; DB 5; Length 108;
 Best Local Similarity 100.0%; Pred. No. 3.73e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 asnles 60
 |||||
 Qy 2 ASNLES 7

Search completed: Tue Mar 18 10:10:50 1997
 Job time : 8 secs.

WATERMAN

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 15:55:23 1997; MasPar time 3.55 Seconds
20.295 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-18
Description: (1-7) from US08612929.pep
Perfect Score: 35
Sequence: 1 AASNLES 7

Scoring table: PAM 150
Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 12.478; Variance 29.454; scale 0.424

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				§	
Result No.	Score	Match Length	ID	Description	Pred. No.
1	35	100.0	7 13	R70196	Mab 3B9 light chain C 1.22e+02
2	35	100.0	15 12	R66144	CD-4 antibody variabl 1.22e+02
3	35	100.0	106 6	R33309	MAE15 light chain. 1.22e+02
4	35	100.0	111 11	R60302	Anti HIV antibody lig 1.22e+02
5	35	100.0	111 10	R55127	Mouse-human chimeric 1.22e+02
6	35	100.0	111 11	R60306	Chimeric anti HIV ant 1.22e+02
7	35	100.0	111 10	R55123	Mouse anti-HIV mu5.5 1.22e+02
8	35	100.0	111 1	P90541	Immunoglobulin L chai 1.22e+02
9	35	100.0	112 5	R24575	Human x mouse modifie 1.22e+02
10	35	100.0	115 1	R04134	Anti-Leu 3a light cha 1.22e+02
11	35	100.0	131 13	R70202	Humanized antibody 3B 1.22e+02
12	35	100.0	131 6	R32123	Anti-CD4 antibody MT 1.22e+02

13 35 100.0 131 13 R75355 Humanized antibody 3B 1.22e+02
14 35 100.0 131 1 R04132 Anti-Leu 3a light cha 1.22e+02
15 35 100.0 131 1 P90543 Amino acids sequence 1.22e+02
16 35 100.0 132 13 R70189 Mouse Mab 3B9 light c 1.22e+02
17 31 88.6 7 14 R75490 Mouse antibody variab 4.13e+02
18 31 88.6 7 14 R75489 Mouse antibody variab 4.13e+02
19 31 88.6 8 18 R52530 306 light chain compl 4.13e+02
20 31 88.6 17 16 R85179 GM-CSF receptor alpha 4.13e+02
21 31 88.6 103 9 R47933 Light chain region of 4.13e+02
22 31 88.6 107 6 R30770 Consensus humanised m 4.13e+02
23 31 88.6 109 9 R47041 Sequence of the conse 4.13e+02
24 31 88.6 110 10 R60810 Light chain variable 4.13e+02
25 31 88.6 111 15 R85236 Murine 206 antibody v 4.13e+02
26 31 88.6 111 15 R85242 Humanised antibody va 4.13e+02
27 31 88.6 111 13 R65174 Region producing huma 4.13e+02
28 31 88.6 111 11 R60528 Light chain variable 4.13e+02
29 31 88.6 111 9 R48623 Sequence of the human 4.13e+02
30 31 88.6 111 9 R48622 Sequence of the human 4.13e+02
31 31 88.6 112 15 R79156 Human IgE receptor-bi 4.13e+02
32 31 88.6 112 14 R75431 Human thyroid stimula 4.13e+02
33 31 88.6 112 14 R79249 Light chain variable 4.13e+02
34 31 88.6 112 14 R79158 Human IgE receptor-bi 4.13e+02
35 31 88.6 120 9 R48620 Sequence of the light 4.13e+02
36 31 88.6 121 9 R48615 Sequence of the monoc 4.13e+02
37 31 88.6 131 6 R28668 p12-k2. 4.13e+02
38 31 88.6 131 6 R29008 p64-k4 protein produc 4.13e+02
39 31 88.6 215 12 R74781 Light chain of 59.1 a 4.13e+02
40 31 88.6 218 15 R75459 Mouse antibody F4-7 1 4.13e+02
41 31 88.6 218 15 R75457 Mouse antibody FB3-2 4.13e+02
42 31 88.6 230 11 R59801 Fusarium solani pisi 4.13e+02
43 31 88.6 230 9 R46295 F. solani pisi pre-pr 4.13e+02
44 31 88.6 230 11 R59796 Fusarium solani pisi 4.13e+02
45 31 88.6 260 15 R77617 Anti-C5 Mab N19/8 scf 4.13e+02

ALIGNMENTS

RESULT 1
ID R70196 standard; Protein; 7 AA.
AC R70196;
DT 20-SEP-1995 (first entry)
DE Mab 3B9 light chain CDR.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PIC.
PI Gross MS, Holmes SD, Sylvestre DR;
WP1; 95-123387/16.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Page 55; 97pp; English.
CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC chains were cloned into pGEM/it+ and transformed into E. coli
CC DH5-alpha. A light chain cDNA clone was sequenced (Q83490) that

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CC encoded the protein given in R70189. 3 CDRs (R70195-97) were
CC identified.
SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.22e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 aasles 7
|||||||
Qy 1 AASNLES 7

RESULT 2

ID R66144 standard; peptide; 15 AA.
AC R66144;
DT 12-JUL-1995 (first entry)
DE CD-4 antibody variable region complementary peptide.
KW CD-4 antibody variable region; complementary peptide;
KW extra-corporeal blood circulation; cell filter material.
OS Synthetic.
PN J06269663-A.
PD 27-SEP-1994.
PF 17-MAR-1993; 057206.
PR 17-MAR-1993; JP-057206.
PA (70YM) TOYOH0 KK.
DR WP1; 94-346316/43.
PT Material for collecting cells positive for CD-4 antibody -
PT comprises nonwoven fabric having keto-alkyl halide functional gp
PS Example 2; Page 7; 9pp; Japanese.
CC R66140-R66146 are peptides complementary to the variable region
CC of the CD-4 antibody, these peptides are fixed onto a claimed
CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with
CC keto-alkyl halide functional groups. This material can be used
CC as a filter for CD-4 positive cells in a medical treatment
CC involving the extra-corporeal circulation of blood.
SQ Sequence 15 AA;

Query Match 100.0%; Score 35; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.22e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 aasles 15
|||||||
Qy 1 AASNLES 7

RESULT 3

ID R33309 standard; Protein; 106 AA.
AC R33309;
DT 05-JUL-1993 (first entry)
DE MAE15 light chain.
KW Antibody; high affinity; FCEH; low affinity; FCEL;
KW IgE receptor; histamine; mast cell; basophil; Kabat;
KW CDR; murine; MAE11; MAE13; MAE15; MAE17.
OS Synthetic.
PN W09304173-A.
PD 04-MAR-1993.
PF 14-AUG-1992; U06860.
PR 14-AUG-1991; US-744768.
PR 07-MAY-1992; US-879495.
PA (GETH) GENENTECH INC.
PI Jardieu PM, Presta LG;
DR WP1; 93-094004/11.

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PT Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
PT disorders e.g. allergies
PS Disclosures; Fig 2; 113pp; English.
CC Antibodies capable of binding FCEH-bound IgE but which are
CC substantially incapable of binding FCEH-bound IgE or inducing
CC histamine release from mast cells or basophils, comprise a human
CC Kabat CDR domain into which has been substituted a positionally
CC analogous residue from a Kabat CDR domain of the murine anti-huIgE
CC antibodies MAE11, MAE13, MAE15 or MAE17.
SQ Sequence 106 AA;

Query Match 100.0%; Score 35; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.22e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60
|||||||
Qy 1 AASNLES 7

RESULT 4

ID R60302 standard; Protein; 111 AA.
AC R60302;
DT 09-MAR-1995 (first entry)
DE Anti HIV antibody light chain variable region.
KW Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS; treatment;
KW prophylaxis; Mus musculus; Homo sapiens.
OS Mus musculus.
FH Key Location/Qualifiers
FT Region 1...23
FT /Label= Framework region 1.
FT Region 24...38
FT /Label= CDR1.
FT Region 39..53
FT /Label= Framework region 2.
FT Region 54..60
FT /Label= CDR2.
FT Region 61..92
FT /Label= Framework region 3.
FT Region 93..101
FT /Label= CDR3.
FT Region 102..111
FT /Label= Framework region 4.
PN W09415969-A.
PD 21-JUL-1994.
PF 14-JAN-1993; J00039.
PR 14-JAN-1993; AU-032671.
PR 14-JAN-1993; WO-J00039.
PA (KAGA) CEMO SERO THERAPEUTIC RES INST.
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
PI Tokiyoshi S;
DR WP1; 94-249145/30.
DR N-PSDB; Q70372.
PT Recombinant chimeric anti HIV antibody - useful for the treatment
PT and prevention of HIV
PS Claim 15; Figure 4; 51pp; Japanese.
CC The recombinant antibody light chain has neutralising activity
CC against HIV. Chimeric antibodies comprising both mouse and human
CC sequences are useful in the treatment/prevention of AIDS caused by
CC HIV.
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 11; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.22e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasnles 60
|||||||
Qy 1 AASNLES 7

RESULT 5

ID R55127 standard; Protein; 111 AA.
AC R55127;
DT 30-JAN-1995 (first entry)
DE Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.
KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
KW human immunodeficiency virus; variable region; VL chain; murine;
KW chimeric; humanised.
OS Chimeric Mus musculus.
OS Chimeric Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT /note= "human"
FT Region 24..38
FT /label= CDR1
FT /note= "murine"
FT Region 39..53
FT /label= FR2
FT Region 54..60
FT /label= CDR2
FT /note= "murine"
FT Region 61..92
FT /label= FR3
FT /note= "human"
FT Region 93..101
FT /label= CDR3
FT /note= "murine"
FT Region 102..111
FT /label= FR4
FT /note= "human"
PN 06125783-A.
PD 10-MAY-1994.
PF 28-DEC-1991; JP-359808.
PR (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
DR WPI; 94-187942/23.
DR N-PSDB; Q65558.
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
PT and recombinant antibody consisting of the H- and L-chains,
PT useful in AIDS therapy
PS Claim 5; Fig 12; 22pp; Japanese.
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (R55120-R55123). The murine anti-HIV CDRs were
CC introduced into human framework regions to construct chimeric
CC antibodies (R55124-R55127).
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.22e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasnles 60
|||||||

Qy 1 AASNLES 7

RESULT 6

ID R60306 standard; Protein; 111 AA.
AC R60306;
DT 13-MAR-1995 (first entry)
DE Chimeric anti HIV antibody light chain variable region.
KW Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS; treatment;
KW prophylaxis; Mus musculus; Homo sapiens.
OS Chimeric Homo sapiens
OS Chimeric Mus musculus.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= Framework region 1.
FT Region 24..38
FT /label= CDR1.
FT /note= "Mouse derived amino acid sequence."
FT Region 39..53
FT /label= Framework region 2.
FT Region 54..60
FT /label= CDR2.
FT /note= "Mouse derived amino acid sequence."
FT Region 61..92
FT /label= Framework region 3.
FT Region 93..101
FT /label= CDR3.
FT /note= "Mouse derived amino acid sequence."
FT Region 102..111
FT /label= Framework region 4.
PN W09415969-A.
PD 21-JUL-1994.
PF 14-JAN-1993; J00039.
PR 14-JAN-1993; AU-032671.
PR 14-JAN-1993; WO-J00039.
PA (KAGA) CHEMA SERO THERAPEUTIC RES INST.
PI Eda Y, Kinachi K, Maeda H, Osatomi K, Shiosaki K;
PI Tokiyoshi S;
DR WPI; 94-249145/30.
DR N-PSDB; R60306.
PT Recombinant chimeric anti HIV antibody - useful for the treatment
PT and prevention of HIV
PS Claim 14; Figure 12; 51pp; Japanese.
CC The recombinant antibody light chain has neutralising activity
CC against HIV. Chimeric antibodies comprising both mouse and human
CC sequences are useful in the treatment/prevention of AIDS caused by
CC HIV.
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 11; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.22e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasnles 60
|||||||
Qy 1 AASNLES 7

RESULT 7

ID R55123 standard; Protein; 111 AA.
AC R55123;
DT 27-JAN-1995 (first entry)
DE Mouse anti-HIV mu5.5 light chain variable region.

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KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
KW human immunodeficiency virus; variable region; VH chain; murine.
OS Mus musculus.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT Region 24..38
FT /label= CDR1
FT Region 39..53
FT /label= FR2
FT Region 54..60
FT /label= CDR2
FT Region 61..92
FT /label= FR3
FT Region 93..101
FT /label= CDR3
FT Region 102..111
FT /label= FR4
FN J06125783-A.
PD 10-MAY-1994.
PF 28-DEC-1991; 359808.
PA (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
DR WPI; 94-187942/23.
DR N-PSDB; Q65554.
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
PT and recombinant antibody consisting of the H- and L-chains,
PT useful in AIDS therapy
PS Example 3; Fig 4; 22pp; Japanese.
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (R55120-R55123). The murine anti-HIV CDRs were
CC introduced into human framework regions to construct chimeric
CC antibodies (R55124-R55127).
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.22e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 54 aasles 60
|||||
Qy 1 AASNLES 7

RESULT 8
ID P90541 standard; protein; 111 AA.
AC P90541;
DT 20-OCT-1989 (first entry)
DE Immunoglobulin L chain variable region.
KW Immunoglobulin; L chain variable region; HIV.
OS Mus musculus
FN EP-327000-A.
PD 09-AUG-1989.
PF 30-JAN-1989; 101583.
FR 30-JAN-1988; JP-20255.
PR 08-JUL-1988; JP-171385.
PA (****) The Chemo-Sero-Therapeutic Research Institute.
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,
PI Takatsuki K;
DR WPI; 89-229050/32.
DR N-PSDB; N90491, N90497, N90493.
PT Chimeric anti-human immune virus antibodies - contg. mouse variable
PT regions and human constant regions for diagnosis, treatment and

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PT prevention of AIDS
PS Claim 5; page 15; 33pp; English.
CC The sequence is an L chain variable region from an immunoglobulin with
CC anti-HIV neutralising activity. See N90491-3, and N90495.
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.22e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60
|||||
Qy 1 AASNLES 7

RESULT 9
ID R24575 standard; Protein; 112 AA.
AC R24575;
DT 08-DEC-1992 (first entry)
DE Human x mouse modified anti-HIV antibody Light chain RL0.5beta.
KW Heavy; light; CDR; HIV; AIDS; REI; 0.5beta.
OS Synthetic.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT Region 24..38
FT /label= CDR1
FT Region 39..53
FT /label= FR2
FT Region 54..60
FT /label= CDR2
FT Region 61..92
FT /label= FR3
FT Region 93..101
FT /label= CDR3
FT Region 102..112
FT /label= FR4
FN J04141095-A.
PD 14-MAY-1992; 266091.
PF 02-OCT-1990; JP-266091.
PR 02-OCT-1990; JP-266091.
PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.
DR WPI; 92-212765/26.
PT New recombinant modified anti-HIV antibodies - comprise human x
PT mouse modified antibody H and L chains
PS Disclosure; Fig 2; 15pp; Japanese.
CC The framework regions (FR) are derived from the human antibody
CC REI. The CDRs are mouse monoclonal antibody 0.5beta derived
CC sequences. The anti-HIV modified antibody can be used for the
CC prophylaxis and treatment of AIDS.
CC Specific examples of the H chain are given in R24556-58 and
CC R24560-62. A specific example of the L chain is given in R24575.
SQ Sequence 112 AA;

Query Match 100.0%; Score 35; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.22e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aasles 60
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Qy 1 AASNLES 7

RESULT 10

ID R04134 standard; protein; 115 AA.
 AC R04134;
 DT 06-SEP-1990 (first entry)
 DE Anti-Leu 3a light chain variable region gene product, KOL/206 V1.
 KW HIV; AIDS; anti-Leu3A; vaccine; ds.
 OS Mus musculus.
 PN EP-365209-A.
 PD 25-APR-1990.
 PF 11-OCT-1989; 010415.
 PR 17-OCT-1988; US-260558.
 PA (BECT) Becton Dickinson Co.
 PI Hinton R, Oi VT;
 DR WPI; 90-126329/17.
 DR N-PSDB; Q04041.
 PT New chimeric variants of murine antibody anti-leucine -
 PT contg. human antibody regions, and DNA encoding sequences.
 PS Claim 4; Fig 4; 12pp; English.
 CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
 CC used to form chimeric mouse-variable, human-constant region Abs
 CC suggested as being useful as a vaccine to HIV.
 SQ Sequence 115 AA;

Query Match 100.0%; Score 35; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.22e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 57 aasles 63
 QY 1 AASNLES 7

RESULT 11
 ID R70202 standard; Protein; 131 AA.
 AC R70202;
 DT 20-SEP-1995 (first entry)
 DE Humanized antibody 3B9 light chain.
 KW Humanized antibody; antibody engineering; monoclonal antibody;
 KW MAb; interleukin-4; IL-4; allergy.
 OS Homo sapiens.
 PN WO9507301-A.
 PD 16-MAR-1995.
 PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR N-PSDB; Q83520.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Page 71-72; 97pp; English.
 CC A humanized antibody light chain variable region and signal
 CC sequence is given in R75355. The signal sequence is also
 CC provided in R70194. The sequences of the 3 CDRs
 CC are identical to mouse anti-human IL-4 MAb 3B9 light chain
 CC CDRs (given in R70195-97).
 SQ Sequence 131 AA;

Query Match 100.0%; Score 35; DB 13; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.22e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 73 aasles 79
 QY 1 AASNLES 7

RESULT 12
 ID R32123 standard; Protein; 131 AA.
 AC R32123;
 DT 02-JUN-1993 (first entry)
 DE Anti-CD4 antibody WT 3.10 light chain variable region.
 KW immunosuppression; tissue transplantation; graft; I chain; V region;
 KW T-helper cell inhibition; transplant rejection; MAb;
 KW interleukin-2 receptor.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= signal 21..120
 FT Region
 FT /label= Variable
 FT Region 121..131
 FT /label= J1
 PN DE4143214-A.
 PD 28-JAN-1993.
 PF 30-DEC-1991; 143214.
 PR 25-JUL-1991; DE-124759.
 PR 30-DEC-1991; DE-143214.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 PI Kaluza B, Riethmueller G, Scheuer W, Weidle U;
 DR WPI; 93-037582/05.
 DR N-PSDB; Q36609.
 PT Synergistic antibody compsn. for use as immunosuppressant -
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
 PT alpha- or anti-IL2R beta antibodies
 PS Claim 5; Page 11; 18pp; German.
 CC This sequence is the light chain variable region of a preferred
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic
 CC composition. MAB WT 3.10 is deposited as clone 3.101/sB10 (ECACC
 CC 90030702). The anti-CD4 antibody is used with at least one anti-IL2R
 CC alpha or beta antibody. Individually the antibodies are strongly
 CC inhibiting and when used together their immunosuppressive properties
 CC are improved; they synergistically inhibit T-helper cell
 CC proliferation to effectively inhibit transplant rejection at low
 CC doses without significantly reducing the general immune response.
 CC See also Q36608-Q36616.
 SQ Sequence 131 AA;

Query Match 100.0%; Score 35; DB 6; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.22e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 aasles 80
 QY 1 AASNLES 7

RESULT 13
 ID R75355 standard; Protein; 131 AA.
 AC R75355;
 DT 20-SEP-1995 (first entry)
 DE Humanized antibody 3B9 light chain.
 KW Humanized antibody; antibody engineering; monoclonal antibody;
 KW MAb; interleukin-4; IL-4; allergy.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..20

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FT /label= sig_peptide
FT Region 43..57
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 73..79
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 112..120
FT /label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvestre DR;
DR WPI; 95-123387/16.
DR N-PSDB; Q73986.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.5; 97pp; English.
CC A humanized antibody light chain variable region and signal
CC sequence is given in R75355. The signal sequence is also
CC provided in R70194. The sequences of the first 2 CDRs
CC are identical to mouse anti-human IL-4 MAb 3B9 light chain
CC CDRs (given in R70195-96), but the third (R70201) differs
CC by a single amino acid from the native mouse CDR (R70197).
SQ Sequence 131 AA;

Query Match 100.0%; Score 35; DB 13; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.22e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 73 aasles 79
|||||||
Qy 1 AASNLES 7

RESULT 14
ID R04132 standard; protein; 131 AA.
AC R04132;
DT 06-SEP-1990 (first entry)
DE Anti-Leu 3a light chain variable region gene product, 206 Vx.
KW HIV; AIDS; anti-Leu3A; vaccine; ds.
OS Mus musculus.
PN EP-365209-A.
PD 25-APR-1990.
PF 11-OCT-1989; 010415.
PR 17-OCT-1988; US-260558.
PA (BECT) Becton Dickinson Co.
PI Hinton R, Oi VT;
DR WPI; 90-126329/17.
DR N-PSDB; Q04039.
PT New chimeric variants of murine antibody anti-leucine -
PT contg. human antibody regions, and DNA encoding sequences.
PS Claim 1; Fig 2; 12pp; English.
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
CC used to form chimeric mouse-variable, human-constant region Abs
CC suggested as being useful as a vaccine to HIV.
SQ Sequence 131 AA;

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Query Match 100.0%; Score 35; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.22e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 aasles 80
|||||||
Qy 1 AASNLES 7

RESULT 15
ID P90543 standard; protein; 131 AA.
AC P90543;
DT 20-OCT-1989 (first entry)
DE Amino acids sequence of a V chi region gene.
KW V cji region; immunoglobulin; L chain variable region; HIV.
OS Mus musculus.
PN EP-327000-A.
PD 09-AUG-1989.
PF 30-JAN-1989; 101583.
PR 30-JAN-1988; JP-20255.
PR 08-JUL-1988; JP-171385.
PA The Chemo-Sero-Therapeutic Research Institute.
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,
PI Takatsuki K;
DR WPI; 89-229050/32.
DR N-PSDB; N90495.
PT Chimeric anti-human immune virus antibodies - contg. mouse variable
PT regions and human constant regions for diagnosis, treatment and
PT prevention of AIDS
PS Disclosure; Fig 8; 33pp; English.
CC The sequence is encoded by a V chi region gene (see N90495).
CC The sequence from Asp 21 encodes the L chain variable region.
SQ Sequence 131 AA;

Query Match 100.0%; Score 35; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.22e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 aasles 80
|||||||
Qy 1 AASNLES 7

RESULT 16
ID R70189 standard; Protein; 132 AA.
AC R70189;
DT 20-SEP-1995 (first entry)
DE Mouse MAb 3B9 light chain.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.
OS Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Sig_peptide
FT Region 44..58
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 74..80
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 113..121
FT /label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.

PD 16-MAR-1995.
 PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR N-PSDB; Q83490.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Fig.1; 97pp; English.
 CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 CC chains were cloned into pCEW7f+ and transformed into E. coli
 CC DH5-alpha. The clones were sequenced (Q83490-91), and used for
 CC antibody engineering.
 SQ Sequence 132 AA;

Query Match 100.0%; Score 35; DB 13; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.22e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 aasles 80
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 Qy 1 AASNLES 7

Search completed: Wed Mar 19 15:55:32 1997
 Job time : 9 secs.


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RESULT 2
ENTRY      C38601      #type fragment
TITLE      Ig kappa chain V region (2B5) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change
23-Mar-1993
ACCESSIONS C38601
REFERENCE  A38601
#authors   Goshorn, S.C.; Retzel, E.; Jermerson, R.
#journal   J. Biol. Chem. (1991) 266:2134-2142
#title     Common structural features among monoclonal antibodies
           binding the same antigenic region of cytochrome c.
#cross-references MUID:91115823
#accession C38601
##status   preliminary
##molecule_type mRNA
##residues 1-65 #label GOS
##cross-references GB:M57980
SUMMARY    #length 65 #checksum 8125

Query Match 100.0%; Score 35; DB 12; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 aasnles 13
|||||||
Qy 1 AASNLES 7

RESULT 3
ENTRY      S42189      #type fragment
TITLE      Ig kappa chain V region - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995
ACCESSIONS S42189
REFERENCE  S42176
#authors   Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal   Eur. J. Immunol. (1993) 23:2503-2510
#title     Variable region gene selection of immunoglobulin G-expressing
           B cells with specificity for a defined epitope on type II
           collagen.
#accession S42189
##status   preliminary
##molecule_type DNA
##residues 1-85 #label MOJ
##cross-references EMBL:Z25448
SUMMARY    #length 85 #checksum 7866

Query Match 100.0%; Score 35; DB 12; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 aasnles 46
|||||||
Qy 1 AASNLES 7

RESULT 4
ENTRY      S42190      #type fragment
TITLE      Ig kappa chain V region - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
```

```
DATE       13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
13-Jan-1995
ACCESSIONS S42190
REFERENCE  S42176
#authors   Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal   Eur. J. Immunol. (1993) 23:2503-2510
#title     Variable region gene selection of immunoglobulin G-expressing
           B cells with specificity for a defined epitope on type II
           collagen.
#accession S42190
##status   preliminary
##molecule_type DNA
##residues 1-87 #label MOJ
##cross-references EMBL:Z25450
SUMMARY    #length 87 #checksum 2354

Query Match 100.0%; Score 35; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 42 aasnles 48
|||||||
Qy 1 AASNLES 7

RESULT 5
ENTRY      S42194      #type fragment
TITLE      Ig kappa chain V region - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995
ACCESSIONS S42194
REFERENCE  S42176
#authors   Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal   Eur. J. Immunol. (1993) 23:2503-2510
#title     Variable region gene selection of immunoglobulin G-expressing
           B cells with specificity for a defined epitope on type II
           collagen.
#accession S42194
##status   preliminary
##molecule_type DNA
##residues 1-88 #label MOJ
##cross-references EMBL:Z25458
SUMMARY    #length 88 #checksum 4364

Query Match 100.0%; Score 35; DB 12; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 aasnles 49
|||||||
Qy 1 AASNLES 7

RESULT 6
ENTRY      S42187      #type fragment
TITLE      Ig kappa chain V region - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995
ACCESSIONS S42187
REFERENCE  S42176
#authors   Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal   Eur. J. Immunol. (1993) 23:2503-2510
```


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#title Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II

collagen.

#accession S42187

##status preliminary

##molecule_type DNA

##residues 1-90 ##label MOJ

##cross-references EMBL:Z25444

SUMMARY #length 90 #checksum 9303

Query Match 100.0%; Score 35; DB 12; Length 90;

Best Local Similarity 100.0%; Pred. No. 1.09e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 45 aaslns 51

|||||||

Qy 1 AASNLES 7

RESULT 7

ENTRY A38601 #type fragment

TITLE Ig kappa chain V region (1G3) - mouse (fragment)

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change

23-Mar-1993

ACCESSIONS A38601

REFERENCE A38601

##authors Goshorn, S.C.; Retzel, E.; Jermerson, R.

##journal J. Biol. Chem. (1991) 266:2134-2142

##title Common structural features among monoclonal antibodies

binding the same antigenic region of cytochrome c.

##cross-references MUID:91115823

##accession A38601

##status preliminary

##molecule_type mRNA

##residues 1-93 ##label GOS

##cross-references GB:M5798

SUMMARY #length 93 #checksum 6635

Query Match 100.0%; Score 35; DB 12; Length 93;

Best Local Similarity 100.0%; Pred. No. 1.09e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 35 aaslns 41

|||||||

Qy 1 AASNLES 7

RESULT 8

ENTRY KWMS10 #type complete

TITLE Ig kappa chain V region (PC7210) - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change

30-Sep-1993

ACCESSIONS D01937; A01937

REFERENCE A93204

##authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

##journal Nature (1978) 276:785-790

##title Rearrangement of genetic information may produce

immunoglobulin diversity.

##cross-references MUID:79073152

##accession D01937

##molecule_type protein

##residues 1-110 ##label WEI

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CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS immunoglobulin

FEATURE

23-92 #disulfide_bonds #status predicted

SUMMARY #length 110 #molecular_weight 11950 #checksum 6378

Query Match 100.0%; Score 35; DB 2; Length 110;

Best Local Similarity 100.0%; Pred. No. 1.09e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aaslns 60

|||||||

Qy 1 AASNLES 7

RESULT 9

ENTRY KWMS1 #type complete

TITLE Ig kappa chain V region (CBPC 101) - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change

05-Apr-1995

ACCESSIONS A01936

REFERENCE A93822

##authors McKean, D.J.; Bell, M.; Potter, M.

##journal Proc. Natl. Acad. Sci. U.S.A. (1978) 75:3913-3917

##title Mechanisms of antibody diversity: multiple genes encode

structurally related mouse kappa variable regions.

##cross-references MUID:79012520

##accession A01936

##molecule_type protein

##residues 1-111 ##label MCK

COMMENT This chain was isolated from a myeloma protein.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

FEATURE

23-92

SUMMARY #length 111 #molecular_weight 11964 #checksum 1507

Query Match 100.0%; Score 35; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 1.09e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aaslns 60

|||||||

Qy 1 AASNLES 7

RESULT 10

ENTRY KWMS69 #type complete

TITLE Ig kappa chain V region (PC7769) - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change

30-Sep-1993

ACCESSIONS E01937; A01937

REFERENCE A93204

##authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

##journal Nature (1978) 276:785-790

##title Rearrangement of genetic information may produce

immunoglobulin diversity.

##cross-references MUID:79073152

##accession E01937

##molecule_type protein

##residues 1-111 ##label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS immunoglobulin

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FEATURE

23-92 #disulfide bonds #status predicted
SUMMARY #length 111 #molecular-weight 12011 #checksum 662
Query Match 100.0%; Score 35; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 54 aasnlcs 60
|||||||
Qy 1 AASNLES 7

RESULT 11
ENTRY KWMS83 #type complete
TITLE Ig kappa chain V region (PC7183) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
30-Sep-1993
ACCESSIONS B01937; A01937
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce immunoglobulin diversity.
#cross-references M01D:79073152
#accession B01937
#molecule_type protein
#residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
23-92 #disulfide bonds #status predicted
SUMMARY #length 111 #molecular-weight 11952 #checksum 9

Query Match 100.0%; Score 35; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 54 aasnlcs 60
|||||||
Qy 1 AASNLES 7

RESULT 12
ENTRY KWMS43 #type complete
TITLE Ig kappa chain V region (PC7043) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
05-Apr-1995
ACCESSIONS A01937
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce immunoglobulin diversity.
#cross-references M01D:79073152
#accession A01937
#molecule_type protein
#residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
23-92 #disulfide bonds #status predicted
SUMMARY #length 111 #molecular-weight 12002 #checksum 438

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Query Match 100.0%; Score 35; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 54 aasnlcs 60
|||||||
Qy 1 AASNLES 7

RESULT 13
ENTRY S19971 #type fragment
TITLE Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
01-Dec-1995
ACCESSIONS S19971; S19973
REFERENCE S19963
#authors Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
#submission submitted to the EMBL Data Library, March 1992
#description Structural characterization of CD4 mAb.
#accession S19971
#molecule_type mRNA
#residues 1-112 ##label WEI
#cross-references EMBL:X65091
#experimental_source clone M-T310
#accession S19973
#molecule_type mRNA
#residues 1-112 ##label WEW
#cross-references EMBL:X65092
#experimental_source M-T404
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 112 #checksum 4782

Query Match 100.0%; Score 35; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 54 aasnlcs 60
|||||||
Qy 1 AASNLES 7

RESULT 14
ENTRY S19976 #type fragment
TITLE Ig kappa chain V region (M-T413) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
12-Apr-1995
ACCESSIONS S19976
REFERENCE S19963
#authors Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
#submission submitted to the EMBL Data Library, March 1992
#description Structural characterization of CD4 mAb.
#accession S19976
#status preliminary
#molecule_type mRNA
#residues 1-112 ##label WEI
#cross-references EMBL:X65093
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 112 #checksum 4816
Query Match 100.0%; Score 35; DB 5; Length 112;

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```
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 aaslns 60
|||||||
Qy 1 AASNIES 7

RESULT 15
ENTRY PH1226 #type fragment
TITLE Ig kappa chain precursor V region (M-T310) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
30-Apr-1995
ACCESSIONS PH1226
REFERENCE PH1224
#authors Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.;
Reiter, C.; Flieger, D.; Lenz, H.; Weiss, E.H.; Rieber,
E.P.; Riethmuller, G.; Weidle, U.H.
#journal Gene (1992) 121:271-278
#title Combinatorial functions of two chimeric antibodies directed
to human CD4 and one directed to the alpha-chain of the
human interleukin-2 receptor.
#accession PH1226
#molecule_type mRNA
#residues 1-131 #label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
1-20 #domain signal sequence #status predicted #label SIG\
21-131 #product Ig light chain V region #status predicted
#label WAI
SUMMARY #length 131 #checksum 4648

Query Match 100.0%; Score 35; DB 5; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 aaslns 80
|||||||
Qy 1 AASNIES 7

RESULT 16
ENTRY B64160 #type complete
TITLE hypothetical protein HI0852 - Haemophilus influenzae (strain
Rd KW20)
ORGANISM #formal_name Haemophilus influenzae
DATE 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
18-Aug-1995
ACCESSIONS B64160
REFERENCE A64000
#authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kervavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
#journal Science (1995) 269:496-512
#title Whole-genome random sequencing and assembly of Haemophilus
```

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```
#accession B64160
#status preliminary; sequence not shown; translation not shown
#molecule_type DNA
#residues 1-463 #label TIGR
#cross-references GB:I42023; TIGR:HI0852
#note best homolog was a hypothetical protein from Escherichia
coli
SUMMARY #length 463 #molecular-weight 50002 #checksum 8725

Query Match 100.0%; Score 35; DB 8; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 94 aaslns 100
|||||||
Qy 1 AASNIES 7

Search completed: Wed Mar 19 15:55:06 1997
Job time : 12 secs.
```

WPPSRLH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:13:17 1997; MaePar time 2.37 Seconds

Tabular output not generated. 54.788 Million cell updates/sec

Title: >US-08-612-929-22

Description: (1-7) from US08612929.pep

Perfect Score: 45

Sequence: 1 TSCMGVS 7

Scoring table: PAM 150

Gap 15

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot33

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10

Statistics: Mean 19.683; Variance 19.771; scale 0.996

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	40	88.9	336	3	FLA1_BORBU	FLAGELLAR FILAMENT 41	7.43e+00
2	40	88.9	793	7	PPSA_ECOLI	PHOSPHOENOLPYRUVATE S	7.43e+00
3	40	88.9	857	5	MEDB_GIALA	MEDIAN BODY PROTEIN.	7.43e+00
4	40	88.9	1274	8	SRE3_BACSO	SURFACTIN SYNTHETASE	7.43e+00
5	39	86.7	58	2	CITB_SALTY	CITB PROTEIN (FRAGMEN	1.28e+01
6	39	86.7	417	4	GELS_XENLA	GELSOLIN (ACTIN-DEPOL	1.28e+01
7	39	86.7	841	6	MYFC_YEREN	OUTER MEMBRANE USHER	1.28e+01
8	38	84.4	130	3	FLAE_SALTY	FLAGELLAR PROTEIN FLH	2.18e+01
9	38	84.4	194	10	YF09_HAEIN	HYPOTHETICAL PROTEIN	2.18e+01
10	38	84.4	238	10	Y2AK_STRGR	HYPOTHETICAL 24.7 KD	2.18e+01
11	38	84.4	300	4	GLTC_BACSO	REGULATORY PROTEIN GL	2.18e+01
12	38	84.4	348	2	CTGF_MOUSE	CONNECTIVE TISSUE GRO	2.18e+01
13	38	84.4	349	2	CTGF_HUMAN	CONNECTIVE TISSUE GRO	2.18e+01

14	38	84.4	361	5	LIG_PHLRA	LIGNINASE III PRECURS	2.18e+01
15	38	84.4	719	6	PGCA_BOVIN	CARTILAGE-SPECIFIC PR	2.18e+01
16	37	82.2	384	7	POQ3_ACICA	COENZYME POQ SYNTHESI	3.68e+01
17	37	82.2	505	3	FIXL_RHME	SENSOR PROTEIN FIXL (3.68e+01
18	37	82.2	541	4	HXT2_YEAST	HIGH-AFFINITY GLUCOSE	3.68e+01
19	37	82.2	546	4	HYT0_YEAST	HEXOSE TRANSPORTER HX	3.68e+01
20	37	82.2	669	10	HY06_HAEIN	PROBABLE TRANSPORT PR	3.68e+01
21	36	80.0	205	7	PRCT_RAT	PROTEASOME THETA CHAI	6.13e+01
22	36	80.0	262	1	BACR_HALHA	BACTERIORHODOPSIN PRE	6.13e+01
23	36	80.0	317	2	CFXR_ALCEU	RUBISCO OPERON TRANSC	6.13e+01
24	36	80.0	325	1	ARCB_HAEIN	AEROBIC RESPIRATION C	6.13e+01
25	36	80.0	376	10	YJ9M_YEAST	HYPOTHETICAL 41.6 KD	6.13e+01
26	36	80.0	449	6	NDOB_PSEPU	NAPHTHALENE 1,2-DIOXY	6.13e+01
27	36	80.0	457	4	HEMN_ECOLI	OXYGEN-INDEPENDENT CO	6.13e+01
28	36	80.0	462	7	PPB3_BACSO	ALKALINE PHOSPHATASE	6.13e+01
29	36	80.0	464	3	GALP_ECOLI	GALACTOSE-PROTON SYMP	6.13e+01
30	36	80.0	467	1	6PGD_SNP7	6-PHOSPHOGLUCONATE DE	6.13e+01
31	36	80.0	507	9	VGLG_VHSV0	SPIKE GLYCOPROTEIN PR	6.13e+01
32	36	80.0	524	7	PPBT_RAT	ALKALINE PHOSPHATASE,	6.13e+01
33	36	80.0	524	7	PPBT_BOVIN	ALKALINE PHOSPHATASE,	6.13e+01
34	36	80.0	530	7	PPB1_HUMAN	ALKALINE PHOSPHATASE,	6.13e+01
35	36	80.0	535	7	PPB1_HUMAN	ALKALINE PHOSPHATASE,	6.13e+01
36	36	80.0	538	8	TOMA_STRGA	TETRACENOMYCIN C RESI	6.13e+01
37	36	80.0	548	3	FUMB_ECOLI	FUMARATE HYDRATASE CL	6.13e+01
38	36	80.0	573	9	UREL_LACFE	ACID UREASE ALPHA SUB	6.13e+01
39	36	80.0	617	4	HEMA_MEASI	HEMAGGLUTININ-NEURAMI	6.13e+01
40	36	80.0	617	4	HEMA_MEASH	HEMAGGLUTININ-NEURAMI	6.13e+01
41	36	80.0	617	4	HEMA_MEASH	HEMAGGLUTININ-NEURAMI	6.13e+01
42	36	80.0	620	4	HEMA_MEASY	HEMAGGLUTININ-NEURAMI	6.13e+01
43	36	80.0	713	2	COGU_BACCI	CYCLOMALTODEXTRIN GIU	6.13e+01
44	36	80.0	1161	7	POL_SFV1	POL POLYPROTEIN (CONT	6.13e+01
45	36	80.0	2149	8	RRPL_RVFEVZ	RNA-DIRECTED RNA POLY	6.13e+01

ALIGNMENTS

RESULT	1	
ID	FLA1_BORBU	STANDARD; PRT; 336 AA.
AC	P11089; P15295;	
DT	01-JUL-1989 (REL. 11, CREATED)	
DT	01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)	
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)	
DE	FLAGELLAR FILAMENT 41 KD CORE PROTEIN (FLAGELLIN).	
GN	FLA.	
OS	BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).	
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; SPIROCHETES; SPIROCHAETALES;	
OC	SPIROCHAETACEAE.	
RN	[1]	
RP	SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.	
RC	STRAIN=GEHO, AND ATCC 35210 / B31;	
RX	MEDLINE; 89263802.	
RA	GASSMANN G.S., KRAMER M.D., GOEBEL U.B., WALLICH R.;	
RL	NUCLEIC ACIDS RES. 17:3590-3590(1989).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=GEHO;	
RX	MEDLINE; 91139587.	
RA	GASSMANN G.S., JACOBS E., DEUTZMANN R., GOEBEL U.B.;	
RL	J. BACTERIOL. 173:1452-1459(1991).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=ATCC 35210 / B31;	
RX	MEDLINE; 90256248.	
RA	WALLICH R., MOTER S.E., SIMON M.M., EBNET K., HEIBERGER A.,	

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RA KRAMER M.D.;
 RL INFECT. IMMUN. 58:1711-1719(1990).
 CC -!- FUNCTION: COMPONENT OF THE CORE OF THE FLAGELLA.
 CC -!- SUBUNIT: OUTER LAYER COMPOSED OF REPEATING UNITS OF FLAA AND A
 CC CORE THAT CONTAINS ONE OR ALL OF FIVE ANTIGENICALLY RELATED
 CC POLYPEPTIDE.
 CC -!- SUBCELLULAR LOCATION: PERIPLASMIC FLAGELLUM.
 CC -!- SIMILARITY: TO OTHER BACTERIAL FLAGELLINS.
 DR EMBL; X15660; G39359; -.
 DR EMBL; X15661; G39361; -.
 DR EMBL; X16833; G39357; -.
 DR EMBL; X56334; G289000; -.
 DR PIR; A41470; FLYYB3.
 DR PIR; A60276; A60276.
 DR PIR; A38450; A38450.
 DR PIR; S04091; S04091.
 DR PROSITE; PS00588; FLAGELLA_BB_ROD.
 KW FLAGELLA; PERIPLASMIC.
 FT VARIANT 180 180 N -> T (IN STRAIN B31).
 FT VARIANT 279 279 D -> N (IN STRAIN B31).
 SQ SEQUENCE 336 AA; 35765 MW; 77882759 CRC32;

Query Match 88.9%; Score 40; DB 3; Length 336;
 Best Local Similarity 71.4%; Pred. No. 7.43e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aaamgvs 49
 :|||
 QY 1 TSGMGVS 7

RESULT 2
 ID PPSA ECOLI STANDARD; PRT; 793 AA.
 AC P23538;
 DT 01-NOV-1991 (REL. 20, CREATED)
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE PHOSPHENOLPYRUVATE SYNTHASE (EC 2.7.9.2) (PYRUVATE, WATER DIKINASE)
 DE (PEP SYNTHASE).
 GN PPSA OR PPS.
 OS ESCHERICHIA COLI.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HOLZSCHU D.L., MCELVER J.A., LIAO C.C., BERRY A.J.
 RL SUBMITTED (JUN-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE; 92140374.
 RA NIRSCHACH M., KREUZALER F., GERSE R.H., POSTMA P., HIRSCH H.J.;
 RL MOL. GEN. GENET. 232:332-336(1992).
 CC -!- PATHWAY: ESSENTIAL STEP IN GLUCONEOGENESIS WHEN PYRUVATE AND
 CC LACTATE ARE USED AS A CARBON SOURCE.
 CC -!- CATALYTIC ACTIVITY: ATP + PYRUVATE + H(2)O = AMP +
 CC PHOSPHENOLPYRUVATE + PHOSPHATE.
 CC -!- SIMILARITY: TO OTHER PEP-UTILIZING ENZYMES.
 DR EMBL; M69116; G147146; -.
 DR EMBL; X59381; G42481; -.
 DR PIR; S20554; S20554.
 DR SWISS-2DPAGE; P23538; COLI.
 DR ECO2DBASE; B083.0; 6TH EDITION.
 DR ECOGENE; EG10759; PPSA.

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DR PROSITE; PS00370; PEP ENZYMES PHOS SITE.
 DR PROSITE; PS00742; PEP ENZYMES 2.
 KW TRANSFERASE; KINASE; ATP-BINDING; PHOSPHORYLATION.
 FT MOD RES 422 422 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 194 196 AGL -> RM (IN REF. 2).
 FT CONFLICT 342 344 AHA -> RSRQ (IN REF. 2).
 FT CONFLICT 346 361 RSMVIRCIHVRVLS -> MERYTLHSQKIIA
 (IN REF. 2).
 SQ SEQUENCE 793 AA; 87402 MW; BF0F2A9E CRC32;

Query Match 88.9%; Score 40; DB 7; Length 793;
 Best Local Similarity 100.0%; Pred. No. 7.43e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 39 sgmgvs 44
 :|||
 QY 2 SGMGVS 7

RESULT 3
 ID MEDB GIALA STANDARD; PRT; 857 AA.
 AC Q08014;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE MEDIAN BODY PROTEIN.
 OS GIARDIA LAMBLIA.
 OC EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; DIPLOMONADIDA;
 OC HEXAMITIDAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PORTLAND-1;
 RX MEDLINE; 93287123.
 RA MARSHALL J., HOLBERTON D.V.;
 RL J. MOL. BIOL. 231:521-530(1993).
 CC -!- FUNCTION: MAY HAVE A ROLE IN IMMOBILISING THE MICROTUBULES
 CC BETWEEN CELL DIVISIONS.
 CC -!- SUBCELLULAR LOCATION: MEDIAN BODY.
 CC -!- DOMAIN: SHOWS AN ALPHA-HELICAL COILED COIL STRUCTURE (30
 CC REPEATING HEPTADS).
 DR EMBL; X64517; G312671; -.
 KW CYTOSKELETON; MICROTUBULES; COILED COIL; HEPTAD REPEAT PATTERN.
 SQ SEQUENCE 857 AA; 100583 MW; 5E2BBA84 CRC32;

Query Match 88.9%; Score 40; DB 5; Length 857;
 Best Local Similarity 71.4%; Pred. No. 7.43e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 795 stgmgs 801
 :|||
 QY 1 TSGMGVS 7

RESULT 4
 ID SRF3 BACSU STANDARD; PRT; 1274 AA.
 AC Q08787;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE SURFACTIN SYNTHETASE SUBUNIT 3.
 GN SRFAC OR SRFAC3.
 OS BACILLUS SUBTILIS.
 OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=168 / JH642;
 RX MEDLINE; 93360813.
 RA COSMINA P., RODRIGUEZ F., DE FERRA F., GRANDI G., PEREGO M.,
 RA VAREMA G., VAN SINDEREN D.;
 RL MOL. MICROBIOL. 8:821-831(1993).
 CC -!- FUNCTION: PROBABLY ACTIVATES A LEUCINE.
 CC -!- PATHWAY: NON-RIBOSOMAL BIOSYNTHESIS OF THE CYCLIC PEPTIDE
 CC ANTI-BIOTIC SURFACTIN.
 CC -!- COFACTOR: CONTAINS A COVALENTLY BOUND PHOSPHOPANTHETHEINE.
 CC -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
 CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
 DR ENBL; X70356; G396483; -.
 DR SUBTILIST; BG10170; SEFAC.
 DR PROSITE; PS00455; AMP BINDING.
 KW ANTI-BIOTIC BIOSYNTHESIS; LIGASE; SPORULATION; PHOSPHOPANTHETHEINE.
 FT REPEAT 1 1044 DOMAIN 1 (LED-ACTIVATING).
 FT BINDING 1003 1003 PHOSPHOPANTHETHEINE (POTENTIAL).
 SQ SEQUENCE 1274 AA; 143817 MW; A3B95100 CRC32;

Query Match 88.9%; Score 40; DB 8; Length 1274;
 Best Local Similarity 100.0%; Pred. No. 7.43e+00;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 809 sgmgvs 814

Qy 2 SGMGVS 7

RESULT 5

ID CITB SALTY STANDARD; PRT; 58 AA.
 AC P37463;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE CITB PROTEIN (FRAGMENT).
 GN CITB.
 OS SALMONELLA TYPHIMURIUM.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RX MEDLINE; 92041761.
 RA SHIMAMOTO T., IZAWA H., DAIMON H., ISHIGURO N., SHINAGAWA M.,
 RA SAKANO Y., TSUDA M., TSUCHIYA T.;
 RL J. BIOCHEM. 110:22-28(1991).
 DR ENBL; D90203; E42680; -.
 DR PIR; PQ0098; PQ0098.
 DR STIGENE; SG10059; CITB.
 KW CITRATE UTILIZATION.
 FT NON TER 1 1
 SQ SEQUENCE 58 AA; 6271 MW; E33DD8EB CRC32;

Query Match 86.7%; Score 39; DB 2; Length 58;

Best Local Similarity 83.3%; Pred. No. 1.28e+01;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 4 tsqmgj 9

Qy 1 TSCMGV 6

RESULT 6

ID CELS XENIA STANDARD; PRT; 417 AA.
 AC P14885;
 DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE GELSOLIN (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (FRAGMENT).
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARY;
 RX MEDLINE; 89008590.
 RA ANKENBAUER T., KLEINSCHMIDT J.A., VANDEKERCKHOVE J., FRANK W.W.;
 RL J. CELL BIOL. 107:1489-1498(1988).
 CC -!- FUNCTION: GELSOLIN IS A CALCIUM-REGULATED, ACTIN-MODULATING
 CC PROTEIN THAT BINDS TO THE PLUS (OR BARBED) ENDS OF ACTIN MONOMERS
 CC OR FILAMENTS, PREVENTING MONOMER EXCHANGE (END-BLOCKING OR
 CC CAPPING). IT CAN PROMOTE THE ASSEMBLY OF MONOMERS INTO FILAMENTS
 CC (NUCLEATION) AS WELL AS SEVER FILAMENTS ALREADY FORMED.
 CC -!- IN ADDITION TO ITS ROLE IN ACTIN REGULATION, THIS PROTEIN IS KNOWN
 CC TO BIND WITH HIGH AFFINITY TO FIBRONECTIN.

DR ENBL; M36652; G214176; -.
 DR ENBL; X13319; G64716; -.
 DR HSP; P02640; I5W0.
 KW ACTIN-BINDING; REPEAT; CALCIUM.
 FT NON TER 1 1
 SQ SEQUENCE 417 AA; 46024 MW; B71940E2 CRC32;

Query Match 86.7%; Score 39; DB 4; Length 417;

Best Local Similarity 71.4%; Pred. No. 1.28e+01;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 38 tdgmga 44

Qy 1 TSGMGVS 7

RESULT 7

ID MYFC YEREN STANDARD; PRT; 841 AA.
 AC P33408;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE OUTER MEMBRANE USHER PROTEIN MYFC PRECURSOR.
 GN MYFC.
 OS YERSINIA ENTEROCOLITICA.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W1024 / SEROTYPE 0:9;
 RX MEDLINE; 94018646.
 RA TRIARTE M., VANOOTECHEM J.-C., DELOR I., DIAZ R., KNUITON S.,
 RA CORNELIS G.R.;
 RL MOL. MICROBIOL. 9:507-520(1993).
 CC -!- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF THE MYFA
 CC FIMBRIAL SUBUNIT.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
 CC (BY SIMILARITY).
 CC -!- SIMILARITY: TO OTHER FIMBRIAL EXPORT USHER PROTEINS.
 DR ENBL; Z21953; G402172; -.
 DR PIR; S39365; S39365.
 DR PROSITE; PS01151; FIMBRIAL_USHER.
 KW OUTER MEMBRANE; TRANSMEMBRANE; FIMBRIA; TRANSPORT; SIGNAL.

FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 841 OUTER MEMBRANE USHER PROTEIN MYFC.
 FT DISULFID 817 840 POTENTIAL.
 SQ SEQUENCE 841 AA; 93414 MW; 19A34962 CRC32;

Query Match 86.7%; Score 39; DB 6; Length 841;
 Best Local Similarity 83.3%; Pred. No. 1.28e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 412 tagmqv 417
 I:||||
 Qy 1 TSGMGV 6

RESULT 8
 ID FLHE SALTY STANDARD; PRT; 130 AA.

AC P40728;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE FLAGELLAR PROTEIN FLHE PRECURSOR.
 GN FLHE.
 OS SALMONELLA TYPHIMURIUM.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 17-25.
 RC STRAIN-KK1004;
 RX MEDLINE; 95095932.
 RA MINAMINO T., IINO T., KITSUKAKE K.;
 RL J. BACTERIOL. 176:1630-1637(1994).
 CC -/- FUNCTION: NOT ESSENTIAL FOR FLAGELLAR FORMATION AND FUNCTION.

DR EMBL; D32203; G633117; -;
 DR STYGENE; SG10528; FLHE.
 KW FLAGELLA; SIGNAL.
 FT SIGNAL 1 16
 FT CHAIN 17 130 FLAGELLAR PROTEIN FLHE.
 SQ SEQUENCE 130 AA; 14073 MW; F9805A38 CRC32;

Query Match 84.4%; Score 38; DB 3; Length 130;
 Best Local Similarity 83.3%; Pred. No. 2.18e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 25 sgmqvt 30
 I:||||
 Qy 2 SGMGVS 7

RESULT 9
 ID YF09 HAEIN STANDARD; PRT; 194 AA.

AC P44231;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL PROTEIN H11509.
 GN H11509.
 OS HAEMOPHILUS INFLUENZAE.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC PASTEURACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20;
 RX MEDLINE; 95350630.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,

RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,
 RA UTTERRACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
 RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
 RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RL SCIENCE 269:496-512(1995).
 DR EMBL; L46140; G1007674; -;
 DR EMBL; U32827; G926588; -;
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 194 AA; 21817 MW; 71374765 CRC32;

Query Match 84.4%; Score 38; DB 10; Length 194;
 Best Local Similarity 83.3%; Pred. No. 2.18e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 134 sgmgva 139
 I:||||
 Qy 2 SGMGVS 7

RESULT 10
 ID Y24K STRGR STANDARD; PRT; 238 AA.

AC P12752;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 24.7 KD PROTEIN IN PHOTOLYASE 5' REGION.
 OS STREPTOMYCES GRISEUS.
 OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89315214.
 RA KOBAYASHI T., TAKAO M., OIKAWA A., YASUI A.;
 RL NUCLEIC ACIDS RES. 17:4731-4744(1989).
 DR EMBL; X15060; G47082; -;
 DR PIR; S05572; S05572.
 KW HYPOTHETICAL PROTEIN.

Qy 2 SGMGVS 7
 SQ SEQUENCE 238 AA; 24655 MW; 313A8012 CRC32;

Query Match 84.4%; Score 38; DB 10; Length 238;
 Best Local Similarity 57.1%; Pred. No. 2.18e+01;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 209 asgmqit 215
 I:||||
 Qy 1 TSGMGVS 7

RESULT 11
 ID GLTC BACSU STANDARD; PRT; 300 AA.

AC P20668;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE REGULATORY PROTEIN GLTC.

GN GLTC.
 OS BACILLUS SUBTILIS.
 OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89359102.

RA BOHANNON D.E., SONENSHIN A.L.;
RL J. BACTERIOL. 171:4718-4727(1989).
RN [2]
RP REVISIONS.
RA SONENSHIN A.L.;
RL SUBMITTED (FEB-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: POSITIVE REGULATOR OF GLUTAMATE BIOSYNTHESIS (GLTAB
CC GENES). GLTC ALSO REPRESSSES ITS OWN TRANSCRIPTION.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC EMBL; M28509; G457514; -.
DR PIR; A33951; A33951.
DR SUBTILIST; BG10810; GLTC.
DR PROSITE; PS00044; HTH LYSR FAMILY.
KW GLUTAMATE BIOSYNTHESIS; TRANSCRIPTION REGULATION; ACTIVATOR;
KW DNA-BINDING.
FT DNA BIND 18 37 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 300 AA; 34019 MW; 3CF46232 CRC32;

Query Match 84.4%; Score 38; DB 4; Length 300;
Best Local Similarity 57.1%; Pred. No. 2.18e+01;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 233 eagmgtv 239

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Qy 1 TSGMGVS 7

RESULT 12

ID CTGF MOUSE STANDARD; PRT; 348 AA.
AC P29268;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (CTGF) (FISP-12 PROTEIN).
GN CTGF OR FISP12 OR FISP-12.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91363290.
RA RYSECK R.-P., MACDONALD-BRAVO H., MATTEI M.-G., BRAVO R.;
RL CELL GROWTH DIFFER. 2:225-233(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91229699.
RA BRUNNER A., CHINN J., NEUBAUER M.G., PURCHIO A.F.;
RL DNA CELL BIOL. 10:293-300(1991).
CC -!- INDUCTION: BY GROWTH FACTORS.
CC -!- TISSUE SPECIFICITY: TESTIS, SPLEEN, KIDNEY, LUNG, HEART, AND BRAIN
CC (LOWEST LEVEL IN TESTIS AND HIGHEST IN LUNG).
CC -!- SIMILARITY: TO INSULIN-LIKE GROWTH FACTOR BINDING PROTEINS AND
CC TO THE CEF-10/CYR61/CTGF/FISP-12/NOV PROTEIN FAMILY.
CC -!- SIMILARITY: CONTAINS A C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
DR EMBL; M70641; G193314; -.
DR EMBL; M70642; G193316; -.
DR EMBL; M80263; G201946; -.
DR PIR; A53228; A53228.
DR PROSITE; PS00222; IGF_BINDING.
KW GROWTH FACTOR BINDING; SIGNAL.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 348 CONNECTIVE TISSUE GROWTH FACTOR.
FT DOMAIN 255 329 CTCK.

FT DISULFID 255 292 BY SIMILARITY.
FT DISULFID 272 306 BY SIMILARITY.
FT DISULFID 283 322 BY SIMILARITY.
FT DISULFID 286 324 BY SIMILARITY.
FT DISULFID 291 328 BY SIMILARITY.
FT CONFLICT 161 161 K -> E (IN REF. 2).
SQ SEQUENCE 348 AA; 37793 MW; EAB92BE0 CRC32;

Query Match 84.4%; Score 38; DB 2; Length 348;
Best Local Similarity 71.4%; Pred. No. 2.18e+01;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 211 tcgmjls 217

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Qy 1 TSGMGVS 7

RESULT 13

ID CTGF HUMAN STANDARD; PRT; 349 AA.
AC P29279;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
GN CTGF.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UMBILICAL VEIN ENDOTHELIAL CELLS;
RX MEDLINE; 91373462.
RA BRADHAM D.M., IGARASHI A., POTTER R.L., GROTEENDORST G.R.;
RL J. CELL BIOL. 114:1285-1294(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=UMBILICAL VEIN ENDOTHELIAL CELLS;
RX MEDLINE; 93187114.
RA IGARASHI A., BRADHAM D.M., OKOCHI H., GROTEENDORST G.R.;
RL J. DERMATOL. 19:642-643(1992).
RN [3]
RP SEQUENCE FROM N.A.
RA OEMAR B.S., WERNER A., YANG Z., GARNIER J.M., GENTZ R., LUESCHER T.F.;
RL SUBMITTED (APR-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED BY
CC HUMAN VASCULAR ENDOTHELIAL CELLS. THIS IMMEDIATE-EARLY PROTEIN
CC MAY BIND ONE OF THE PDGF CELL SURFACE RECEPTORS.
CC -!- SUBUNIT: MONOMER.
CC -!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY BE PRODUCED BY
CC -!- ALTERNATIVE SPLICING OF THE SAME GENE.
CC -!- SIMILARITY: TO INSULIN-LIKE GROWTH FACTOR BINDING PROTEINS AND
CC TO THE CEF-10/CYR61/CTGF/FISP-12/NOV PROTEIN FAMILY.
CC -!- SIMILARITY: CONTAINS A C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
DR EMBL; M92934; G180924; -.
DR EMBL; S56201; G266235; -.
DR EMBL; X78947; G474934; -.
DR PIR; A40551; A40551.
DR PIR; S44205; S44205.
DR MIM; 121009; 11TH EDITION.
DR PROSITE; PS00222; IGF_BINDING.
KW GROWTH FACTOR BINDING; SIGNAL; ALTERNATIVE SPLICING.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 349 CONNECTIVE TISSUE GROWTH FACTOR.
FT DOMAIN 256 330 CTCK.

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FT DISULFID 256 293 BY SIMILARITY.
 FT DISULFID 273 307 BY SIMILARITY.
 FT DISULFID 284 323 BY SIMILARITY.
 FT DISULFID 287 325 BY SIMILARITY.
 FT DISULFID 292 329 BY SIMILARITY.
 FT CARBOHYD 28 28 POTENTIAL.
 FT CARBOHYD 225 225 POTENTIAL.
 FT VARSPLIC 172 198 MISSING (IN SHORT FORM).
 SQ SEQUENCE 349 AA; 38069 MW; C21E9662 CRC32;

Query Match 84.4%; Score 38; DB 2; Length 349;
 Best Local Similarity 71.4%; Pred. No. 2.18e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 212 tcgmgis 218
 | |||:
 QY 1 TSGMGVS 7

RESULT 14

ID LIG_PHLRA STANDARD; PRT; 361 AA.
 AC P20010;
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DE LIGNINASE III PRECURSOR (EC 1.11.1.-) (LIGNIN PEROXIDASE).
 OS PHLEBIA RADIATA (WHITE-ROT FUNGUS).
 CC EUKARYOTA; FUNGI; BASIDIOMYCOTINA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=79;
 RX MEDLINE; 90185208.
 RA SALOHEIMO M., BARAJAS V., NIKU-PAAYOLA M.L., KNOWLES J.K.C.;
 RL GENE 85:343-351(1989).
 CC -/- CATALYTIC ACTIVITY: DEPOLYMERIZATION OF LIGNIN. CATALYSES THE
 C (ALPHA)-C (BETA) CLEAVAGE OF THE PROPYL SIDE CHAINS OF LIGNIN.
 CC -/- PATHWAY: FIRST STEP IN LIGNIN DEGRADATION.

DR PIR; JQ0374; JQ0374.
 DR HSP; P31837; ILGA.
 DR PROSITE; PS00435; PEROXIDASE 1.
 DR PROSITE; PS00436; PEROXIDASE 2.
 KW OXIDOREDUCTASE; PEROXIDASE; HEME; GLYCOPROTEIN; MULTIGENE FAMILY;
 KW LIGNIN DEGRADATION; SIGNAL.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 361 LIGNINASE.
 FT ACT SITE 66 66 BY SIMILARITY.
 FT ACT SITE 70 70 DISTAL HISTIDINE (BY SIMILARITY).
 FT ACT SITE 199 199 PROXIMAL HISTIDINE (HEME AXIAL LIGAND).
 FT CARBOHYD 268 268 POTENTIAL.
 SQ SEQUENCE 361 AA; 38439 MW; F65A5254 CRC32;

Query Match 84.4%; Score 38; DB 5; Length 361;
 Best Local Similarity 83.3%; Pred. No. 2.18e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 124 sgmgva 129
 | |||:
 QY 2 SGMGVS 7

RESULT 15

ID PGCA_BOVIN STANDARD; PRT; 719 AA.
 AC P13608;
 DT 01-JAN-1990 (REL. 13, CREATED)

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DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
 DE CARTILAGE-SPECIFIC PROTEOGLYCAN CORE PROTEIN (CSPCP) (AGGREGAN)
 DE (FRAGMENT).
 OS BOS TAURUS (BOVINE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87270630.
 RA OLDREGE A., ANTONSSON P., HEINEGARD D.;
 RL BIOCHEM. J. 243:255-259(1987).
 RN [2]
 RP PARTIAL SEQUENCE.
 RX MEDLINE; 85027710.
 RA PERIN J.P., BONNET F., JOLLES J., JOLLES P.;
 RL FEBS LETT. 176:37-42(1984).
 RN [3]
 RP PARTIAL SEQUENCE.
 RX MEDLINE; 87005253.

RA PERIN J.P., BONNET F., JOLLES P.;
 RL FEBS LETT. 206:73-77(1986).
 CC -/- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR
 MATRIX OF CARTILAGINOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN
 IS TO RESIST COMPRESSION IN CARTILAGE.
 CC -/- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE
 CHAINS, N-LINKED AND O-LINKED OLIGOSACCHARIDES.
 CC -/- SIMILARITY: CONTAINS A C-TYPE LECTIN FAMILY DOMAIN.

DR EMBL; X16486; G282; -.
 DR PIR; A27752; A27752.
 DR PIR; A29164; A29164.
 DR PIR; B29164; B29164.
 DR PIR; E29164; E29164.
 DR PIR; G27751; G27751.
 DR HSP; P20693; IHLJ.
 DR PROSITE; PS00615; C TYPE LECTIN.
 KW GLYCOPROTEIN; CARTILAGE; PROTEOGLYCAN; LECTIN.
 FT NON_TER 1 1
 FT DOMAIN 513 631 C-TYPE LECTIN.
 FT CARBOHYD 353 353 POTENTIAL.
 SQ SEQUENCE 719 AA; 74501 MW; FAF270AE CRC32;

Query Match 84.4%; Score 38; DB 6; Length 719;
 Best Local Similarity 85.7%; Pred. No. 2.18e+01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 369 taglqvs 375
 | |||:
 QY 1 TSGMGVS 7

Search completed: Tue Mar 18 10:13:26 1997
 Job time : 9 secs.

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```
RESULT 2
ENTRY PT0174 #type fragment
TITLE Ig heavy chain precursor V region (IDB5.7) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
12-Apr-1995
ACCESSIONS PT0174
REFERENCE PT0174
#authors Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.
#journal Mol. Immunol. (1991) 28:505-515
#title Specificity and variable region cDNA sequence of an isogenic monoclonal antidiotype to an anti-alpha (1-6) dextran.
#cross-references MUID:91287738
#accession PT0174
##molecule_type mRNA
##residues 1-143 ##label PER
##experimental_source strain BALB/c
COMMENT IDB5.7 is an antibody to anti-alpha (1-6) dextran.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 143 #checksum 3660

Query Match 100.0%; Score 45; DB 5; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.75e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 tsgmgs 56
|||||
Qy 1 TSGMGVS 7

RESULT 3
ENTRY S26465 #type complete
TITLE Ig heavy chain V region - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
12-Apr-1995
ACCESSIONS S26465
REFERENCE S26459
#authors Kavalier, J.
#submission submitted to the EMBL Data Library, April 1991
#accession S26465
##status preliminary
##molecule_type mRNA
##residues 1-113 ##label KAV
##cross-references EMBL:X59115
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 113 #molecular_weight 12508 #checksum 2993

Query Match 93.3%; Score 42; DB 5; Length 113;
Best Local Similarity 85.7%; Pred. No. 7.9e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 22 tsgmgs 28
|||||
Qy 1 TSGMGVS 7

RESULT 4
ENTRY S39304 #type complete
TITLE flagellin - Borrelia afzelii
ORGANISM #formal_name Borrelia afzelii
DATE 25-Dec-1994 #sequence_revision 25-Dec-1994 #text_change
```

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```
25-Dec-1994
ACCESSIONS S39304
REFERENCE S39302
#authors Noppa, L.; Burman, N.; Sadziene, A.; Barbour, A.G.; Bergstrom, S.
#submission submitted to the EMBL Data Library, September 1993
#accession S39304
##status preliminary
##residues 1-336 ##label NOP
##cross-references EMBL:X75202
SUMMARY #length 336 #molecular_weight 35737 #checksum 8921

Query Match 88.9%; Score 40; DB 14; Length 336;
Best Local Similarity 71.4%; Pred. No. 2.12e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagmgs 49
|||||
Qy 1 TSGMGVS 7

RESULT 5
ENTRY A38450 #type complete
TITLE flagellin - Lyme disease spirochete (strain GeHo)
ORGANISM #formal_name Borrelia burgdorferi #common_name Lyme disease spirochete
DATE 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change
18-Nov-1994
ACCESSIONS A38450; S04091; A60276; A61075
REFERENCE A38450
#authors Gassmann, G.S.; Jacobs, E.; Deutzmann, R.; Goebel, U.B.
#journal J. Bacteriol. (1991) 173:1452-1459
#title Analysis of the Borrelia burgdorferi GeHo fla gene and antigenic characterization of its gene product.
#cross-references MUID:91139587
#accession A38450
##molecule_type DNA
##residues 1-336 ##label GAS
##cross-references CB:X56334
REFERENCE S04091
#authors Gassmann, G.S.; Kramer, M.; Goebel, U.B.; Wallich, R.
#journal Nucleic Acids Res. (1989) 17:3590
#title Nucleotide sequence of a gene encoding the Borrelia burgdorferi flagellin.
#cross-references MUID:89263802
#accession S04091
##molecule_type DNA
##residues 1-336 ##label GA2
##cross-references EMBL:X14941
##note translation of nucleotide sequence not given
REFERENCE A60276
#authors Collins, C.; Peltz, G.
#journal Infect. Immun. (1991) 59:514-520
#title Immunoreactive epitopes on an expressed recombinant flagellar protein of Borrelia burgdorferi.
#accession A60276
##status not compared with conceptual translation
##molecule_type mRNA
##residues 1-336 ##label COL
##experimental_source strain CAL2
##note the authors say this sequence from strain CAL2 differs from the sequence from strain GeHo, but the GeHo sequence shown for comparison is inconsistent with reference A38450
```


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```

REFERENCE      A61075
#authors      Gasmann, G.S.; Deutzmann, R.; Vogt, A.; Goebel, U.B.
#journal      FEMS Microbiol. Lett. (1989) 60:101-106
#title        N-terminal amino acid sequence of the Borrelia burgdorferi
              flagellin.
#accession    A61075
#molecule_type protein
##residues_   1-15,'X',17-29 ##label GA3
GENETICS
#gene         fla
#superfamily flagellin
#flagellum
#length 336 #molecular-weight 35765 #checksum 9490
Query Match   88.9%; Score 40; DB 6; Length 336;
Best Local Similarity 71.4%; Pred. No. 2.12e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aaqmgvs 49
   ::|||
Qy 1 TSGMGVS 7

RESULT 6
ENTRY      S39303 #type complete
TITLE      flagellin - Borrelia garinii
#formal_name Borrelia garinii
ORGANISM   25-Dec-1994 #sequence_revision 25-Dec-1994 #text_change
DATE       25-Dec-1994
ACCESSIONS S39303
REFERENCE   S39302
#authors   Noppa, L.; Burman, N.; Sadziene, A.; Barbour, A.G.;
            Bergstrom, S.
#submission submitted to the EMBL Data Library, September 1993
#accession  S39303
#status     preliminary
##residues 1-336 ##label NOP
##cross-references EMBL:X75203
SUMMARY     #length 336 #molecular-weight 35765 #checksum 9778

Query Match   88.9%; Score 40; DB 14; Length 336;
Best Local Similarity 71.4%; Pred. No. 2.12e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aaqmgvs 49
   ::|||
Qy 1 TSGMGVS 7

RESULT 7
ENTRY      S39305 #type complete
TITLE      flagellin - Lyme disease spirochete
#formal_name Borrelia burgdorferi #common_name Lyme disease
ORGANISM   spirochete
DATE       06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change

ACCESSIONS S39305
REFERENCE   S39302
#authors   Noppa, L.; Burman, N.; Sadziene, A.; Barbour, A.G.;
            Bergstrom, S.
#submission submitted to the EMBL Data Library, September 1993
#accession  S39305
#status     preliminary
##molecule_type DNA

```

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```

##residues    1-336 ##label NOP
##cross-references EMBL:X75200
SUMMARY       #length 336 #molecular-weight 35789 #checksum 9643

Query Match   88.9%; Score 40; DB 7; Length 336;
Best Local Similarity 71.4%; Pred. No. 2.12e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aaqmgvs 49
   ::|||
Qy 1 TSGMGVS 7

RESULT 8
ENTRY      FLLYB3 #type complete
TITLE      flagellin - Lyme disease spirochete (strain B31)
ALTERNATE_NAMES 41K antigen
ORGANISM      #formal_name Borrelia burgdorferi #common_name Lyme disease
              spirochete
DATE          31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
              18-Nov-1994
ACCESSIONS    A41470; S04696; B60118; A60705; S08541
REFERENCE      A41470
#authors      Wallich, R.; Motor, S.E.; Simon, M.M.; Ebnet, K.; Heiberger,
              A.; Kramer, M.D.
#journal      Infect. Immun. (1990) 58:1711-1719
#title        The Borrelia burgdorferi flagellum-associated 41-kilodalton
              antigen (flagellin): molecular cloning, expression, and
              amplification of the gene.
#cross-references MUID:90256248
#accession    A41470
#molecule_type DNA
##residues    1-336 ##label WA2
##cross-references GB:X16833
REFERENCE      S04091
#authors      Gasmann, G.S.; Kramer, M.; Goebel, U.B.; Wallich, R.
#journal      Nucleic Acids Res. (1989) 17:3590
#title        Nucleotide sequence of a gene encoding the Borrelia
              burgdorferi flagellin.
#cross-references MUID:89263802
#accession    S04696
#molecule_type DNA
##residues    1-336 ##label GAS
##cross-references EMBL:X15661
#note         translation of nucleotide sequence not given
REFERENCE      A60118
#authors      Luft, B.J.; Jiang, W.; Munoz, P.; Battwyler, R.J.; Gorevic,
              P.D.
#journal      Infect. Immun. (1989) 57:3637-3645
#title        Biochemical and immunological characterization of the surface
              proteins of Borrelia burgdorferi.
#cross-references MUID:90035442
#accession    B60118
#molecule_type protein
##residues    1-9,'A',11-13,'X',15-18 ##label LUF
REFERENCE      A60705
#authors      Coleman, J.L.; Benach, J.L.
#journal      J. Clin. Invest. (1989) 84:322-330
#title        Identification and characterization of an endoflagellar
              antigen of Borrelia burgdorferi.
#accession    A60705
#molecule_type protein
##residues    1-10 ##label COL
CLASSIFICATION #superfamily flagellin

```


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```
KEYWORDS      flagellum; periplasmic space
SUMMARY       #length 336 #molecular-weight 35751 #checksum 54

Query Match      88.9%; Score 40; DB 3; Length 336;
Best Local Similarity 71.4%; Pred. No. 2.12e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagmgvs 49
   ::|||||
Oy 1 TSGMGVS 7

RESULT 9
ENTRY   S37728 #type complete
TITLE   P41 protein - Lyme disease spirochete
ORGANISM #formal_name Borrelia burgdorferi #common_name Lyme disease
         spirochete
DATE    20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
        20-Feb-1995
ACCESSIONS S37728
REFERENCE  S37726
#authors  Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.;
           Schwab, E.; Soutschek, E.; Will, G.; Wilcke, B.
#journal  Med. Microbiol. Immunol. (1993) 182:37-50
#title    Genetic heterogeneity of the genes coding for the outer
           surface protein C (OspC) and the flagellin of Borrelia
           burgdorferi.
#accession S37728 preliminary
##status  #molecule type DNA
##residues_ 1-336 ##label JAU
##cross-references EMBL:X69598
SUMMARY    #length 336 #molecular-weight 35754 #checksum 9781

Query Match      88.9%; Score 40; DB 7; Length 336;
Best Local Similarity 71.4%; Pred. No. 2.12e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagmgvs 49
   ::|||||
Oy 1 TSGMGVS 7

RESULT 10
ENTRY   S37729 #type complete
TITLE   P41 protein - Lyme disease spirochete
ORGANISM #formal_name Borrelia burgdorferi #common_name Lyme disease
         spirochete
DATE    20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
        20-Feb-1995
ACCESSIONS S37729
REFERENCE  S37726
#authors  Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.;
           Schwab, E.; Soutschek, E.; Will, G.; Wilcke, B.
#journal  Med. Microbiol. Immunol. (1993) 182:37-50
#title    Genetic heterogeneity of the genes coding for the outer
           surface protein C (OspC) and the flagellin of Borrelia
           burgdorferi.
#accession S37729 preliminary
##status  #molecule type DNA
##residues_ 1-336 ##label JAU
##cross-references EMBL:X69597
SUMMARY    #length 336 #molecular-weight 35753 #checksum 9281
```

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```
Query Match      88.9%; Score 40; DB 7; Length 336;
Best Local Similarity 71.4%; Pred. No. 2.12e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagmgvs 49
   ::|||||
Oy 1 TSGMGVS 7

RESULT 11
ENTRY   I39171 #type complete
TITLE   cyclin A/CDK2-associated p45 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change
        23-Feb-1996
ACCESSIONS I39171
REFERENCE  I39170
#authors  Zhang, H.; Kobayashi, R.; Galaktionov, K.; Beach, D.
           Cell (1995) 82:915-925
#journal  p19Skl and p45Skp2 are essential elements of the cyclin
           A-CDK2 S phase kinase.
#title    A-CDK2 S phase kinase.
#cross-references MUID:96016087
#accession I39171 preliminary
##status  #molecule type mRNA
##residues_ 1-435 ##label RES
##cross-references EMBL:U33761; NID:g995825; CDS_PID:g995826
GENETICS
#note     gene name Skp2
SUMMARY    #length 435 #molecular-weight 48989 #checksum 8642

Query Match      88.9%; Score 40; DB 11; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.12e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 46 sgmgvs 51
   |||||
Oy 2 SCMGVS 7

RESULT 12
ENTRY   S20554 #type complete
TITLE   pyruvate,water dikinase (EC 2.7.9.2) - Escherichia coli
ALTERNATE_NAMES phosphoenolpyruvate synthase
ORGANISM #formal_name Escherichia coli
DATE    16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
        28-Apr-1993
ACCESSIONS S20554; S14838
REFERENCE  S20554
#authors  Niersbach, M.; Kreuzaler, F.; Geerse, R.H.; Postma, P.W.;
           Hirsch, H.J.
#journal  Mol. Gen. Genet. (1992) 231:332-336
#title    Cloning and nucleotide sequence of the Escherichia coli K-12
           ppsA gene, encoding PEP synthase.
#cross-references MUID:92140374
#accession S20554
##molecule type DNA
##residues_ 1-792 ##label NIE
##cross-references EMBL:X59381
GENETICS
#gene     ppsA
#keywords transferase
SUMMARY    #length 792 #molecular-weight 87434 #checksum 1665
```


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Query Match 88.9%; Score 40; DB 7; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.12e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 39 sgmgvs 44
|||||
Qy 2 SCMGVS 7

RESULT 13
ENTRY S33821 #type complete
TITLE median body protein - Giardia lamblia
ORGANISM #formal name Giardia lamblia
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
ACCESSIONS S33821
REFERENCE S33821
#authors Marshall, J.; Holberton, D.V.
#journal J. Mol. Biol. (1993) 231:521-530
#title Sequence and structure of a new coiled coil protein from a microtubule bundle in Giardia.
#accession S33821
##status preliminary
##molecule_type mRNA
##residues 1-857 ##label MAR
##cross-references EMBL:X64517
SUMMARY #length 857 #molecular-weight 100583 #checksum 6805

Query Match 88.9%; Score 40; DB 10; Length 857;
Best Local Similarity 71.4%; Pred. No. 2.12e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 795 sgmgvs 801
:|||||
Qy 1 TSCMGVS 7

RESULT 14
ENTRY PQ0098 #type fragment
TITLE citB protein - Salmonella typhimurium (fragment)
ORGANISM #formal name Salmonella typhimurium
DATE 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Mar-1993
ACCESSIONS PQ0098
REFERENCE J00576
#authors Shinamoto, T.; Iwawa, H.; Daimon, H.; Ishiguro, N.; Shinagawa, M.; Sakano, Y.; Tsuda, M.; Tsuchiya, T.
#journal J. Biochem. (1991) 110:22-28
#title Cloning and nucleotide sequence of the gene (citA) encoding a citrate carrier from Salmonella typhimurium.
#cross-references MUID:92041761
#accession PQ0098
##molecule_type DNA
##residues 1-58 ##label SH1
##experimental_source strain LT2
GENETICS
#gene citB
SUMMARY #length 58 #checksum 2672

Query Match 86.7%; Score 39; DB 6; Length 58;
Best Local Similarity 83.3%; Pred. No. 3.41e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 4 tsgmgi 9
|||||
Qy 1 TSCMGV 6

RESULT 15
ENTRY A31142 #type fragments
TITLE gelsolin, ovary - African clawed frog (fragments)
ORGANISM #formal name Xenopus laevis #common name African clawed frog
DATE 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 08-Jul-1994
ACCESSIONS A31142; B31142
REFERENCE A31142
#authors Ankenbauer, T.; Kleinschmidt, J.A.; Vandekerckhove, J.; Franke, W.W.
#journal J. Cell Biol. (1988) 107:1489-1498
#title Proteins regulating actin assembly in oogenesis and early embryogenesis of Xenopus laevis: gelsolin is the major cytoplasmic actin-binding protein.

#cross-references MUID:89008590
#accession A31142
##molecule_type mRNA
##residues 21-437 ##label AN1
#accession B31142
##molecule_type protein
##residues 1-20 ##label AN2
##cross-references EMBL:X13319
CLASSIFICATION #superfamily gelsolin; gelsolin repeat homology
KEYWORDS actin binding
FEATURE 101-419
SUMMARY #domain gelsolin repeat homology #label GEL2
#length 437 #checksum 6465

Query Match 86.7%; Score 39; DB 5; Length 437;
Best Local Similarity 71.4%; Pred. No. 3.41e+01;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 58 tdmgva 64
|||||
Qy 1 TSCMGVS 7

Search completed: Tue Mar 18 10:13:56 1997
Job time : 12 secs.

MAREK'S DISEASE VIRUS

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:14:13 1997; MasPar time 1.70 Seconds

42.284 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-22

Description: (1-7) from US08612929.pep

Perfect Score: 45

Sequence: 1 TSGMGVS 7

Scoring table: PAM 150

Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 13.161; Variance 34.970; scale 0.376

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	45	100.0	7	13	R70198	Mab 3B9 heavy chain C
2	45	100.0	140	13	R70190	Mouse Mab 3B9 heavy c
3	45	100.0	141	13	R70192	Humanized antibody 3B
4	45	100.0	141	13	R70191	Chimeric antibody 3B9
5	45	100.0	246	11	R58612	IL-6 binding inhibito
6	42	93.3	111	12	R66304	Human immunoglobulin
7	42	93.3	120	17	R88109	Murine anti-Protein C
8	42	93.3	139	17	R88107	Murine anti-Protein C
9	40	88.9	336	17	R75747	B. burgdorferi strain
10	40	88.9	336	5	R25897	Flagellar protein of
11	40	88.9	341	3	R13142	B. burgdorferi strain
12	40	88.9	1074	4	R24102	Marek's disease virus

13	40	88.9	1274	7	R34714	Bacillus subtilis srf	6.77e+01
14	39	86.7	1128	9	R49994	Mouse carboxypeptidas	8.99e+01
15	38	84.4	22	6	R31612	Fragment XXXI homolog	1.19e+02
16	38	84.4	348	5	R25566	Beta-IG-M2.	1.19e+02
17	38	84.4	349	16	R79964	Connective tissue gro	1.19e+02
18	38	84.4	530	10	R57091	Small round virus SRS	1.19e+02
19	37	82.2	7	10	R54104	Humanised anti-HIV MA	1.57e+02
20	37	82.2	122	11	R54101	Humanised MAB H-chain	1.57e+02
21	37	82.2	122	10	R54110	Humanised anti-HIV MA	1.57e+02
22	36	80.0	52	1	R04577	Recombinant polypepti	2.08e+02
23	36	80.0	120	16	R92089	Anti-RSV F glycoprote	2.08e+02
24	36	80.0	120	16	R92088	CDR-grafted anti-RSV	2.08e+02
25	36	80.0	248	12	R60692	Mature H. halobium ba	2.08e+02
26	36	80.0	262	12	R60691	Fragment of H. halobi	2.08e+02
27	36	80.0	262	1	R26419	Bacteriorhodopsin dou	2.08e+02
28	36	80.0	453	12	R63790	Aspergillus aculeatus	2.08e+02
29	36	80.0	457	14	R78184	E.coli cell division	2.08e+02
30	36	80.0	506	10	R50010	Secretory alkaline ph	2.08e+02
31	36	80.0	573	2	R22670	Gamma peptide of acid	2.08e+02
32	36	80.0	617	8	R42392	MCI haemagglutinin.	2.08e+02
33	36	80.0	617	8	R42393	JM haemagglutinin.	2.08e+02
34	36	80.0	617	8	R42388	Consensus haemaggluti	2.08e+02
35	36	80.0	617	8	R42391	Chicago 2 haemaggluti	2.08e+02
36	36	80.0	617	8	R49925	Consensus haemaggluti	2.08e+02
37	36	80.0	617	8	R42389	San Diego haemaggluti	2.08e+02
38	36	80.0	617	8	R42387	Moratan haemagglutini	2.08e+02
39	36	80.0	617	8	R42390	Chicago 1 haemaggluti	2.08e+02
40	36	80.0	687	12	R63188	Variant cyclomaltodex	2.08e+02
41	36	80.0	713	1	R06110	Sequence of cyclomalt	2.08e+02
42	36	80.0	713	3	R12743	Enzyme with starch de	2.08e+02
43	36	80.0	713	3	R10052	Cyclomaltodextrin glu	2.08e+02
44	36	80.0	775	15	R79950	Enzyme Q36.	2.08e+02
45	36	80.0	3647	1	R05041	Filamentous haemagglu	2.08e+02

ALIGNMENTS

RESULT	1
ID	R70198 standard; Protein; 7 AA.
AC	R70198;
DT	20-SEP-1995 (first entry)
DE	MAB 3B9 heavy chain CDR.
KW	Chimeric antibody; humanized antibody; antibody engineering;
KW	monoclonal antibody; Mab; interleukin-4; IL-4; allergy; CDR;
KW	complementarity determining region.
OS	Mus sp.
PN	W09507301-A.
PD	16-MAR-1995.
PF	07-SEP-1994; U10308.
PR	07-SEP-1993; US-117366.
PR	14-OCT-1993; US-136783.
PA	(SMIK) SMITHKLINE BEECHAM CORP.
PI	(SMIK) SMITHKLINE BEECHAM PLC.
PI	Gross MS, Holmes SD, Sylvester DR;
DR	WPI; 95-123387/16.
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT	from high affinity mAbs - useful in treatment of IL-4-mediated
PT	and IgE-mediated allergic conditions
PS	Disclosure; Page 56; 97pp; English.
CC	Spleen cells from mice immunized with human IL-4 were used to prepare
CC	hybridomas, which were screened for anti-IL-4 Mab secretion. Only
CC	clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC	chains were cloned into pGEM7f+ and transformed into E. coli
CC	DH5-alpha. A heavy chain cDNA clone was sequenced (083491) that

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3

CC encoded the protein given in R70190. 3 CDRs (R70198-200) were
CC identified.
SQ Sequence 7 AA;

Query Match 100.0%; Score 45; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.59e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 tsgmgvs 7
|||||
Qy 1 TSGMGVS 7

RESULT 2

ID R70190 standard; Protein; 140 AA.

AC R70190;

DT 20-SEP-1995 (first entry)

DE Mouse MAb 3B9 heavy chain.

KW Chimeric antibody; humanized antibody; antibody engineering;

KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.

OS Mus sp.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig_peptide

FT Region 50..56

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 71..86

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 119..129

FT /label= CDR

FT /note= "complementarity determining region"

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

DR N-PSDB; 083491.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Fig.2; 97pp; English.

CC Spleen cells from mice immunized with human IL-4 were used to prepare

CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only

CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy

CC chains were cloned into pGEM7f+ and transformed into E. coli

CC DH5-alpha. The clones were sequenced (083490-91), and used for

CC antibody engineering.

SQ Sequence 140 AA;

Query Match

Best Local Similarity 100.0%; Score 45; DB 13; Length 140;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 tsgmgvs 56
|||||
Qy 1 TSGMGVS 7

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RESULT 3

ID R70192 standard; Protein; 141 AA.

AC R70192;

DT 20-SEP-1995 (first entry)

DE Humanized antibody 3B9 heavy chain.

KW Humanized antibody; antibody engineering; monoclonal antibody;

KW MAb; interleukin-4; IL-4; allergy.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig_peptide

FT Region 51..57

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 72..87

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 120..130

FT /label= CDR

FT /note= "complementarity determining region"

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

DR N-PSDB; 083493.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Fig.4; 97pp; English.

CC A humanized antibody heavy chain variable region and signal

CC sequence is given in R70192. The signal sequence is also

CC provided in R70193. The CDR sequences of the construct are

CC identical to the native CDRs of mouse anti-human IL-4 MAb

CC 3B9 (R70198-200).

SQ Sequence 141 AA;

Query Match

Best Local Similarity 100.0%; Score 45; DB 13; Length 141;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 51 tsgmgvs 57
|||||
Qy 1 TSGMGVS 7

RESULT 4

ID R70191 standard; Protein; 141 AA.

AC R70191;

DT 20-SEP-1995 (first entry)

DE Chimeric antibody 3B9 heavy chain.

KW Chimeric antibody; antibody engineering; monoclonal antibody;

KW MAb; interleukin-4; IL-4; allergy.

OS Homo sapiens; Mus sp.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig_peptide

FT Region 51..57

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 72..87
FT /label= CDR
FT /note= "complementarity determining region"
FT Peptide 120..130
FT /label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvestre DR;
DR WPI; 95-123387/16.
DR N-PSDB; Q83492.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions
PS Disclosure; Fig.3; 97pp; English.
CC A human/mouse chimeric antibody heavy chain variable region was CC constructed (given in R70191) that contained the mouse anti-human CC IL-4 Mab 3B9 variable region including 3 CDRs (R70198-200) and a CC human antibody signal peptide (R70193). The construct was used CC for humanized antibody production.
SQ Sequence 141 AA;

Query Match 100.0%; Score 45; DB 13; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.59e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 51 tsgmgvs 57
|||||
Qy 1 TSGMGVS 7

RESULT 5
ID R58612 standard; Protein; 246 AA.
AC R58612;
DT 28-APR-1995 (first entry)
DE IL-6 binding inhibitor.
KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
KW septic shock; multiple myeloma; ss.
OS Homo sapiens.
PN EP-617126-A.
PD 28-SEP-1994.
PF 16-FEB-1994; 102346.
PR 17-FEB-1993; JP-028173.
PA (AJIN) AJINOMOTO KK.
PI Hamuro J, Nakazawa H, Shimamura T;
DR WPI; 94-295777/37.
DR N-PSDB; Q70612.
PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to PT its receptor - useful for treating autoimmune disease induced PT or aggravated by IL-6
PS Claim 5; Page 18; 26pp; English.
CC Q70612 codes for human interleukin-6 binding inhibitor, the CC polypeptide described in R58612. This polypeptide inhibits the CC binding of human IL-6 to its receptor, and can therefore be CC useful in the treatment of a variety of autoimmune diseases;
CC specifically in the treatment of rheumatoid arthritis, septic CC shock due to bacterial infection and multiple myeloma.
SQ Sequence 246 AA;

Query Match 100.0%; Score 45; DB 11; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.59e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 153 tsgmgvs 159
|||||
Qy 1 TSGMGVS 7

RESULT 6
ID R66304 standard; Protein; 111 AA.
AC R66304;
DT 02-AUG-1995 (first entry)
DE Human immunoglobulin variable heavy chain #10.
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW cosmid; placenta; vector; pJ881; E.coli; mammalian.
OS Homo sapiens.
PN W09426895-A.
PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PR 10-MAY-1993; WO-J00603.
PA (NIBS) JAPAN TOBACCO INC.
PI Honjo T, Matsuda F;
DR WPI; 95-006791/01.
DR N-PSDB; Q78948.
PT DNA fragment comprising human immunoglobulin Vh genes - for the PT production of human immunoglobulin in mammalian hosts
PS Claim 19; Page 43-44; 130pp; Japanese.
CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were CC isolated and cloned from a series of cosmid constructs: Y202, Y103, Y21; CC Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using primers CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The CC fragments cover a region of 800 kb. The DNA fragments were isolated from CC high molecular weight DNA from human placenta. The DNA was partially CC digested with TagI restriction enzyme. The fragments were separated by CC gel electrophoresis and 35-45 kb fractions were collected. The fragments CC were ligated with ClaI-digested cosmid vector pUB81. The ligation CC products were in vitro packed and infected into E.coli 490A. The CC fragments were then subcloned by colony hybridisation. The Vh genes and CC the DNA fragments encoding them are useful in producing human CC immunoglobulin in mammalian hosts.

Query Match 93.3%; Score 42; DB 12; Length 111;
Best Local Similarity 85.7%; Pred. No. 3.81e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 49 tsgmgvs 55
|||||
Qy 1 TSGMGVS 7

RESULT 7
ID R88109 standard; peptide; 120 AA.
AC R88109;
DT 25-JUL-1996 (first entry)
DE Murine anti-Protein C Mab HPC-4 Vh gamma mature peptide.
KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
KW zymogen; cleavage; mouse; humanised antibody; variable region;
KW light chain; inhibition; antithrombin; coagulation; tumour.
OS Mus musculus.
PN W09534652-A1.
PD 21-DEC-1995.

PF 09-JUN-1995; U07372.
PR 10-JUN-1994; US-259321.
PA (OKLA-) OKLAHOMA MED RES FOUND.
PI Esmon CT, Rezaie A;
DR WPI; 96-049681/05.
DR N-PSDB; T09300.
PT Calcium-binding monoclonal antibody immunoreactive with Protein C -
PT inhibits Protein C anticoagulant activation by
PT thrombin-thrombomodulin, e.g. for treating tumours
PS Claim 2; Page 29; 41pp; English.
CC This is the amino acid sequence of the mature peptide from the murine
CC anti-protein C monoclonal antibody HPC-4 heavy chain variable region.
CC HPC-4 recognises the activation peptide region (R88106) of the heavy
CC chain of protein C, a vitamin K-dependent plasma protein zymogen.
CC Protein C is converted to activated protein C (APC) by cleavage between
CC the Arg-Leu amino acid contained within the activation peptide sequence.
CC HPC-4 prevents protein C activation to APC by binding to this region.
CC The DNA sequences encoding the variable regions of the heavy and light
CC chains of the antibody (T09299-302) were used to construct humanised
CC antibodies using the PCR primers T09303-9. The humanised antibodies are
CC useful as inhibitors of coagulation and can be used for the treatment of
CC tumours by inhibiting the anticoagulant activity of APC by preventing
CC conversion of protein C to APC.
SQ Sequence 120 AA;

Query Match 93.3%; Score 42; DB 17; Length 120;
Best Local Similarity 85.7%; Pred. No. 3.81e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 31 tsgmgvg 37
|||||:
Qy 1 TSGMGVS 7

RESULT 8

ID R88107 standard; Protein; 139 AA.
AC R88107;
DT 25-JUL-1996 (first entry)
DE Marine anti-Protein C MAb HPC-4 VH gamma protein.
KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
KW zymogen; cleavage; mouse; humanised antibody; variable region;
KW light chain; inhibition; anticoagulant; coagulation; tumour.
OS Mus musculus.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "signal peptide"
FT Peptide 20..139
FT /note= "mature peptide"
PN W09534652-AL.
PD 21-DEC-1995.
PF 09-JUN-1995; U07372.
PR 10-JUN-1994; US-259321.
PA (OKLA-) OKLAHOMA MED RES FOUND.
PI Esmon CT, Rezaie A;
DR WPI; 96-049681/05.
DR N-PSDB; T09299.
PT Calcium-binding monoclonal antibody immunoreactive with Protein C -
PT inhibits Protein C anticoagulant activation by
PT thrombin-thrombomodulin, e.g. for treating tumours
PS Claim 2; Page 29; 41pp; English.
CC This is the amino acid sequence of the heavy chain variable region from
CC the murine anti-protein C monoclonal antibody HPC-4 which recognises
CC the activation peptide region (R88106) of the heavy chain of protein C,
CC a vitamin K-dependent plasma protein zymogen. Protein C is converted to

CC activated protein C (APC) by cleavage between the Arg-Leu amino acid
CC contained within the activation peptide sequence. HPC-4 prevents protein
CC C activation to APC by binding to this region. The DNA sequences encoding
CC the variable regions of the heavy and light chains of the antibody
CC (T09299-302) were used to construct humanised antibodies using the PCR
CC primers T09303-9. The humanised antibodies are useful as inhibitors of
CC coagulation and can be used for the treatment of tumours by inhibiting
CC the anticoagulant activity of APC by preventing conversion of protein C
CC to APC.
SQ Sequence 139 AA;

Query Match 93.3%; Score 42; DB 17; Length 139;
Best Local Similarity 85.7%; Pred. No. 3.81e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 50 tsgmgvg 56
|||||:
Qy 1 TSGMGVS 7

RESULT 9

ID R15747 standard; Protein; 336 AA.
AC R15747;
DT 30-JUL-1996 (first entry)
DE B. burgdorferi strain B31 antigen P41 (P41-B31).
KW Strain B31; P41 antigen; antigenic domain; chimaeric protein;
KW treatment; diagnosis; infection; vaccine; Lyme borreliosis;
KW immunodiagnostic assay; antibody; T-cell reactivity;
KW chimeric.
OS Borrelia burgdorferi.
PN W09512676-AL.
PD 11-MAY-1995.
PF 27-OCT-1994; U12352.
PR 01-NOV-1993; US-148191.
PR 29-APR-1994; US-235836.
PA (ASU-) ASSOC UNIVERSITIES INC.
PI Dunn JJ, Luft BJ;
DR WPI; 95-215034/28.
DR N-PSDB; 090744.
PT Chimeric protein comprising 2 or more antigenic Borrelia
PT polypeptide(s) - useful in a vaccine against Lyme borreliosis and in
PT immuno:diagnostic assays
PS Example 1; Fig 40; 200pp; English.
CC The present sequence is the B. burgdorferi strain B31, antigen
CC P41 (P41-B31). Using chemical or enzymatic methods, peptide
CC fragments of P41-B31 were prep'd., and analysed by western blot to
CC assess their ability to bind different anti-P41 monoclonal
CC antibodies. The information obt'd. was used to locate antigenic
CC domains in P41-B31, the epitopes of which were mapped with the
CC aid of site directed mutagenesis. Identical analyses were performed
CC on a selection of antigens purified from a variety of B. burgdorferi
CC strains, the results from which were utilised in the prepn. of a
CC pool of antigenic Borrelia polypeptides, and corresponding
CC polynucleotides. Chimaeric proteins comprising 2 or more antigenic
CC Borrelia polypeptides, that do not naturally occur in the same
CC protein, can be used in the treatment and diagnosis of Borrelia
CC infections, i.e. as a vaccine against Lyme borreliosis, in
CC immunodiagnostic assays to detect anti-Borrelia antibodies or to
CC measure T-cell reactivity.
SQ Sequence 336 AA;

Query Match 88.9%; Score 40; DB 17; Length 336;
Best Local Similarity 71.4%; Pred. No. 6.77e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagmgvs 49
 ::|||
 Qy 1 TSGMGVS 7

RESULT 10
 ID R25897 standard; Protein; 336 AA.
 AC R25897;
 DT 25-JAN-1993 (first entry)
 DE Flagellar protein of *Borrelia burgdorferi*.
 KW Flagella-less; vaccine; immunoassay; Lyme disease; epidemic bovine;
 KW abortion; avian spirochetosis; relapsing fever; flagellin.
 OS *Borrelia burgdorferi*.
 PN W09212235-A.
 PD 23-JUL-1992.
 PF 10-JAN-1992; U00181.
 PR 11-JAN-1991; US-641143.
 PA (TEXA) UNIV TEXAS.
 PI Barbour AG, Bundoc V;
 DR WPI; 92-268660/32.
 DR N-PSDB; Q27078.
 PT New flagella-less *Borrelia* and derived antigens - useful for
 PT vaccinating against and diagnosing *Borrelia* infections e.g. Lyme
 PT disease or relapsing fever
 PS Example 1; Fig 1; 88pp; English.
 CC The sequence shows a *Borrelia burgdorferi* flagellin protein whose
 CC sequence was deduced from that of the flagellin gene (fla gene)
 CC which was prep. by screening a genomic library of strain HB19 of *B.*
 CC *burgdorferi* in lambda FIX II with an oligonucleotide probe having a
 CC DNA sequence based on a conserved sequence of fla genes from two
 CC other strains of *B. burgdorferi* (Gassman, et al., 1989). The fla
 CC gene may be mutagenised to form an inactive fla gene e.g. by deletion
 CC of the entire coding region, or mutagenesis of the RBS, etc. so that
 CC functional flagellar protein is not produced. This mutated gene may
 CC be reintroduced into *Borrelia* species and cultures of flagellales
 CC *Borrelia* microbes produced. Antigens to the flagellales *Borrelia*
 CC sp. and vaccines can be used for the prevention and treatment of
 CC Lyme disease, epidemic bovine abortion, avian spirochetosis or
 CC relapsing fever. Since the transformed microorganism lacks the
 CC flagella antigen associated with autoantibody, it can be used to
 CC immunise individuals against Lyme disease without the risk of vaccine
 CC induced autoantibody formation.
 SQ Sequence 336 AA;

Query Match 88.9%; Score 40; DB 5; Length 336;
 Best Local Similarity 71.4%; Pred. No. 6.77e+01;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagmgvs 49
 ::|||
 Qy 1 TSGMGVS 7

RESULT 11
 ID R13142 standard; Protein; 341 AA.
 AC R13142;
 DT 27-SEP-1991 (first entry)
 DE *B. burgdorferi* strain PKo p41 protein.
 KW Lyme borreliosis; vaccine; flagellin.
 OS *Borrelia burgdorferi*.
 PN W09109870-A.
 PD 11-JUL-1991.
 PF 21-DEC-1990; E02282.

PR 22-DEC-1989; DE-942728.
 PR 13-JUN-1990; DE-018988.
 PA (MIKR-) MIKROGEN MOLEKULARB.
 PI Fuchs R, Wilske B, Preac-Mursic V, Motz M, Soutschek E.
 DR WPI; 91-222844/30.
 PT New *Borrelia burgdorferi* proteins - useful as immunoassay
 PT reagents and antigens for vaccine prodn.
 PS Claim 6; Page 48; 68pp; German.
 CC p41(flagellin) is a 41kD protein isolated from *B. burgdorferi*. The
 CC p41 coding sequence was isolated from a *B. burgdorferi* cDNA library
 CC and is used for recombinant production of the protein. p41 is
 CC immunologically active and is useful as an immunoassay reagent for
 CC detecting antibodies directed against *Borrelia* spp., esp. for early
 CC diagnosis of Lyme borreliosis.
 CC See Q12744-7, Q13297-8, R13139-R13142.
 SQ Sequence 341 AA;

Query Match 88.9%; Score 40; DB 3; Length 341;
 Best Local Similarity 71.4%; Pred. No. 6.77e+01;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 48 aagmgvs 54
 ::|||
 Qy 1 TSGMGVS 7

RESULT 12
 ID R24102 standard; Protein; 1074 AA.
 AC R24102;
 DT 14-NOV-1992 (first entry)
 DE Marek's disease virus MD20 polypeptide.
 KW Antibodies; vaccine; recombinant; poultry; passive immunotherapy;
 KW diagnostic immunoassay; anti-idiotypic; antigen.
 OS Marek's disease virus.
 PN EP-486106-A.
 PD 20-MAY-1992.
 PF 13-NOV-1991; 202947.
 PR 16-NOV-1990; US-615211.
 PA (ALAU) AKZO NV.
 PI Morgan RW;
 DR WPI; 92-168713/21.
 DR N-PSDB; Q24789.
 PT DNA encoding Marek's disease virus polypeptides MD18 and MD20 -
 PT and antibodies and vaccine useful for the protection of poultry
 PT against MDV infection
 PS Claim 8; Page 18; 31pp; English.
 CC The protein sequence of MDV MD20 was deduced from the DNA sequence
 CC obt'd. by screening a lambda EMBL 3 library made by infecting chicken
 CC embryo fibroblasts with a tissue-culture adapted passage of Marek's
 CC disease virus (MDV) strain GA, and incubating until a 90 percent
 CC cytopathic effect had developed. Vectors and host cells contg. the
 CC MDV MD20 gene and MDV polypeptides can be used in a vaccine to protect
 CC poultry against Marek's disease. Antibodies or antiserum raised by
 CC the polypeptides may be used in passive immunotherapy, diagnostic
 CC immunoassays and in the generation of anti-idiotypic antibodies for
 CC use in a test kit for Marek's disease. The vaccine may also contain
 CC immunogens related to other poultry pathogens, e.g. infectious
 CC bronchitis-virus, Newcastle disease-virus or infectious bursal
 CC disease-virus to produce a multivalent vaccine.
 CC See also R24102.
 SQ Sequence 1074 AA;

Query Match 88.9%; Score 40; DB 4; Length 1074;
 Best Local Similarity 71.4%; Pred. No. 6.77e+01;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 99 asgmva 105
:|||||
Qy 1 TSGMGVS 7

RESULT 13

ID R34714 standard; Protein; 1274 AA.
AC R34714;
DT 17-AUG-1993 (first entry)
DE Bacillus subtilis srfA operon ORF3 prod.
KW Multienzyme complex; surfactin synthetase; MCSS; ORF; surfactant.
OS Bacillus subtilis.
FH Key Location/Qualifiers
FT Peptide 146..152
FT /note= "repeat sequence"
FT Peptide 613..623
FT /note= "repeat sequence"
FT Peptide 857..877
FT /note= "repeat sequence"
FN EP-540074-A.
PD 05-MAY-1993.
PF 03-OCT-1992; 203037.
PR 09-OCT-1991; IT-MI2683.
PR 02-SEP-1992; IT-MI2044.
PA (ENIE) ENIRICERHE SPA.
PI Carrera P, Cosmina P, De FERRA E, Grandi G, Perego M;
PI Rodriguez F;
DR WPI; 93-145447/18.
DR N-PSDB; Q40706.
PT Multi-enzyme complex surfactin synthetase DNA - is isolated from
PT Bacillus subtilis, and used for prodn. of surfactin for use in
PT pharmaceutical prods.
PS Claim 15; Page 43-45; 70pp; English.
CC The Bacillus subtilis chromosomal DNA region comprises the srfA
CC operon which encodes the multienzyme complex surfactin synthetase
CC (MCSS). Analysis of the sequence showed four regions potentially
CC coding for proteins, a zone upstream of the first ORF contg. the
CC srfA operon promoter and a presumed terminator positioned downstream
CC of the stop codon of the fourth ORF. ORF3 encodes a protein
CC (shown) contg. a 1008 amino acid region (module 7) which can be
CC aligned with the modules of ORFs 1 and 2 to show highly conserved
CC sequences. The last 243 amino acids of the protein show no homology
CC with any modules or sequences of antibiotic peptide synthetases.
CC See also R34712-21.
SQ Sequence 1274 AA;

Query Match 88.9%; Score 40; DB 7; Length 1274;
Best Local Similarity 100.0%; Pred. No. 6.77e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Db 809 sgmgvs 814
:|||||
Qy 2 SGMGVS 7

RESULT 14

ID R49994 standard; Protein; 1128 AA.
AC R49994;
DT 23-SEP-1994 (first entry)
DE Mouse carboxypeptidase-like bone-specific protein OSF-5.
KW Mouse OSF-5; bone-related carboxypeptidase-like protein;
KW growth factor; adhesion molecule; osteogenesis; bone induction;

KW bone metabolism disorder; osteoporosis; osteopetrosis;
KW Paget's disease.
OS Mus musculus (osteoblastic cell line MC3T3E1).
FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= signal_sequence
FT Region 116..159
FT /label= Repeat region
FT /note= "contains 4 tandem copies of 11mer repeat"
FT Region 116..126
FT /label= Repeat unit
FT /note= "Lysine- and Proline-rich repeat; shows weak
FT homology with receptors for prolactin, FGF,
FT GABA, serotonin and Histone H1"
FT Domain 423..531
FT /label= Factor VIII-like domain
FT /note= "homologous with phospholipid binding domain
FT of blood coagulation factor VIII"
FT Domain 544..1027
FT /label= Carboxypeptidase-like domain
FT /note= "acts as a controlling element for peptide
FT hormones and cytokines during bone
FT metabolism"
FN EP-588118-A.
PD 23-MAR-1994.
PF 25-AUG-1993; 113604.
PR 28-AUG-1992; JP-230029.
PR 03-DEC-1992; JP-324033.
PA (FARH) HOECHST JAPAN LTD.
PA (FARH) HOECHST JAPAN KK.
PI Amann E, Kawai S, Okazaki M, Takeshita S;
PI WPI; 94-093794/12.
DR N-PSDB; Q58708.
PT New bone-related carboxypeptidase OSF-5 - used to obtain prods.
PT for the diagnosis and treatment of bone metabolic diseases, e.g.
PT osteoporosis, or Paget's disease
PS Claim 1; Page 13-19; 26pp; English.
CC OSF-5 is a bone-specific carboxypeptidase which acts as an adhesion
CC molecule or growth factor; it takes part in osteogenesis at the site
CC of bone induction. OSF-5 can be used to treat bone metabolic diseases,
CC e.g. osteoporosis, Paget's disease, osteomalacia, hyperostosis or
CC osteopetrosis.
SQ Sequence 1128 AA;

Query Match 86.7%; Score 39; DB 9; Length 1128;
Best Local Similarity 83.3%; Pred. No. 8.99e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;Db 831 tsqmg 836
:|||||
Qy 1 TSGMGV 6

RESULT 15

ID R31612 standard; Protein; 22 AA.
AC R31612;
DT 24-MAY-1993 (first entry)
DE Fragment XXXI homologous to chicken nov protein fragment.
KW avian nephroblastoma; avian myeloblastoma virus;
KW stringent hybridisation.
OS Homo sapiens.
FN W09300430-A.
PD 07-JAN-1993.
PF 25-JUN-1992; F00589.

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PR 25-JUN-1991; FR-007807;
PA (CNRS) CENT NAT RECH SCI.
PI Martinerie C, Perbal B;
DR WPI; 93-036377/04.
PT Nucleotide sequences hybridising to regions of chicken nov gene -
PT useful as probes for detecting complementary sequences to
PT evaluate development and/or differentiation of tumours
PS Disclosure; Page 42; 67pp; French.
CC The invention includes nucleotide sequences which encode amino acid
CC sequences with at least 80% homology to sequence XXX (R31611), i.e
CC to part of the chicken nov protein encoded by the 4th. exon. Such
CC sequences preferably encode the amino acid sequence XXXI (R31612).
SQ Sequence 22 AA;

Query Match 84.4%; Score 38; DB 6; Length 22;
Best Local Similarity 71.4%; Pred. No. 1.19e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 9 tcgmgis 15
| | | | |
Qy 1 TSGMGVS 7

Search completed: Tue Mar 18 10:14:23 1997
Job time : 10 secs.

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FT SIGNAL 1 20
 FT CHAIN 21 131
 FT DOMAIN 21 43
 FT DOMAIN 44 58
 FT DOMAIN 59 73
 FT DOMAIN 74 80
 FT DOMAIN 81 112
 FT DOMAIN 113 121
 FT DOMAIN 122 131
 FT DISULFID 43 112
 FT NON TER 131 131
 SQ SEQUENCE 131 AA; 14291 MW; 9055A06B CRC32;

Query Match 86.7%; Score 812; DB 5; Length 131;
 Best Local Similarity 86.3%; Pred. No. 2.01e-158;
 Matches 113; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Db 1 metdtllllwvllwvpgstgnivltqspaslavslgqratiscrasvdygnsfmhwy 60
 Qy 1 METDTILLWVLLWVPGSGTGNIVLTQSPASLAVSLGQRATISCKASQSDYDGDGYMNY 60
 Db 61 qkqgqpklllylasnlesgvpafsgsgstftitldpveadfaatycqnnedpw 120
 Qy 61 QKQGPQPKLLIYAASNLSEGPAPFSGSGSGTFTLINHPVEEDAAATYCCQSNEDPP 120

Db 121 tfgggtkleik 131
 Qy 121 TFGGGTKLEIK 131

RESULT 2

ID KV3F MOUSE STANDARD; PRT; 132 AA.
 AC P01658;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 321).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN {}
 RP SEQUENCE OF 1-37.
 RX MEDLINE; 78235887.
 RA BURSTEIN Y., SCHECHTER I.;
 RL BIOCHEMISTRY 17:2392-2400(1978).
 RN {}
 RP SEQUENCE OF 21-132.
 RX MEDLINE; 73140224.
 RA MCKEAN D.J., POTTER M., HOOD L.E.;
 RL BIOCHEMISTRY 12:749-759(1973).
 CC -I- THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN
 CC WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE
 CC MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.
 DR PIR; A01933; KVM532.
 DR HSP; P01679; IGGB.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 132
 FT DOMAIN 21 43
 FT DOMAIN 44 58
 FT DOMAIN 59 73
 FT DOMAIN 74 80
 FT DOMAIN 81 112
 FT DOMAIN 113 121

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FT DOMAIN 122 131
 FT DISULFID 43 112
 FT NON TER 132 132
 SQ SEQUENCE 132 AA; 14523 MW; E572F824 CRC32;

Query Match 86.3%; Score 809; DB 5; Length 132;
 Best Local Similarity 77.3%; Pred. No. 1.02e-157;
 Matches 102; Conservative 21; Mismatches 9; Indels 0; Gaps 0;

Db 1 metdtllllwvllwvpgstgdivltqspaslavslgqratiscrasvntygnsfmwy 60
 Qy 1 METDTILLWVLLWVPGSGTGNIVLTQSPASLAVSLGQRATISCKASQSDYDGDGYMNY 60
 Db 61 zzkqg2pkllyrasnlzsgiparfsgsgstbftitibpvabdvatyczabzbpw 120
 Qy 61 QKQGPQPKLLIYAASNLSEGPAPFSGSGSGTFTLINHPVEEDAAATYCCQSNEDPP 120
 Db 121 tfgggtkleik 132
 Qy 121 TFGGGTKLEIK 132

RESULT 3

ID KV3M MOUSE STANDARD; PRT; 111 AA.
 AC P01665;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (PC 7043).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN {}
 RP SEQUENCE.
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 DR PIR; A01937; KVM543.
 DR HSP; P01679; IGGB.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12002 MW; ADC728CA CRC32;

Query Match 79.6%; Score 746; DB 5; Length 111;
 Best Local Similarity 98.2%; Pred. No. 6.11e-143;
 Matches 109; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslavslgqratisckasqsdvdygnsymwyqkqgpkpkllyaaenles 60
 Qy 21 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDGYMNYQKQGPQPKLLIYAASNL 80
 Db 61 giparfsgsgstftlinhpveedfaatycqnsdftfgsgtkleik 111
 Qy 81 GIPARFSGSGSGTFTLINHPVEEDAAATYCCQSNEDPPTFGGGTKLEIK 131

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RESULT 4
ID KV3N MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7183).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; B01937; KVM583.
DR HSP; P01679; ICG8.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 041902B8 CRC32;

Query Match 79.4%; Score 744; DB 5; Length 111;
Best Local Similarity 97.3%; Pred. No. 1.80e-142;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslavslgqraticskasqsvdydgsymwvyqqkpgppklliyaasnles 60
QY 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQQKPGPPKLLIYAASNLES 80
|||||
Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpwtfgsgtkleik 111
QY 81 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPPTFGGKLEIK 131
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RESULT 5
ID KV3O MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 6308).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; C01937; KVM508.
DR HSP; P01679; ICG8.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
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FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; F7865271 CRC32;

Query Match 79.2%; Score 742; DB 5; Length 111;
Best Local Similarity 97.3%; Pred. No. 5.27e-142;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslavslgqraticskasqsvdydgsymwvyqqkpgppklliyaasnles 60
QY 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQQKPGPPKLLIYAASNLES 80
|||||
Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpwtfgsgtkleik 111
QY 81 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPPTFGGKLEIK 131
|||||

RESULT 6
ID KV3Q MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7769).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; E01937; KVM569.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 9CB705B9 CRC32;

Query Match 78.1%; Score 732; DB 5; Length 111;
Best Local Similarity 96.4%; Pred. No. 1.15e-139;
Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslavslgqraticskasqsvdydgsymwvyqqkpgppkllifaasnles 60
QY 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQQKPGPPKLLIYAASNLES 80
|||||
Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpwtfgsgtkleik 111
QY 81 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPPTFGGKLEIK 131
|||||

RESULT 7
ID KV3L MOUSE STANDARD; PRT; 111 AA.
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AC P01664;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (CBPC 101).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KWSCL.
DR HSSP; P01679; IIGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 36 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; A2AC84C7 CRC32;

Query Match 77.9%; Score 730; DB 5; Length 111;
Best Local Similarity 95.5%; Pred. No. 3.38e-139;
Matches 106; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1 divltqspaslavslqqraticskasqsdvdygdsymnywqkpgppklliyaasnl 60
|||||
Qy 21 DIVLTQSPASLAVSLQQRATISCKASQSDVDYDGSYNNWYQQKPGPPKLLIYAASNL 80
|||||

Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpytfgggtkleik 111
|||||
Qy 81 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPPTFGGGTKLEIK 131
|||||

RESULT 8
ID KV3P MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7210).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATHAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; D01937; KWS10.
DR HSSP; P01679; IIGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.

FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 101 110 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; BF45B542 CRC32;

Query Match 76.7%; Score 719; DB 5; Length 110;
Best Local Similarity 95.5%; Pred. No. 1.26e-136;
Matches 106; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Db 1 divltqspaslavslqqraticskasqsdvdygdsymnywqkpgppklliyaasnl 60
|||||
Qy 21 DIVLTQSPASLAVSLQQRATISCKASQSDVDYDGSYNNWYQQKPGPPKLLIYAASNL 80
|||||

Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpytfgggtkleik 110
|||||
Qy 81 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPPTFGGGTKLEIK 131
|||||

RESULT 9
ID KV3R MOUSE STANDARD; PRT; 111 AA.
AC P01670;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 6684).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATHAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; A01938; KWS84.
DR HSSP; P01679; IACV.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 102 111 FRAMEWORK 4.
FT NON_TER 111 111 BY SIMILARITY.
SQ SEQUENCE 111 AA; 12039 MW; F4B1FA93 CRC32;

Query Match 71.9%; Score 674; DB 5; Length 111;
Best Local Similarity 88.3%; Pred. No. 3.88e-126;
Matches 98; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Db 1 divltqspaslavslqqraticskasqsdvdygdsymnywqkpgppklliyaasnl 60
|||||
Qy 21 DIVLTQSPASLAVSLQQRATISCKASQSDVDYDGSYNNWYQQKPGPPKLLIYAASNL 80
|||||

Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpytfgggtkleik 111
|||||
Qy 81 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPPTFGGGTKLEIK 131
|||||

RESULT 10
ID KV3T MOUSE STANDARD; PRT; 111 AA.
AC P01672;

DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7940).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; C01938; KVM540.
DR HSSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12038 MW; 4856B39D CRC32;

Query Match 71.5%; Score 670; DB 5; Length 111;
Best Local Similarity 88.3%; Pred. No. 3.30e-125;
Matches 98; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Db 1 divltqpaslaqlgratiscraskesvafgyymhwqyqgqgppklllylaenles 60
|||||
Qy 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYMNWYQKPGQPPKLLIYAASNLES 80
|||||
Db 61 gvarfegsgsgtdftlnihpveedavtyycqhsrelpbtfgggtkleik 111
|-:|||||
Qy 81 GIPARFSGSGTDFTLNHPVEEDAATYYCQSNEDPPTFGGGTKLEIK 131
|||||

RESULT 11
ID KV3H MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 3741 AND TEPC 111).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
CC -/- THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A01934; KVM637.
DR HSSP; P01679; IAGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
SQ SEQUENCE 1. FRAMEWORK 1.

FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; 76502E89 CRC32;

Query Match 70.8%; Score 663; DB 5; Length 111;
Best Local Similarity 86.5%; Pred. No. 1.40e-123;
Matches 96; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Db 1 divltqpaslaqlgratiscraskesvdfgymhwqyqgqgppklllyraenles 60
|||||
Qy 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYMNWYQKPGQPPKLLIYAASNLES 80
|||||
Db 61 gparfegsgsgtdftlnihpveedavtyycqhsrelpbtfgggtkleik 111
|||||
Qy 81 GIPARFSGSGTDFTLNHPVEEDAATYYCQSNEDPPTFGGGTKLEIK 131
|||||

RESULT 12
ID KV3S MOUSE STANDARD; PRT; 111 AA.
AC P01671;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7175).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; B01938; KVM575.
DR HSSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12010 MW; AA8039B3 CRC32;

Query Match 70.4%; Score 660; DB 5; Length 111;
Best Local Similarity 86.5%; Pred. No. 6.98e-123;
Matches 96; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Db 1 divltqpaslaqlgratiscraskesvdfgymhwqyqgqgppklllylaenles 60
|||||
Qy 21 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYMNWYQKPGQPPKLLIYAASNLES 80
|||||
Db 61 gvarfegsgsgtdftlnihpveedavtyycqhsrelpbtfgggtkleik 111
|-:|||||
Qy 81 GIPARFSGSGTDFTLNHPVEEDAATYYCQSNEDPPTFGGGTKLEIK 131
|||||

RESULT 13
ID KV3C MOUSE STANDARD; PRT; 112 AA.
AC P01659;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (TEPC 124).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 73140225.
RA MCKEAN D.J., POTTER M., HOOD L.E.;
RL BIOCHEMISTRY 12:760-771(1973).
DR PIR; A01933; KVMS32.
DR HSP; P01679; IGB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12339 MW; 4504DD0E CRC32;

Query Match 70.2%; Score 658; DB 5; Length 112;
Best Local Similarity 74.1%; Pred. No. 2.03e-122;
Matches 83; Conservative 20; Mismatches 9; Indels 0; Gaps 0;

Db 1 divltqpaslavlgqratiscrasvsvdysvgnfwmvzypkzppklliyraenls 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQSPASLAVSLGORATISCKASQSDYDGDYSYNNWYQKPGQPPKLLIYAASNL 80
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 giparfsgsgtftltpvzabdvatfczszbzapwtfgsgtkleikr 112
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 GIPARFSGSGTFTLNHPVEEDATYYCQSNEDPPTFGGKLEIKR 132

RESULT 14
ID KV3J MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (ABPC 22 AND PC 9245).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
CC -!- THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.

DR PIR; A01935; KVMS6.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; 711C554A CRC32;

Query Match 70.1%; Score 657; DB 5; Length 111;
Best Local Similarity 84.7%; Pred. No. 3.47e-122;
Matches 94; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Db 1 nivltqpaslavlgqratiscrasvsvdysvgnfwmvzypkzppklliyraenls 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQSPASLAVSLGORATISCKASQSDYDGDYSYNNWYQKPGQPPKLLIYAASNL 80
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 gyparfsgsgtftltpvzabdvatfczszbzapwtfgsgtkleik 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 GIPARFSGSGTFTLNHPVEEDATYYCQSNEDPPTFGGKLEIK 131

RESULT 15
ID KV3K MOUSE STANDARD; PRT; 111 AA.
AC P01663;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 4050).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; A01935; KVMS6.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 5EBF3264 CRC32;

Query Match 69.4%; Score 650; DB 5; Length 111;
Best Local Similarity 82.9%; Pred. No. 1.47e-120;
Matches 92; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Db 1 nivltqpaslavlgqratiscrasvsvdysvgnfwmvzypkzppklliyraenls 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQSPASLAVSLGORATISCKASQSDYDGDYSYNNWYQKPGQPPKLLIYAASNL 80

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Db 61 gyparfsgsgrtdftltidpveaddaatyycqgnedpltfagqklelk 111
Qy 81 GIPARFSGSGGTDTTINHPVEEDAATYCOQSNEDPPTFGGKTLEIK 131

Search completed: Tue Mar 18 10:00:08 1997
Job time : 34 secs.


```
Best Local Similarity 96.9%; Pred. No. 2.87e-95;
Matches 127; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 metdtdllwllwpgstgdlvtqspaelmslqgratiscasqslgdydgsymnw 60
|||||
Qy 1 METDTLLWLLWVPGSTGDLVTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWY 60
|||||

Db 61 qkqgqpkllyaaanlesgiparfsgsgtdftlinhpveedaatyccasedpp 120
|||||
Qy 61 QKQGPQPKLLIYAASNLSEGPAPRFSGSGCTDFTLINHPVEEDAATYCCQSNEDPP 120
|||||

Db 121 tfgggtkleik 131
|||||
Qy 121 TFGGGTKLEIK 131

RESULT 2
ENTRY KVMS6 #type complete
TITLE Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 31-Dec-1993
ACCESSIONS B90412; B90374; B93822; C93822; C93204; D93204; A01935
REFERENCE A90412
#authors Burstein, Y.; Schechter, I.
#journal Biochemistry (1978) 17:2392-2400
#title Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.
#cross-references MUID:78235887
#contents M63
#accession B90412
#molecule_type protein
#residues 1-35 ##label BUR
REFERENCE A90374
#authors McKean, D.; Potter, M.; Hood, L.
#journal Biochemistry (1973) 12:760-771
#title Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.
#cross-references MUID:73140225
#contents M63
#accession B90374
#molecule_type protein
#residues 21-46, 'Q', 48-53, 'B', 55-57, '2', 59-86, 'F', 88-131 ##label MCK
#note this sequence has since been revised in reference A93822
REFERENCE A93822
#authors McKean, D.J.; Bell, M.; Potter, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1978) 75:3913-3917
#title Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.
#cross-references MUID:79012520
#contents M63; AB22
#accession B93822
#molecule_type protein
#residues 1-53; 69-107 ##label MC2
#accession C93822
#molecule_type protein
#residues 21-119, 'Y', 121-131 ##label MC3
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
```

```
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce immunoglobulin diversity.
#cross-references MUID:79073152
#contents PC9245; PC4050
#accession C93204
#molecule_type protein
#residues 21-119, 'Y', 121-131 ##label WEI
#accession D93204
#molecule_type protein
#residues 21-119, 'L', 121-123, 'A', 125-129, 'L', 131 ##label WE2
COMMENT The M63 precursor sequence is shown.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
1-20 #domain signal sequence #status experimental #label SIG
SUMMARY #length 131 #molecular-weight 14291 #checksum 5945

Query Match 86.7%; Score 812; DB 2; Length 131;
Best Local Similarity 86.3%; Pred. No. 5.42e-83;
Matches 113; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Db 1 metdtdllwllwpgstgdlvtqspaelmslqgratiscasqslgdydgsymnw 60
|||||
Qy 1 METDTLLWLLWVPGSTGDLVTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWY 60
|||||

Db 61 qkqgqpkllyaaanlesgiparfsgsgtdftlinhpveedaatyccqsnedpw 120
|||||
Qy 61 QKQGPQPKLLIYAASNLSEGPAPRFSGSGCTDFTLINHPVEEDAATYCCQSNEDPP 120
|||||

Db 121 tfgggtkleik 131
|||||
Qy 121 TFGGGTKLEIK 131

RESULT 3
ENTRY KVMS32 #type complete
TITLE Ig kappa chain precursor V regions (MOPC 321, TEPC 124) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 31-May-1979 #sequence_revision 31-May-1979 #text_change 04-Nov-1994
ACCESSIONS A90412; A90373; A90374; A01933
REFERENCE A90412
#authors Burstein, Y.; Schechter, I.
#journal Biochemistry (1978) 17:2392-2400
#title Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.
#cross-references MUID:78235887
#contents MOPC 321
#accession A90412
#molecule_type protein
#residues 1-37 ##label BUR
#note this precursor was synthesized in a cell-free system directed by mRNA isolated from myeloma polyomes
REFERENCE A90373
#authors McKean, D.; Potter, M.; Hood, L.
#journal Biochemistry (1973) 12:749-759
#title Mouse immunoglobulin chains. Partial amino acid sequence of a kappa chain.
#cross-references MUID:73140224
#contents MOPC 321
```



```
#accession A90373
##molecule_type protein
##residues 21-132 ##label MCK
##note the partial sequence of the C region of this Bence Jones
protein was also determined; it differs from that
reported for mouse MOPC 21 only in the transposition
of two nearby residues

REFERENCE
#authors McKean, D.; Potter, M.; Hood, L.
#journal Biochemistry (1973) 12:760-771
#title Mouse immunoglobulin chains. Pattern of sequence variation
among kappa chains with limited sequence differences.
#cross-references MUID:73140225
#contents TEPC 124
#accession A90374
##molecule_type protein
##residues 21-131 ##label MC2
##note the sequence is compatible with that of MOPC 321 except
in having 47-Glx, 51-Trp, and 118-Ala

COMMENT The MOPC 321 sequence is shown.
COMMENT Residues 1-20 are the signal sequence.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
36-114 #domain immunoglobulin homology #label IMM
SUMMARY #length 132 #molecular-weight 14523 #checksum 370

Query Match 86.3%; Score 809; DB 2; Length 132;
Best Local Similarity 77.3%; Pred. No. 1.28e-82;
Matches 102; Conservative 21; Mismatches 9; Indels 0; Gaps 0;

Db 1 metdtllllwllwpqstgdivltqspaslavslgqratiscrasksvntygnsmfzwy 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1 METDTILLWLLWVPGSGTGDIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWY 60
::||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:

Db 61 zdkqpgpkllyrasnlzsgiparfsgsgtdftlnihpveedaatyycqherypl 120
::||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:
Qy 61 QKQPGQPPLLIIYAASNLGSGIPARFSGSGTDFTLNIHPVEEDAATYYCQSQSNEDPP 120
||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:

Db 121 tfqggtkleikr 132
||||:|||||
Qy 121 TFGGGTKLEIKR 132
||||:|||||

RESULT 4
ENTRY S55027 #type fragment
TITLE immunoglobulin light chain variable region precursor - mouse
ORGANISM (fragment)
#formal name Mus musculus #common name house mouse
DATE 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change
19-Oct-1995
ACCESSIONS S55027
REFERENCE S55027
#authors Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.;
Margolies, M.N.; Sheriff, S.
#journal J. Mol. Biol. (1995) 248:344-360
#title Structure and specificity of the anti-digoxin antibody 40-50.
#accession S55027
##status preliminary
##molecule_type mRNA
##residues 1-131 ##label JEF
##cross-references EMBL:L31404
SUMMARY #length 131 #checksum 6089

Query Match 83.2%; Score 780; DB 12; Length 131;
```

```
Best Local Similarity 84.7%; Pred. No. 5.34e-79;
Matches 111; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Db 1 metdtllllwllwpqstgdivltqspaslavslgqratiscrasksvatgshihwy 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1 METDTILLWLLWVPGSGTGDIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 61 qdkpgqpkllylasilesgvparfsgsgtdftlnihpveedaatyycqherypl 120
||||:||||| || ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:
Qy 61 QKQPGQPPLLIIYAASNLGSGIPARFSGSGTDFTLNIHPVEEDAATYYCQSQSNEDPP 120
||||:||||| || ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:

Db 121 tfqggtkleik 131
||||:|||||
Qy 121 TFGGGTKLEIK 131
||||:|||||

RESULT 5
ENTRY PN0446 #type fragment
TITLE Ig kappa chain precursor V-II region - human (fragment)
ORGANISM #formal name Homo sapiens #common name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
30-Apr-1995
ACCESSIONS PN0446
REFERENCE PN0444
#authors Kaluza, B.; Betzl, G.; Shao, H.; Diamantein, T.; Weidle,
U.H.
#journal Gene (1992) 122:321-328
#title A general method for chimerization of monoclonal antibodies
by inverse polymerase chain reaction which conserves
authentic N-terminal sequences.
#accession PN0446
##molecule_type mRNA
##residues 1-140 ##label KAL
##cross-references GB:I02345
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
1-20 #domain signal sequence #status predicted #label SIG\
21-140 #product Ig light chain kappa-2 V region #status
predicted #label MAT
SUMMARY #length 140 #checksum 3597

Query Match 82.3%; Score 771; DB 5; Length 140;
Best Local Similarity 84.8%; Pred. No. 7.07e-78;
Matches 112; Conservative 6; Mismatches 12; Indels 2; Gaps 1;

Db 1 metdtllllwllwpqstgdivltqspaslavslgqratiscrasksvatgshihwy 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1 METDTILLWLLWVPGSGTGDIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 61 qdkpgqpkllylvsnlesgvparfsgsgtdftlnihpveedaatyycqherypl 118
||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:
Qy 61 QKQPGQPPLLIIYAASNLGSGIPARFSGSGTDFTLNIHPVEEDAATYYCQSQSNEDPP 120
||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||:

Db 119 tfqggtkleikr 130
||||:|||||
Qy 121 TFGGGTKLEIKR 132
||||:|||||

RESULT 6
ENTRY S19971 #type fragment
TITLE Ig kappa chain V region (CD4 mAb clone M-T310 and others) -
mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
```


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```
DATE          06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
ACCESSIONS    S19971; S19973
REFERENCE      S19963
#authors      Weissenhorn, M.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
#submission   submitted to the EMBL Data Library, March 1992
#description   Structural characterization of CD4 mAb.
#accession    S19971
##molecule_type mRNA
##residues    1-112 ##label WEI
##cross-references EMBL:X65091
##experimental_source clone M-T310
#accession    S19973
##molecule_type mRNA
##residues    1-112 ##label WEM
##cross-references EMBL:X65092
##experimental_source M-T404
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY       #length 112 #checksum 4782

Query Match      80.9%; Score 758; DB 5; Length 112;
Best Local Similarity 96.4%; Pred. No. 2.94e-16;
Matches 108; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 divltqspaslpmslqgratiscasgldydgdsymwvqqkpgppklliyaasnl 60
    |||||
Qy 21 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWYQQRPGPPKLLIYAASNL 80
    |||||

Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpftfgggtkleikr 112
    |||||
Qy 81 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPFTFGGGTKLEIKR 132
    |||||

RESULT 7
ENTRY   KWMS43      #type complete
TITLE   Ig kappa chain V region (PC7043) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE    01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
        05-Apr-1995
ACCESSIONS A01937
REFERENCE  A93204
#authors  Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal  Nature (1978) 276:785-790
#title    Rearrangement of genetic information may produce
          immunoglobulin diversity.
#cross-references MUID:79073152
#accession A01937
##molecule_type protein
##residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
23-92
SUMMARY   #disulfide bonds #status predicted
          #length 111 #molecular-weight 12002 #checksum 438

Query Match      79.6%; Score 746; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 9.16e-75;
Matches 109; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslpmslqgratiscasgldydgdsymwvqqkpgppklliyaasnl 60
    |||||
Qy 21 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWYQQRPGPPKLLIYAASNL 80
    |||||

Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpftfgggtkleik 111
    |||||
```

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```
Qy 81 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPFTFGGGTKLEIK 131
    |||||

RESULT 8
ENTRY   KWMS83      #type complete
TITLE   Ig kappa chain V region (PC7183) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE    30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
        30-Sep-1993
ACCESSIONS B01937; A01937
REFERENCE  A93204
#authors  Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal  Nature (1978) 276:785-790
#title    Rearrangement of genetic information may produce
          immunoglobulin diversity.
#cross-references MUID:79073152
#accession B01937
##molecule_type protein
##residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS    immunoglobulin
FEATURE
23-92
SUMMARY   #disulfide bonds #status predicted
          #length 111 #molecular-weight 11952 #checksum 9

Query Match      79.4%; Score 744; DB 2; Length 111;
Best Local Similarity 97.3%; Pred. No. 1.62e-74;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslpmslqgratiscasgldydgdsymwvqqkpgppklliyaasnl 60
    |||||
Qy 21 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWYQQRPGPPKLLIYAASNL 80
    |||||

Db 61 giparfsgsgtdftlnihpveedaatyccqsnedpftfgggtkleik 111
    |||||
Qy 81 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPFTFGGGTKLEIK 131
    |||||

RESULT 9
ENTRY   KWMS08      #type complete
TITLE   Ig kappa chain V region (PC6308) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE    30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
        30-Sep-1993
ACCESSIONS C01937; A01937
REFERENCE  A93204
#authors  Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal  Nature (1978) 276:785-790
#title    Rearrangement of genetic information may produce
          immunoglobulin diversity.
#cross-references MUID:79073152
#accession C01937
##molecule_type protein
##residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS    immunoglobulin
FEATURE
23-92
SUMMARY   #disulfide bonds #status predicted
          #length 111 #molecular-weight 12071 #checksum 2195

Query Match      79.2%; Score 742; DB 2; Length 111;
Best Local Similarity 97.3%; Pred. No. 2.88e-74;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```


Db 1 divltqpsaslavlgratiasckasgvdgdymwyqkqppklllytaasles 60
|||||
Qy 21 DIVLTQPSASLAVSIGQRATISCKASQSDVDYDGSYNNWYQKQPPKLLIYAASNLES 80
|||||
Db 61 giparfsgsgtdftlinhpveedaatyccgsnedpwtfgsgtkleik 111
|||||
Qy 81 GIPARFSGSGTDFTLNHPVEEDAATYCCQSNEDPPTFGGKTLEIK 131
|||||

RESULT 10
ENTRY KWMS69 #type complete
TITLE Ig kappa chain V region (PC7769) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 30-Sep-1993

ACCESSIONS E01937; A01937
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce immunoglobulin diversity.
#cross-references MUID:79073152
#accession E01937
#molecule_type protein
##residues 1-111 ##label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE 23-92
#disulfide_bonds #status predicted
SUMMARY #length 111 #molecular_weight 12011 #checksum 662

Query Match 78.1%; Score 732; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 5.04e-73;
Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqpsaslavlgratiasckasgvdgdymwyqkqppkllifaasles 60
|||||
Qy 21 DIVLTQPSASLAVSIGQRATISCKASQSDVDYDGSYNNWYQKQPPKLLIYAASNLES 80
|||||

Db 61 giparfsgsgtdftlinhpveedaatyccgsnedpwtfgsgtkleik 111
|||||
Qy 81 GIPARFSGSGTDFTLNHPVEEDAATYCCQSNEDPPTFGGKTLEIK 131
|||||

RESULT 11
ENTRY KWMSCL #type complete
TITLE Ig kappa chain V region (CBPC 101) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 05-Apr-1995

ACCESSIONS A01936
REFERENCE A93822
#authors McKean, D.J.; Bell, M.; Potter, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1978) 75:3913-3917
#title Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.
#cross-references MUID:79012520
#accession A01936
#molecule_type protein
##residues 1-111 ##label MCK

COMMENT This chain was isolated from a myeloma protein.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE 23-92
#disulfide_bonds #status predicted

SUMMARY #length 111 #molecular_weight 11964 #checksum 1507

Query Match 77.9%; Score 730; DB 2; Length 111;
Best Local Similarity 95.3%; Pred. No. 8.94e-73;
Matches 106; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1 divltqpsaslavlgratiasckasgvdgtgesymwyqnpqgpklliyaasles 60
|||||
Qy 21 DIVLTQPSASLAVSIGQRATISCKASQSDVDYDGSYNNWYQKQPPKLLIYAASNLES 80
|||||

Db 61 giparfsgsgtdftlinhpveedaatyccgsnedpwtfgsgtkleik 111
|||||
Qy 81 GIPARFSGSGTDFTLNHPVEEDAATYCCQSNEDPPTFGGKTLEIK 131
|||||

RESULT 12
ENTRY S19976 #type fragment
TITLE Ig kappa chain V region (M-T413) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 12-Apr-1995

ACCESSIONS S19976
REFERENCE S19963
#authors Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
#submission Submitted to the EMBL Data Library, March 1992
#description Structural characterization of CD4 mAb.
#accession S19976
##status preliminary
##molecule_type mRNA
##residues 1-112 ##label WEI
##cross-references EMBL:X65093

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 112 #checksum 4816

Query Match 77.7%; Score 728; DB 5; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.58e-72;
Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 1 divltqpsaslavlgratiasckasgldydadsymhvyqkqppklliyaasles 60
|||||
Qy 21 DIVLTQPSASLAVSIGQRATISCKASQSDVDYDGSYNNWYQKQPPKLLIYAASNLES 80
|||||

Db 61 giparfsgsgtdftlinhpveedaatyccgsiqdpytfgggtkleikr 112
|||||
Qy 81 GIPARFSGSGTDFTLNHPVEEDAATYCCQSNEDPPTFGGKTLEIKR 132
|||||

RESULT 13
ENTRY S06731 #type complete
TITLE Ig kappa chain precursor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995

ACCESSIONS S06731
REFERENCE S06731
#authors Alanen, A.; Weiss, S.
#journal Eur. J. Immunol. (1989) 19:1961-1963
#title Sequence and linkage of the V(kappa)21A and G germ-line gene segments in the mouse.
#cross-references MUID:90060210
#accession S06731
##status preliminary
##molecule_type DNA
##residues 1-120 ##label ALA

WAP50LH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:01:42 1997; MsePar time 4.25 Seconds
319,919 Million cell updates/sec
Tabular output not generated.

Title: >US-08-612-929-2
Description: (1-132) from US08612929.pep
Perfect Score: 937
Sequence: 1 MEYDTILLWLLWPGSTG.....QQSNEDPPTFGGKLEIKR 132

Scoring table: PAM 150
Gap 11

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 30.011; Variance 164.394; scale 0.183

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	937	100.0	132	13	Mouse MAB 3B9 light c	9.23e-62
2	910	97.1	131	6	Anti-CD4 antibody WT	1.12e-59
3	905	96.6	131	1	Anti-Leu 3a light cha	2.72e-59
4	895	95.5	131	1	Amino acids sequence	1.61e-58
5	819	87.4	131	6	p12-k2.	1.15e-52
6	816	87.1	131	6	p64-k4 protein produc	1.96e-52
7	801	85.5	131	1	Light chain variable	2.78e-51
8	790	84.3	131	6	Antibody 4A2 light ch	1.95e-50
9	789	84.2	132	3	kappa light chain var	2.33e-50
10	776	82.8	132	3	Mouse 4C10 anti-Idiot	2.32e-49
11	767	81.9	130	14	Anti-idiotype antibod	1.14e-48
12	747	79.7	111	10	Mouse anti-HIV mu5.5	3.90e-47

13	747	79.7	111	11	R60302	Anti HIV antibody lig	3.90e-47
14	734	78.3	111	1	P90541	Immunoglobulin L chai	3.87e-46
15	727	77.6	146	14	R74966	Anti-idiotype antibod	1.33e-45
16	719	76.7	120	9	R48618	Sequence of the monoc	5.46e-45
17	708	75.6	131	13	R70202	Humanized antibody 3B	3.80e-44
18	705	75.2	111	6	R33305	MaE11 light chain.	6.45e-44
19	701	74.8	131	13	R75355	Humanized antibody 3B	1.30e-43
20	700	74.7	106	6	R33309	MaE15 light chain.	1.56e-43
21	670	71.5	111	9	R47494	Murine anti-CD18 Ab 6	3.06e-41
22	665	71.0	112	3	R13089	Murine 1B4 light chai	7.38e-41
23	657	70.1	260	15	R77617	Anti-C5 MAb N19/8 scF	3.01e-40
24	655	69.9	112	14	R80272	V1 region from an ant	4.28e-40
25	653	69.7	112	14	R75431	Human thyroid stimula	6.09e-40
26	653	69.7	112	2	R10539	Chimeric MAb 9.2.27 1	6.09e-40
27	651	69.5	111	15	R85236	Murine 206 antibody v	8.65e-40
28	650	69.4	113	16	R79892	Anti-EGFR antibody li	1.03e-39
29	649	69.3	111	13	R65172	Murine NM-01 variable	1.23e-39
30	648	69.2	110	11	R60564	Anti-carcinoembryonic	1.47e-39
31	647	69.1	121	9	R48615	Sequence of the monoc	1.75e-39
32	646	68.9	218	15	R75459	Mouse antibody F4-7 1	2.08e-39
33	646	68.9	218	15	R75457	Mouse antibody FB3-2	2.08e-39
34	645	68.8	113	16	R79893	Anti-EGFR antibody li	2.48e-39
35	645	68.8	113	16	R79882	Anti-EGFR antibody li	2.48e-39
36	645	68.8	121	6	R33346	Sequence of the varia	2.48e-39
37	644	68.7	120	9	R48620	Sequence of the light	2.96e-39
38	643	68.6	112	14	R79158	Human IgE receptor-bi	3.53e-39
39	641	68.4	239	16	R79866	Anti-EGFR single chai	5.01e-39
40	639	68.2	212	10	R52659	Porphyrin antibody li	7.12e-39
41	637	68.0	599	16	R90837	3B1 single chain anti	1.01e-38
42	635	67.8	110	10	R60810	Light chain variable	1.44e-38
43	635	67.8	112	15	R79156	Human IgE receptor-bi	1.44e-38
44	635	67.8	113	16	R79891	Anti-EGFR antibody li	1.44e-38
45	633	67.6	133	10	R59511	Sequence of the light	2.04e-38

ALIGNMENTS

RESULT 1
ID R70189 standard; Protein; 132 AA.
AC R70189;
DT 20-SEP-1995 (first entry)
DE Mouse MAB 3B9 light chain.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAB; interleukin-4; IL-4; allergy.
OS Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Sig_peptide
FT Region 44..58
FT /label= CDR
FT /note= *complementarity determining region*
FT Region 74..80
FT /label= CDR
FT /note= *complementarity determining region*
FT Region 113..121
FT /label= CDR
FT /note= *complementarity determining region*
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.

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PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR N-PSDB; Q83490.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.1; 97pp; English.
CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC chains were cloned into pCEWf+ and transformed into E. coli
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for
CC antibody engineering.
SQ Sequence 132 AA;

Query Match 100.0%; Score 937; DB 13; Length 132;
Best Local Similarity 100.0%; Pred. No. 9,23e-62;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 metdtkllwllwvpgstgdivltqspaslavslgqratisckasqsvdydgsymw 60
|||||
Qy 1 METDTLLWVLLWVPGSTGDIVLTQSPASLAVSLGQRATISCKASQSVDYDGSYMWY 60
|||||
Db 61 qkpgqppklliyaanlesgiparfsgsgtdftlnihpveedaatyccgsedpp 120
|||||
Qy 61 QKPGQPPLKLLIYAANLESIGIPARFSGSGTDFTLNHPVEEDAATYCCQSNEDPP 120
|||||

Db 121 tfgggtkleikr 132
|||||
Qy 121 TFGGGTKLEIKR 132
|||||

RESULT 2

ID R32123 standard; Protein; 131 AA.
AC R32123;
DT 02-JUN-1993 (first entry)
DE Anti-CD4 antibody MT 3.10 light chain variable region.
KW Immunosuppression; tissue transplantation; graft; I chain; V region;
KW T-helper cell inhibition; transplant rejection; Mab;
KW interleukin-2 receptor.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= signal 21..120
FT Region
FT /label= Variable
FT Region 121..131
FT /label= J1
PN DE143214-A.
PD 28-JAN-1993.
PF 30-DEC-1991; 143214.
PR 25-JUL-1991; DE-124759.
PR 30-DEC-1991; DE-143214.
PA (BOEY) BOEHRINGER MANNHEIM GMBH.
PI Kaluza B, Rietmüller G, Scheuer W, Weidle U;
DR WPI; 93-037582/05.
DR N-PSDB; Q36609.
PT Synergistic antibody compsn. for use as immunosuppressant -
PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
PT alpha- or anti-IL2R beta antibodies
PS Claim 5; Page 11; 18pp; German.
CC This sequence is the light chain variable region of a preferred
CC anti-CD4 monoclonal antibody for use in the claimed synergistic
CC composition. Mab MT 3.10 is deposited as clone 3.101/8B10 (ECACC
CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R

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CC alpha or beta antibody. Individually the antibodies are strongly
CC inhibiting and when used together their immunosuppressive properties
CC are improved; they synergistically inhibit T-helper cell
CC proliferation to effectively inhibit transplant rejection at low
CC doses without significantly reducing the general immune response.
CC See also Q36608-Q36616.
SQ Sequence 131 AA;

Query Match 97.1%; Score 910; DB 6; Length 131;
Best Local Similarity 96.9%; Pred. No. 1.12e-59;
Matches 127; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 metdtkllwllwvpgstgdivltqspaslavslgqratisckasqsvdydgsymw 60
|||||
Qy 1 METDTLLWVLLWVPGSTGDIVLTQSPASLAVSLGQRATISCKASQSVDYDGSYMWY 60
|||||
Db 61 qkpgqppklliyaanlesgiparfsgsgtdftlnihpveedaatyccgsedpp 120
|||||
Qy 61 QKPGQPPLKLLIYAANLESIGIPARFSGSGTDFTLNHPVEEDAATYCCQSNEDPP 120
|||||
Db 121 tfgggtkleik 131
|||||
Qy 121 TFGGGTKLEIK 131
|||||

RESULT 3

ID R04132 standard; protein; 131 AA.
AC R04132;
DT 06-SEP-1990 (first entry)
DE Anti-Leu 3a light chain variable region gene product, 206 Vx.
KW HIV; AIDS; anti-Leu3A; vaccine; ds.
OS Mus musculus.
PN EP-365209-A.
PD 25-APR-1990.
PF 11-OCT-1989; 010415.
PR 17-OCT-1988; US-260558.
PA (BECT) Becton Dickinson Co.
PI Hinton R, Oi VT;
DR WPI; 90-126329/17.
DR N-PSDB; Q04039.
PT New chimeric variants of murine antibody anti-leucine -
PT contg. human antibody regions, and DNA encoding sequences.
PS Claim 1; Fig 2; 12pp; English.
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
CC used to form chimeric mouse-variable, human-constant region Abs
CC suggested as being useful as a vaccine to HIV.
SQ Sequence 131 AA;

Query Match 96.6%; Score 905; DB 1; Length 131;
Best Local Similarity 96.2%; Pred. No. 2.72e-59;
Matches 126; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 1 metdtkllwllwvpgstgdivltqspaslavslgqratisckasqsvdydgsymw 60
|||||
Qy 1 METDTLLWVLLWVPGSTGDIVLTQSPASLAVSLGQRATISCKASQSVDYDGSYMWY 60
|||||
Db 61 qkpgqppklliyaanlesgiparfsgsgtdftlnihpveedaatyccgsedpp 120
|||||
Qy 61 QKPGQPPLKLLIYAANLESIGIPARFSGSGTDFTLNHPVEEDAATYCCQSNEDPP 120
|||||
Db 121 tfaggtkleik 131
|||||
Qy 121 TFGGGTKLEIK 131
|||||

RESULT 4
 ID P90543 standard; protein; 131 AA.
 AC P90543;
 DT 20-OCT-1989 (first entry)
 DE Amino acids sequence of a V chi region gene.
 KW V cji region; immunoglobulin; L chain variable region; HIV.
 OS Mus musculus
 PN EP-327000-A.
 PD 09-AUG-1989.
 PF 30-JAN-1989; 101583.
 PR 30-JAN-1988; JP-20255.
 PR 08-JUL-1988; JP-171385.
 PA The Chemo-Sero-Therapeutic Research Institute.
 PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsuhashita S, Hattori T, Takatsuki K;
 DR N-PSDB; N90495.
 DR WPI; 89-229050/32.
 PT Chimeric anti-human immune virus antibodies - contg. mouse variable regions and human constant regions for diagnosis, treatment and prevention of AIDS
 PS Disclosure; Fig 8; 33pp; English.
 CC The sequence is encoded by a V chi region gene (see N90495).
 CC The sequence from Asp 21 encodes the L chain variable region.
 SQ Sequence 131 AA;

Query Match 95.5%; Score 895; DB 1; Length 131;
 Best Local Similarity 97.7%; Pred. No. 1.61e-58;
 Matches 128; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 metdtillwllwvpgstgdlvtqpsaslqslqgratiscaskvsgvdydgdsymwy 60
 ||:|||||
 Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPASLAVSLGQRATISCKASQSDYDGDYNNWY 60
 ||:|||||
 Db 61 qkqpgqpklliyasnlsgiparfsgsgtdftlnihpveeedaatyycqgsnedpf 120
 ||:|||||
 Qy 61 QKPGQPKLLIYAASNLSEGPARGSGSGTDFTLNIHPVEEEDAATYYCQGSNEDPP 120
 ||:|||||
 Db 121 tfgsgtkleik 131
 ||:|||||
 Qy 121 TFGGGTKLEIK 131

RESULT 5
 ID R28668 standard; protein; 131 AA.
 AC R28668;
 DT 30-MAR-1993 (first entry)
 DE p12-k2.
 KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
 KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20;
 KW plasmid; p12-k2; p12-h2.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "Signal peptide"
 FT Protein 21..131
 FT /note= "Mature peptide"
 PN W09219759-A.
 PD 12-NOV-1992.
 PF 24-APR-1992; J00544.
 PR 25-APR-1991; JP-095476.
 PR 19-FEB-1992; JP-032084.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
 DR N-PSDB; Q30757.
 PT Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 PS Disclosure; Page 124-125; 207pp; Japanese.
 CC The sequences given in R29008-09 were encoded by plasmids which were
 CC used in example to illustrate the production of a human antibody which
 CC recognises human interleukin-6 receptor (IL-6R). The antibody
 CC comprises light (L) chain and heavy (H) chain variable regions which
 CC comprises derived from a mouse monoclonal antibody produced from the

DR WPI; 92-398882/48.
 DR N-PSDB; Q30753.
 PT Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 PS Disclosure; Page 118; 207pp; Japanese.
 CC The sequences given in R28668-69 were encoded by plasmid sequences
 CC which were used in example to illustrate the production of a human
 CC antibody which recognises human interleukin-6 receptor (IL-6R). The
 CC antibody comprises light (L) chain and heavy (H) chain variable
 CC regions which were derived from a mouse monoclonal antibody produced
 CC from the hybridoma AUK12-20 which contained the plasmids p12-k2 and
 CC p12-h2.
 SQ Sequence 131 AA;

Query Match 87.4%; Score 819; DB 6; Length 131;
 Best Local Similarity 87.0%; Pred. No. 1.15e-52;
 Matches 114; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Db 1 mesdtillwllwvpgstgdlvtqpsaslqslqgratiscaskvsgvsgymhy 60
 ||:|||||
 Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPASLAVSLGQRATISCKASQSDYDGDYNNWY 60
 ||:|||||
 Db 61 qkqpgqpklliyasnlsgiparfsgsgtdftlnihpveeedaatyycqgsrenpy 120
 ||:|||||
 Qy 61 QKPGQPKLLIYAASNLSEGPARGSGSGTDFTLNIHPVEEEDAATYYCQGSNEDPP 120
 ||:|||||
 Db 121 tfgsgtkleik 131
 ||:|||||
 Qy 121 TFGGGTKLEIK 131

RESULT 6
 ID R29008 standard; protein; 131 AA.
 AC R29008;
 DT 30-MAR-1993 (first entry)
 DE p64-k4 protein product.
 KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
 KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
 KW plasmid; p64-k4; p64-h2.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "Signal peptide"
 FT Protein 21..131
 FT /note= "Mature peptide"
 PN W09219759-A.
 PD 12-NOV-1992.
 PF 24-APR-1992; J00544.
 PR 25-APR-1991; JP-095476.
 PR 19-FEB-1992; JP-032084.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
 DR N-PSDB; Q30757.
 PT Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 PS Disclosure; Page 124-125; 207pp; Japanese.
 CC The sequences given in R29008-09 were encoded by plasmids which were
 CC used in example to illustrate the production of a human antibody which
 CC recognises human interleukin-6 receptor (IL-6R). The antibody
 CC comprises light (L) chain and heavy (H) chain variable regions which
 CC comprises derived from a mouse monoclonal antibody produced from the

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CC hybridoma AUK64-7 which contained the plasmids p64-k4 and p64-h2.
SQ Sequence 131 AA;

Query Match 87.1%; Score 816; DB 6; Length 131;
Best Local Similarity 85.5%; Pred. No. 1.96e-52;
Matches 112; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Db 1 mesdtllllwllwvpgstgdivltqspaslvslgqrattiscasqsdvdydgsymnwy 60
||:|||||
Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPASLVSLGQRATISCKASQSDVDYDGSYNNWY 60

Db 61 qkqpgqpklliyasnlsgiparfsgsgtrdftlinhpveedatyyccqsnedpp 120
|||||
Qy 61 QKQPGQPKLLIYAASNLSEGIPIARFSGSGTDFTLNHPVEEDATYYCCQSNEDPP 120

Db 121 tfgggtkleik 131
||:|||||
Qy 121 FGGGTKLEIK 131

;

RESULT 7

ID R05089 standard; protein; 131 AA.
AC R05089;
DT 04-OCT-1990 (first entry)
DE Light chain variable domain of human chorion gonadotropin-binding peptd.
KW Human chorionic gonadotropin; antibodies; choriocarcinoma; abortion;
KW tumour detection; complementary determining regions;
KW pregnancy prevention; light chain.
OS Mus musculus.

FH Key Location/Qualifiers
FT Binding-site 44..58
FT /label=CDR
FT Binding-site 74..80

FT /label=CDR 113..120

FT /label=CDR

FN EP-370581-A.

PD 30-MAY-1990.

PF 21-NOV-1989; 202951.

PR 25-NOV-1988; NL-002902.

PA (ALKO) AKZO NV.

PI van Wezenbeek PM;

DR WPI; 90-155307/22.

DR N-PSDB; Q04694.

PT Polypeptide(s) which specifically bind human chorionic gonadotropin -
PT contg. antigen-binding domains comprising complementary
PT determining domains.
PS Disclosure; p; English.
CC Together with the heavy chain variable domain (R05090) the sequence forms
CC a hCh-binding antibody fragment (FhCG). For the production of Abs
CC the variable region was fused to a constant region of human origin.
CC The product can be used to prevent pregnancy or for combatting
CC choriocarcinomas or other hCG-producing tumours.
CC They also have diagnostic applications as immune reagents for in vivo
CC diagnosis, eg for localisation of tumours and for in vitro diagnosis for
CC detection of hCG in body fluids.

SQ Sequence 131 AA;

Query Match 85.5%; Score 801; DB 1; Length 131;

Best Local Similarity 82.4%; Pred. No. 2.78e-51;
Matches 108; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

Db 1 mekdtllllwllwvpgstgdivltqspaslvslgqrattiscasqsdvdydgsymnwf 60
||:|||||

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8

Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPASLVSLGQRATISCKASQSDVDYDGSYNNWY 60

Db 61 qkqpgqpklliyasnlsgiparfsgsgtrdftlinhpveedatyyccqsnedpp 120
|||||

Qy 61 QKQPGQPKLLIYAASNLSEGIPIARFSGSGTDFTLNHPVEEDATYYCCQSNEDPP 120
|||||

Db 121 tfgggtkleik 131
||:|||||

Qy 121 FGGGTKLEIK 131

RESULT 8

ID R30881 standard; Protein; 131 AA.
AC R30881;
DT 10-MAY-1993 (first entry)
DE Antibody 4A2 light chain constant region.
KW Fd'; fragment; human; 4A2; constant region; Fab'; F(ab')2; antibody;
KW light chain; primer.
OS Mus musculus.

PN W09222324-A.

PD 23-DEC-1992.

PF 15-JUN-1992; U04976.

PR 14-JUN-1991; US-714175.

PA (XOMA) XOMA CORP.

PI Better MD, Carroll S, Horwitz AH;

DR WPI; 93-017909/02.

DR P-PSDB; Q34575.

PT Polynucleotide sequences encoding Fab' and F(ab')2 fragments -
PT used to produce, e.g. antibody-ricin A chain immuno:toxin(s)
PS Disclosure; Fig 10; 92pp; English.

CC This sequence represents the light chain constant domain (CL) from
CC mouse antibody 4A2. This sequence was used in conjunction
CC with the Fd' sequences given in Q34567-72 to produce chimeric Fd'
CC vectors.
SQ Sequence 131 AA;

Query Match 84.3%; Score 790; DB 6; Length 131;
Best Local Similarity 84.0%; Pred. No. 1.95e-50;
Matches 110; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Db 1 mesdtllllwllwvpgstgdivltqspaslvslgqrattiscasqsdvdydgsymnwy 60
||:|||||

Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPASLVSLGQRATISCKASQSDVDYDGSYNNWY 60
|||||

Db 61 qkqpgqpklliyasnlsgiparfsgsgtrdftlinhpveedatyyccqsnedpp 120
|||||

Qy 61 QKQPGQPKLLIYAASNLSEGIPIARFSGSGTDFTLNHPVEEDATYYCCQSNEDPP 120
|||||

Db 121 tfgggtkleik 131
||:|||||

Qy 121 FGGGTKLEIK 131

RESULT 9

ID R10920 standard; Protein; 132 AA.
AC R10920;
DT 08-MAY-1991 (first entry)
DE kappa light chain variable region of T84.66 monoclonal antibody.
KW Mab T84.66; kappa light chain; carcinoembryonic antigen; CEA;
KW human adenocarcinoma; mouse-human chimaeric antibody.
OS Mus musculus.
FH Key Location/Qualifiers
FT Peptide 21..38
FT /label= tryptic peptide

FT	/note= "sequenced as peptide fragment"	
Region	44..57	
FT	/label= complementarity determining region	
FT		
Region	70..80	
FT	/label= complementarity determining region	
FT		
Region	110..121	
FT	/label= complementarity determining region	
PN	W09101990-A.	
PD	21-FEB-1991.	
PF	19-JUL-1990; U04049.	
PR	26-JUL-1989; US-385102.	
PA	(CITY) CITY OF HOPE.	
PI	Shively JE, Riggs AD, Neumaier M;	
DR	WP1; 91-073486/10.	
DR	N-PSDB; Q10834.	
PT	Novel anti-CEA antibody - comparable to ATCC Accession No. BH	
PT	8747, produced by recombinant DNA, used in diagnosis of tumours	
PS	Claim 4; Page 18; 24pp; English.	
CC	The light chain variable region of murine MAb 84.66 was cloned and	
CC	sequenced. It was used to produce mouse V-human C antibodies with high	
CC	affinity for CEA. Chimeric murine-human anti-CEA Abs are used to	
CC	diagnose human colon adenocarcinomas.	
CC	See also Q11098 and Q10835-Q10848.	
SQ	Sequence 132 AA;	

Query Match	84.2%;	Score 789;	DB 3;	Length 132;
Best Local Similarity	82.6%;	Pred. No. 2.33e-50;		
Matches	109;	Conservative	12;	Mismatches 11; Indels 0; Gaps 0;

Db	1 metdtllwlllwpqstgdviltgspastavlqgratmcraagevdifvgvfihwy 60
	: : : :
Qy	1 METDTLLWLLWPVGTGDIVLTQSPASTAVLSIGQRATISCKASQVDYDGDSTMYNY 60

Db	61 qkbpqpklllyaaenlesipvrfgtqsrtdftliidpveadvatyycaqtndep 120
	: : : :
Qy	61 QKBPQP KLLLYAAENLESIPARSGSGTGF TLIHPVEEADATYYCQNEDPP 120

Db 121 tfgggtkleikr 132
|||
QY 121 TFGGgTKLEIKR 132

RESULT		10	R37116 standard; Protein; 132 AA.
ID	AC	R37116;	
DT	30-SEP-1993	(first entry)	
DE	Mouse 4C10 anti-idiotypic Ab light chain V region.		
KW	MALTA; monoclonal antibody; hybridoma; organ transplant rejection;		
KW	immuno-modulator; cancer; treatment; diagnosis; melanoma;		
KW	anti-cancer immunity; enhancement; suppression.		
OS	Mus musculus.		
FH	Key	Location/Qualifiers	
FT	Misc difference 31		
ET	/note= "Thr -> Ser, from PCR substituted gene"		
FN	W09310221-A.		
PD	27-MAY-1993.		
Pf	12-NOV-1992; U10166.		
PR	13-NOV-1991; US-791934.		
PA	(REGC) UNIV CALIFORNIA.		
PI	Hastings A, Irie RF, Morrison SL.		
DR	WPI; 93-182538/22.		
PT	Chimeric murine-human anti-idiotypic monoclonal antibodies -		
PT	useful as immuno-modulators for treating and diagnosing cancers,		
PT	and for suppressing organ transplant rejection and auto-immune		

PT diseases
PS Disclosure; Page 30-31; 46pp; English.
CC The sequence is that of the 4C10 anti-idiotype Ab light chain V region
CC which was used in the construction of a murine/human monoclonal
CC anti-idiotype antibody (MA1A). The MA1A elicits an anti-ganglioside
CC response and produces antibodies which induce cytotoxic destruction
CC of cancer cells bearing the gangliosides. It can be used for treating
CC cancers partic. melanomas. It can also be used as an immunomodulator to
CC enhance anti-cancer immunity, suppress organ transplant rejection and
CC suppress autoimmune disease. The MA1A can also be used in the diagnosis
CC of cancers.
SQ Sequence 132 AA;

Query Match	82.8%;	Score 776;	DB 7;	Length 132;
Best Local Similarity	83.3%;	Pred. No.	2.32e-49;	
Matches	110;	Conservative	10;	Mismatches 11; Indels 1; Gaps 1;
Db	1	metcdlllwlwvpgstgdvlvtgspaslavlgratmcrcasevdsvymfmbwy	60	
		: :		
		: :		
Qy	1	METDTILLWLLWPVSGTGIVLTQPASLAVSLGQRATISCRASQSDVDYDGDYSNNWY	60	
Db	61	qdkpgppklllyrasklesgiparfsgsesrtdfcltlnpvaeaddvatyyccqanedpt	120	
		: :		
		: :		
Qy	61	QQKPGPPKLLIYYAANLESIGIPARFSGSGSCTFTINTIHPEEDAAITYYCQNEDPP	120	
Db	121	wfeggwkleik	132	
Qy	121	-TFGGGTGLEIK	131	

RESULT	11
ID	R74967 standard; Protein; 130 AA.
AC	R74967;
DT	02-FEB-1996 (first entry)
DE	Anti-Idiotypic antibody Id1o20 clone 20KB1.
KW	Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; complementarity determining region.
OS	Mus sp.
FH	Key
FT	Location/Qualifiers
FT	Peptide 1..20
FT	/label= signal_peptide
PN	J07101999-A.
PD	18-APR-1995.
PF	06-OCT-1993; 272950.
PR	06-OCT-1993; JP-272950.
PA	(HAGI/) HAGIWARA Y.
DR	WPI; 95-182987/24.
DR	N-PSDB; Q90432.
PT	Novel anti-idiotypic antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
PT	Example 5; Page 20; 28pp; Japanese.
PS	CC R74960-R74969 are clones of the anti-idiotypic antibodies Id1o3, Id1o17, Id1o20, Id1o27 and Id1o33 against a human anticancer monoclonal antibody.
CC	CC These antibodies and DNA encoding them are useful in pharmacological, medical and biochemical fields of research.
CC	Sequence 130 AA;

```
Query Match      81.9%; Score 767; DB 14; Length 130;
Best Local Similarity 83.2%; Pred. No. 1.14e-48;
Matches 109; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

Db 1 metdtkllwvpgstgdvlvtgspaslavslgratitryasksvetsgyymhw 60
|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
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Qy 1 METDTILWLLWPCSTGDIVLTQSPASLASVIGQRATISCKASQSDYDGDSDYNNWY 60

Db 61 cqrpgqprlllylvnldsgvparfsgsgtdftlnihpveeedaatyvcqhl-egay 119
||:||||:|||| ||:||||:||||:||||:||||:||||:||||:||||: ||:

Qy 61 QQRPGQPKLLIYAASNLESIPARFSGSGTDTLTINHPVEEDAAATYYCQSNEDPP 120

Db 120 tfgggtkleik 130
|||||

Qy 121 TFGGKTLEIK 131

RESULT 12

ID R55123 standard; Protein; 111 AA.

AC R55123;

DT 27-JAN-1995 (first entry)

DE Mouse anti-HIV mu5.5 light chain variable region.

KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;

KW human immunodeficiency virus; variable region; VH chain; murine.

OS Mus musculus.

FH Key Location/Qualifiers

FT Region 1..23

FT /label= FR1

FT /label= CDR1

FT /label= FR2

FT /label= CDR2

FT /label= FR3

FT /label= CDR3

FT /label= FR4

PN J06125783-A.

PD 10-MAY-1994.

PF 28-DEC-1991; JP-359808.

PR (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.

PA WP1; 94-187942/23.

DR N-PSDB; Q65554.

PT Mouse-human chimeric anti-HIV antibody heavy and light chains -

PT and recombinant antibody consisting of the H- and L-chains,

PT useful in AIDS therapy

PS Example 3; Fig 4; 22pp; Japanese.

CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.

CC The heavy and light chain variable regions from these antibodies

CC were sequenced (R55120-R55123). The murine anti-HIV CDRe were

CC introduced into human framework regions to construct chimeric

CC antibodies (R55124-R55127).

SQ Sequence 111 AA;

Query Match 79.7%; Score 747; DB 10; Length 111;
Best Local Similarity 98.2%; Pred. No. 3.90e-47;
Matches 109; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslasvlgqratisckasqsdvtdgdSYMNVYQQRPGQPKLLIYAASNLES 60
|||||

Qy 21 DIVLTQSPASLASVIGQRATISCKASQSDYDGDSDYNNWYQQRPGQPKLLIYAASNLES 80

Db 61 gparfsgsgtdftlnihpveeedaatyvcqsnedpwtfgggtkleik 111
|||||

Qy 81 GIPARFSGSGTDTLTINHPVEEDAAATYYCQSNEDPPTFGGKTLEIK 131

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RESULT 13

ID R60302 standard; Protein; 111 AA.

AC R60302;

DT 09-MAR-1995 (first entry)

DE Anti HIV antibody light chain variable region.

KW Antibody; heavy chain; light chain; human immunodeficiency virus;

KW HIV; acquired immune deficiency syndrome; AIDS; treatment;

KW prophylaxis; Mus musculus; Homo sapiens.

OS Mus musculus.

FH Key Location/Qualifiers

FT Region 1..23

FT /label= Framework region 1.

FT /label= CDR1.

FT /label= CDR1.

FT /label= Framework region 2.

FT /label= Framework region 2.

FT /label= CDR2.

FT /label= Framework region 3.

FT /label= CDR3.

FT /label= Framework region 4.

PN W09415969-A.

PD 21-JUL-1994.

PF 14-JAN-1993; J00039.

PR 14-JAN-1993; AU-032671.

PR 14-JAN-1993; WO-J00039.

PA (KAGA) CEMO SERO THERAPEUTIC RES INST.

PI Eda Y, Kimachi K, Maeda H, Otsomi K, Shioaki K;

PI Tokiyoshi S;

DR WP1; 94-249145/30.

DR N-PSDB; Q70372.

PT Recombinant chimeric anti HIV antibody - useful for the treatment

PT and prevention of HIV

PS Claim 15; Figure 4; 51pp; Japanese.

CC The recombinant antibody light chain has neutralising activity

CC against HIV. Chimeric antibodies comprising both mouse and human

CC sequences are useful in the treatment/prevention of AIDS caused by

CC HIV.

SQ Sequence 111 AA;

Query Match 79.7%; Score 747; DB 11; Length 111;
Best Local Similarity 98.2%; Pred. No. 3.90e-47;
Matches 109; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 divltqspaslasvlgqratisckasqsdvtdgdSYMNVYQQRPGQPKLLIYAASNLES 60
|||||

Qy 21 DIVLTQSPASLASVIGQRATISCKASQSDYDGDSDYNNWYQQRPGQPKLLIYAASNLES 80

Db 61 gparfsgsgtdftlnihpveeedaatyvcqsnedpwtfgggtkleik 111
|||||

Qy 81 GIPARFSGSGTDTLTINHPVEEDAAATYYCQSNEDPPTFGGKTLEIK 131

RESULT 14

ID P90541 standard; protein; 111 AA.

AC P90541;

DT 20-OCT-1989 (first entry)

DE Immunoglobulin L chain variable region.

KW Immunoglobulin; L chain variable region; HIV.

OS Mus musculus

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PN EP-327000-A.
PD 09-AUG-1989.
PF 30-JAN-1989; 101583.
PR 30-JAN-1988; JP-20255.
PR 08-JUL-1988; JP-171385.
PA (****) The Chemo-Sero-Therapeutic Research Institute.
PI Maeda H, Eda Y, Kinachi K, Tokiyoshi S, Matsushita S, Hattori T,
PI Takatsuki K;
DR WPI; 89-229050/32.
DR N-PSDB; N90491, N90492, N90493.
PT Chimeric anti-human immune virus antibodies - contg. mouse variable
PT regions and human constant regions for diagnosis, treatment and
PT prevention of AIDS
PS Claim 5; page 15; 33pp; English.
CC The sequence is an L chain variable region from an immunoglobulin with
CC anti-HIV neutralising activity. See N90491-3, and N90495.
SQ Sequence 111 AA;

Query Match 78.3%; Score 734; DB 1; Length 111;
Best Local Similarity 97.3%; Pred. No. 3.87e-46;
Matches 108; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 divltqpsaslavlgqratiackasgvdgdydmymwyqkpgqppklliyaaanles 60
|||||
QY 21 DIVLTQSPASLAVSLGQRATISCKASQSDYDGSYNNWYQKPGQPPKLLIYAASNLES 80
|||||
Db 61 giparfegsgtrdftlnihpveedaatyycqgnedpftfgsgtkleik 111
|||||
QY 81 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPPTFGGTKLEIK 131
|||||

RESULT 15

ID R74966 standard; Protein; 146 AA.
AC R74966;
DT 02-FEB-1996 (first entry)
DE Anti-idiotype antibody Idiol7 clone 17KB1.
KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW complementarity determining region.
OS Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..13
FT /label= signal_peptide
PN J0710199-A.
PD 18-APR-1995.
PF 06-OCT-1993; 272950.
PR 06-OCT-1993; JP-272950.
PA (HAGI/) HAGIWARA Y.
DR WPI; 95-182987/24.
DR N-PSDB; Q90431.
PT Novel anti-idiotype antibody against an human anticancer monoclonal
PT antibody - and DNA sequences encoding the antibody, useful in
PT pharmacology, medicine and biochemical fields.
PS Example 5; Page 19; 28pp; Japanese.
CC R74960-R74969 are clones of the anti-idiotype antibodies Idio3, Idiol7,
CC Idio20, Idio27 and Idio33 against a human anticancer monoclonal antibody.
CC These antibodies and DNA encoding them are useful in pharmacological,
CC medical and biochemical fields of research.
SQ Sequence 146 AA;

Query Match 77.6%; Score 727; DB 14; Length 146;
Best Local Similarity 83.2%; Pred. No. 1.33e-45;
Matches 104; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

Db 1 lwvlllwpqsgtdivltqpsaslavlgqrasiykraskavstsgysymhwnqkpgqp 60

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QY 8 LWVLLWPQSGTGDIVLTQSPASLAVSLGQRATISCKASQSDYDGSYNNWYQKPGQP 67
|||||
Db 61 prlliyvlenlesgvparfsgsgtdftlnihpveedaatyycqghir-gaytfgggk 119
|||||
QY 68 PKLLIYAASNLESIGIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPPTFGGGTK 127
|||||
Db 120 leikr 124
|||||
QY 128 LEIKR 132
|||||

Search completed: Tue Mar 18 10:02:18 1997
Job time : 36 secs.

RESULT 8
 ID HV46 MOUSE STANDARD; PRT; 137 AA.
 AC P01822;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (MOPC 315).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89238351.
 RA RINFRET A., HORNE C., DORRINGTON K.J., KLEIN M.;
 RL MOL. IMMUNOL. 26:431-434(1989).
 RN [2]
 RP SEQUENCE OF 1-31.
 RX MEDLINE; 78094475.
 RA JIJKA R.L., PESTKA S.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 74:5692-5696(1977).
 RN [3]
 RP SEQUENCE OF 1-21.
 RX MEDLINE; 79148758.
 RA SCHECHTER I., WOLF O., ZEMELL R., BURSTEIN Y.;
 RL FED. PROC. 38:1839-1845(1979).
 RN [4]
 RP SEQUENCE OF 19-136.
 RX MEDLINE; 74170779.
 RA FRANCIS S.H., LESLIE R.G.Q., HOOD L., EISEN H.N.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:1123-1127(1974).
 RN [5]
 RP REVISION TO 53.
 RX MEDLINE; 77244979.
 RA HOOD L., MARGOLIES M.N., GIVOL D., ZAKUT R.;
 RL UNPUBLISHED RESULTS, CITED BY:
 RL PADLAN E.A., DAVIES D.R., PECHT I., GIVOL D., WRIGHT C.;
 RL COLD SPRING HARB. SYMP. QUANT. BIOL. 41:627-637(1977).
 CC -1- THIS ALPHA CHAIN HAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS
 CC ANTI-DINITROPHENYL ACTIVITY.
 DR EMBL; M27638; G602707; -;
 DR EMBL; X07880; G295908; -;
 DR PIR; P10102; AVMS35.
 DR HSP; P01789; 2FGH.
 KW IMMUGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 18
 FT CHAIN 19 137 IG HEAVY CHAIN V REGION (MOPC 315).
 FT DOMAIN 19 48 FRAMEWORK 1.
 FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 85 116 FRAMEWORK 3.
 FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 127 137 FRAMEWORK 4.
 FT DISULFID 40 114 BY SIMILARITY.
 FT CONFLICT 15 15 G -> GG (IN G295908).
 FT CONFLICT 15 15 G -> H (IN REF. 2).
 FT CONFLICT 77 78 GY -> YG (IN REF. 4).
 FT CONFLICT 102 102 N -> D (IN REF. 4).
 FT CONFLICT 123 123 MISSING (IN REF. 4).
 FT NON TER 137 137
 SQ SEQUENCE 137 AA; 15399 MW; 155A5E8D CRC32;

Query Match 49.0%; Score 499; DB 4; Length 137;
 Best Local Similarity 55.7%; Pred. No. 1.64e-78;
 Matches 78; Conservative 21; Mismatches 32; Indels 3; Gaps 3;
 Db 1 mkvlelyllltaipg-insdvqlqesgpglvkpsqelsltcvtgysl-tsgyfwvwiqr 58
 QY 1 MNRLLTSSLLLLVPAVILSQVTLKESGPGILQPSQTLSCFSGFSLTSGMGVSWIRQ 60
 Db 59 fpmklewlgfikydgngynpelnkrvsitrdtsenqffliknsvttedatycagdn 118
 QY 61 PSKGLEMLAHYVDDDKRYNPSIKSLRLLTISKDTSSNQVFLKITSVDTADTATYVCARRE 120
 Db 119 dhly-yfdywgqgttlvtss 137
 QY 121 TVFYFDFVWAGAGTTVTVSS 140
 RESULT 9
 ID HV44 MOUSE STANDARD; PRT; 115 AA.
 AC P01820;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (PJ14).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 81012133.
 RA SAKANO H., MAKI R., KUROSAWA Y., ROEDER W., TONEGAWA S.;
 RL NATURE 286:676-683(1980).
 DR PIR; A02095; HVMS14.
 DR HSP; P01772; IFDL.
 KW IMMUGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 115 IG HEAVY CHAIN V REGION (PJ14).
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12447 MW; 6E782F62 CRC32;
 Query Match 47.8%; Score 487; DB 4; Length 115;
 Best Local Similarity 62.3%; Pred. No. 5.49e-76;
 Matches 71; Conservative 21; Mismatches 16; Indels 6; Gaps 6;
 Db 5 allfclvtfpfcilqesgpglvapsgslsitctvsqfal-t-gygvnwvrrqpgk 62
 QY 7 SLL-LIV-PAVILSQVTLKESGPGILQPSQTLSCFSGFSLTSGMGVSWIRQPSCK 64
 Db 63 glewlgml-wgdgstdynsalrleiskdnksqvlkmsalqtdtdtaryyca 115
 QY 65 GLEWLAHYVDDDKR-YNPSIKSLRLLTISKDTSSNQVFLKITSVDTADTATYICA 117
 RESULT 10
 ID HV45 MOUSE STANDARD; PRT; 116 AA.
 AC P01821;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (MC101).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]

KW		IMMUNOGLOBULIN V REGION.		PYRROLIDONE CARBOXYLIC ACID.
FT	MOD RES	I	1	
TT	NON TER	122	122	
SQ	SEQUENCE	122 AA; 13668 MW;	4AF2E3D8 CRC32;	
	Query Match		41.9%; Score 427; DB 4; Length 122;	
	Best Local Similarity	47.6%;	Pred. No. 1.85e-63;	
	Matches	59; Conservative 31; Mismatches 29; Indels 5; Gaps		
Dbl	1 qvelvesggvzvpgsrslrlscasagftsfnyam--hwyrqpqgqlawvaisybgbk 58			
Qy	20 QVTKESGGGLIQ-SQTLSLTCFSFGSLTSGMGVSWIQRPSGRGLEIAH-I-YWDKK 78			
Dbl	59 yyabsvkrfftisrdbskbtlylqmslaetraebavvyccardplyqbgyrafnymwggtlv 118			
Qy	79 RYMPSIKSRLITSKDTSSNQVELFITSVDTDATYYCARRETVE---YWYFDVMWGAGTV 136			
Dbl	119 tvss 122			
Qy	137 TVSS 140			

[illegible]

Query Match	41.1%;	Score 418;	DB 4;	Length 116;
Best Local Similarity	54.4%;	Pred. No. 1.36e-61;		
Matches	62;	Conservative	23;	Mismatches 25;
			Indels	4;
			Gaps	3;

		62
Db	4 lllcllcfatpgilledvqlqesgpdllkbpqealeltctvtgyai--tsgvshwairfpan	62
Qy	8 LLLL-IVPAY--VLSQVTLKESGGICILQLPSLTLTCSFSGFLSTSGMGVSIPQSPCK	64
Db	63 klemwgdythsgntsynpelksisrtdsknffllqvstvedtatyycar	116
Qy	65 GLEWLAHYDDDKRNP SLKSRLTI SKOTSSNQVFKITSDVTADTYTCAR	118

[illegible]

```

Query Match      41.0%; Score 417; DB 4; Length 117;
Best local Similarity 51.7%;
Pred. No. 2.18e-61;
Matches 61; Conservative 26; Mismatches 30; Indels 1; Gaps 1;

Dbb 1 mkmftllylltvpq-ilsdvlqesgplvlpesgialctctvtgisitgnyrswirq 59
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 1 MNRLTSLLLIIVAYVLVSQVTLKESGPIQLQPSQTLSLTCSFSGSLSTGCVSWIRQ 60

Dbb 60 fpgnhlewgiyvaisynpskrtitrdtknqfflemaltaedatvycar 117
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Ov 61 PSKGLEWLAHLWDDKRYNPSLKSLKSLATISQDTSKNQVLTITSDVDTATYTCAR 118

```

Search completed: Tue Mar 18 10:02:50 1997
Job time : 15 secs.

QY	1	MNRLTSSLLLLTPAVYLSQVLTIKESPGILQPQTLSLTCSGFSILTSGMGVSWIRQ	60
Db	61	psgrglewlahiewddnllnypslksrltsktsdrnqvlktsvtdadtatycarre	120
QY	61	PSKGLEGLWLAHIYDDRRKNPSSLKSLRLTSKDTSSNQVFLKITSVDATATYYCARE	120
Db	121	rgygnylgpldywggqgtsvtvss	143
QY	121	TVF—YWY-FDMGAGCTTTWTSS	140

```

2
RESULT#
ENTRY
TITLE Iq heavy chain precursor V-D-J region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
22-Apr-1995
ACCESSIONS S11740
REFERENCE S11740
#authors Hayakawa, K.; Carmarck, C.E.; Hyman, R.; Hardy, R.R.
#submission submitted to the EMBL Data Library, May 1990
#description Natural autoantibodies to thymocytes: Origin, VH genes, fine
specificities, and the role of Thy-1 glycoprotein.
#accession S11740
#molecule_type mRNA
#residues 1-122 #label EMB
#cross-references EMBL:X53097
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
length 122 #checksum 38
SUMMARY

```

```

RESULT      3
ENTRY
TITLE      Iq heavy chain V region - mouse
ORGANISM   Mus musculus #common name house mouse
DATE       06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
           12-Apr-1995
ACCESSIONS S26465 #type complete
REFERENCE   S26465
            #authors Kavalier, J.
            #submission submitted to the EMBL Data Library, April 1991
            #accession S26465
            #status preliminary
            #molecule_type mRNA
            #residues 1-113 #label KAV
            #cross-references EMBL:X59115
CLASSIFICATION
            #superfamily immunoglobulin V region; immunoglobulin homology
            #length 113 #molecular-weight 12508 #checksum 2993
SUMMARY
Query Match 69.4%; Score 706; DB 5; Length 113;
Best Local Similarity 88.5%; Pred. No. 5,80e-69;

```

```

RESULT      4
ENTRY
TITLE      Iq heavy chain V region - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
          13-Jan-1995
ACCESSIONS
REFERENCE   S26328 #type complete
            Iq heavy chain V region - mouse
            #formal_name Mus musculus #common_name house mouse
            13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
            13-Jan-1995
            S26328
            S26309
            Stark, S.E.; Caton, A.J.
            J. Exp. Med. (1991) 174:613-624
            Antibodies that are specific for a single amino acid
            interchange in a protein epitope use structurally distinct
            variable regions.
            #accession S26328
            #status preliminary
            #molecule_type mRNA
            #residues 1-116 #label STA
            #cross-references EMBL:X59198
            #length 116 #molecular-weight 12895 #checksum 8145
SUMMARY

```

```

RESULT      5
ENTRY
TITLE      Iq heavy chain - human
ORGANISM   Homo sapiens
DATE       13-Jan-1995
           12-Apr-1995
ACCESSIONS S31513
           S31515
REFERENCE  Chaetagner, P.; Demaison, C.; Theze, J.; Zouali, M.
           submitted to the EMBL Data Library, December 1992
           Dominance of clonotypic patterns and variable gene usage of
           anti-DNA autoantibodies from patient with lupus.
           S31513
           preliminary
           mRNA
           1-138
           #label CHA
           #residues_
           #cross-references EMBL:X69861
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
                #length 138
                #molecular-weight 15115
                #checksum 3666
SUMMARY

```



```
Query Match 67.5%; Score 687; DB 5; Length 138;
Best Local Similarity 70.1%; Pred. No. 1.27e-66;
Matches 96; Conservative 19; Mismatches 20; Indels 2; Gaps 1;

Db 2 stllltipwlsqitlksesgtlvkptqtlktcsfsgfslstsgvgvqirgpgktt 61
   1:|||||:|:|||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|
Qy 6 SLLLLIPAYVLVSQVTLKESGPGILQPSQTLSTLTCFSFGSLTSGMGVSWIRQPSGKG 65

Db 62 lewliawdddkryspalksrltktdsqnqvlmtmndpvdtdatycacahrgpiavt 121
   1:|||||:|:|||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|
Qy 66 LEWLHAIHWDDDKRYNPSLSKRLTISKDTSSNQVFLKITSVDTDATATYYCARRETFYW 125

Db 122 ggnfdywgqgtlvtpvs 138
   1:|||||:|:|||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|
Qy 126 --YFDVWAGCTTVTVSS 140

RESULT 6
ENTRY S09959 #type fragment
TITLE Ig heavy chain V-D-J region (31-90) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Mar-1993

ACCESSIONS S09959
REFERENCE S09959
#authors Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
#journal Eur. J. Immunol. (1990) 20:771-777
#title Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies from autoimmune NZB mice.
#cross-references MUID:90249328
#accession S09959
#molecule_type mRNA
#residues 1-121 #label REI
#cross-references EMBL:X51847
SUMMARY #length 121 #checksum 7852

Query Match 66.2%; Score 674; DB 12; Length 121;
Best Local Similarity 77.7%; Pred. No. 5.05e-65;
Matches 94; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

Db 1 qvtlksghvlpqsgtlsltcsvsfslsahmgvgwrrpsgkglewlaniwnddky 60
   1:|||||:|:|||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|
Qy 20 QVTIKESGPGILQPSQTLSTLTCFSFGSLTSGMGVSWIRQPSGKGLEWLAHIWDDDKR 79

Db 61 ynavskrltvsdktenqvfllksavtdtdatycaciqvgvdfdwgaqtpvts 120
   1:|||||:|:|||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|
Qy 80 YNPSLSKRLTISKDTSSNQVFLKITSVDTDATATYYCARRETFYWFYFDVWAGCTTVTVS 139

Db 121 s 121
Qy 140 S-140

RESULT 7
ENTRY S18555 #type complete
TITLE Ig heavy chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Apr-1995
ACCESSIONS S18555
REFERENCE S18551
#authors Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Honjo, T.
```

```
#journal EMBO J. (1991) 10:3641-3645
#title Physical map of the 3' region of the human immunoglobulin heavy chain locus: clustering of antibody-related variable segments in one haplotype.
#cross-references MUID:92037524
#accession S18555
#status preliminary
#molecule_type DNA
#residues 1-119 #label SHI
#cross-references EMBL:X62111
GENETICS
#introns 16/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 119 #molecular-weight 13230 #checksum 1886

Query Match 65.8%; Score 670; DB 5; Length 119;
Best Local Similarity 72.3%; Pred. No. 1.57e-64;
Matches 86; Conservative 21; Mismatches 12; Indels 0; Gaps 0;

Db 1 mdtlctllltipswlsqitlksesgtlvkptqtlktctsfsgfslstsgvgvqirg 60
   1:|||||:|:|||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|
Qy 1 MRLTSSLLLLIPAYVLVSQVTLKESGPGILQPSQTLSTLTCFSFGSLTSGMGVSWIRQ 60

Db 61 ppgkalewliawdddkryspalksrltktdsqnqvlmtmndpvdtdatycacahr 119
   1:|||||:|:|||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|
Qy 61 PSQKGLEWLAHIWDDDKRYNPSLSKRLTISKDTSSNQVFLKITSVDTDATATYYCARR 119

RESULT 8
ENTRY A49442 #type fragment
TITLE Ig heavy chain V region (50.1) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-1995
ACCESSIONS A49442
REFERENCE A49442
#authors Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; Simmerman, H.K.B.; Profy, A.T.; Wilson, I.A.
#journal Proteins (1992) 14:499-508
#title Crystallization, sequence, and preliminary crystallographic data for an anti-peptide Fab 50.1 and peptide complexes with the principal neutralizing determinant of HIV-1 gp120.
#accession A49442
#status preliminary; not compared with conceptual translation
#molecule_type DNA
#residues 1-107 #label STU
SUMMARY #length 107 #checksum 9363

Query Match 62.6%; Score 637; DB 12; Length 107;
Best Local Similarity 88.8%; Pred. No. 1.76e-60;
Matches 87; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Db 1 pglqpsqtlsltcsvsfslstsgvgvswirgsgkglewlahifwdgdkrynpkskr 60
   1:|||||:|:|||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|
Qy 28 PGLQPSQTLSTLTCFSFGSLTSGMGVSWIRQPSGKGLEWLAHIWDDDKRYNPSLSKSR 87

Db 61 lkiskdtemqvfllktsavtdtdatycaciqvgv-eggiyw 97
   1:|||||:|:|||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|
Qy 88 LTSKDTSSNQVFLKITSVDTDATATYYCARRETFYW 125

RESULT 9
ENTRY B25913 #type fragment
```



```
RESULT 12
ENTRY
TITLE      A36005      #type complete
ORGANISM    Ig heavy chain V region (M60) - human
DATE        #formal_name Homo sapiens #common_name man
21-Dec-1990 #sequence_revision 13-Sep-1991 #text_change
22-Apr-1995
ACCESSIONS  A36005
REFERENCE    Schroeder Jr., H.W.; Wang, J.Y.
            Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6146-6150
            Preferential utilization of conserved immunoglobulin heavy
            chain variable gene segments during human fetal life.
            #cross-references MUID:90349571
            #accession A36005
            #status preliminary
            #molecule_type mRNA
            #residues 1-121 #label SCH
            #cross-references G8:M340Z1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY       #length 121 #molecular-weight 13557 #checksum 6899

Query Match      56.2%; Score 572; DB 5; Length 121;
Best Local Similarity 68.6%; Pred. No. 1.51e-52;
Matches 83; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

Db 1 evtlresgalkvptqtlitctlygslstsgmcsvwrpgskalewllaldwdddy 60
   :|||:||||: 1:||||:||||: |||||  |||||  |||||  |||||  |||||
Qy 20 QVTIKESGPGILQPSQTLSLTCFSFSLSTSGMGSWIRQPSGKGLEWLAHIYWD DDKR 79

Db 61 ystslkrliskdsknqvltmtmdpvdtdatyyvhrhprt1-afdwgggtkvav 119
   |:|||||  |||  |||  |:|  |||||  :|  |||||  |||  |||  |||
Qy 80 YNPSLKSRLTISKDTSSNQVFIKITSVDATATYYCARRETVFYWFDVWGAGTTTV 139

Db 121 s 121
   |
Qy 140 S 140

RESULT 13
ENTRY
TITLE      G1HUHE      #type complete
ORGANISM    Ig heavy chain V-II region (He) - human
DATE        #formal_name Homo sapiens #common_name man
            #sequence_revision 07-May-1981 #text_change 16-Feb-1996
ACCESSIONS  A02093
REFERENCE    Cunningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman,
            G.M.
            Proc. Natl. Acad. Sci. U.S.A. (1969) 64:997-1003
            Subgroups of amino acid sequences in the variable regions of
            immunoglobulin heavy chains.
            #cross-references MUID:70114712
            #accession A02093
            #molecule_type protein
            #residues 1-121 #label CUN
COMMENT      This gamma-1 chain was isolated from a myeloma protein.
GENETICS
#gene       GDB:IGHV8
#map_position 14q32.33
#cross-references GDB:G00-128-528
#classification #superfamily immunoglobulin V region; immunoglobulin homology
#keywords     pyroglytamic acid
FEATURE
1           #modified_site pyrrolidone carboxylic acid (Gln) #status
            experimental
SUMMARY      #length 125 #molecular-weight 13783 #checksum 9697

Query Match      54.6%; Score 556; DB 2; Length 125;
Best Local Similarity 64.0%; Pred. No. 1.33e-50;
Matches 80; Conservative 21; Mismatches 20; Indels 4; Gaps 3;

Db 1 qitlkesgptlvkptetltctcfsgfslstsgvsgvwirgpgkalewllafinwdddnr 60
   |:|||||  :  |:|||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 20 QVTIKESGPGILQPSQTLSLTCFSFSLSTSGMGSWIRQPSGKGLEWLAHIYWD DDKR 79

Db 61 ypslrsrltktktrnqvltitnmdpvdsgtyfcahrppwfrftgnlggfdwgqgtl 120
   |:|||||  |||  |||  |||  |:|  |||||  :|  |||||  |||  |||  |||
Qy 80 YNPSLKSRLTISKDTSSNQVFIKITSVDATATYYCARRET-VFY-WY--FDVWGAGTT 135

Db 121 vtvs 125
   |||||
Qy 136 VTVSS 140
```

```
Query Match      55.1%; Score 561; DB 2; Length 121;
Best Local Similarity 60.7%; Pred. No. 3.29e-51;
Matches 74; Conservative 27; Mismatches 19; Indels 2; Gaps 2;

Db 1 qvtlksngptlvkptetltctcglstldtdgavgwirgpgkalewllawlywdddk 60
   |||||  ||  :  |:|||||  |||||  |||||  |||||  |||||  |||||
Qy 20 QVTIKESGPGILQPSQTLSLTCFSFSLSTSGMGSWIRQPSGKGLEWLA-HIYWD DDK 78

Db 61 rfpslksrltvtrdtsknqvlmtmdpvdtdatyyvhrhprt1-afdwgggtkvav 119
   |:|||||  |||  |||  |||  |:|  |||||  :|  |||||  |||  |||  |||
Qy 79 RNPVSLKSRLTISKDTSSNQVFIKITSVDATATYYCARRETVFYWFDVWGAGTTTV 138

Db 120 ss 121
   ||
Qy 139 SS 140

RESULT 14
ENTRY
TITLE      MHHUMC      #type complete
ORGANISM    Ig heavy chain V-II region (McE) - human
DATE        #formal_name Homo sapiens #common_name man
            14-Nov-1983 #sequence_revision 22-Nov-1983 #text_change
            16-Feb-1996
ACCESSIONS  A02092
REFERENCE    Gerber-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.;
            Erickson, B.W.; Litman, G.W.
            J. Immunol. (1981) 126:1212-1216
            Molecular basis for the temperature-dependent insolubility of
            cryoglobulins. X. The amino acid sequence of the heavy
            chain variable region of McE.
            #cross-references MUID:81118242
            #accession A02092
            #molecule_type protein
            #residues 1-125 #label GER
            #note      this chain was derived from a monoclonal IgM
                        cryoimmunoglobulin

GENETICS
#gene       GDB:IGHV8
#cross-references GDB:G00-128-528
#map_position 14q32.33
#classification #superfamily immunoglobulin V region; immunoglobulin homology
#keywords     pyroglytamic acid
FEATURE
1           #modified_site pyrrolidone carboxylic acid (Gln) #status
            experimental
SUMMARY      #length 125 #molecular-weight 13783 #checksum 9697

Query Match      54.6%; Score 556; DB 2; Length 125;
Best Local Similarity 64.0%; Pred. No. 1.33e-50;
Matches 80; Conservative 21; Mismatches 20; Indels 4; Gaps 3;

Db 1 qitlkesgptlvkptetltctcfsgfslstsgvsgvwirgpgkalewllafinwdddnr 60
   |:|||||  :  |:|||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 20 QVTIKESGPGILQPSQTLSLTCFSFSLSTSGMGSWIRQPSGKGLEWLAHIYWD DDKR 79

Db 61 ypslrsrltktktrnqvltitnmdpvdsgtyfcahrppwfrftgnlggfdwgqgtl 120
   |:|||||  |||  |||  |||  |:|  |||||  :|  |||||  |||  |||  |||
Qy 80 YNPSLKSRLTISKDTSSNQVFIKITSVDATATYYCARRET-VFY-WY--FDVWGAGTT 135

Db 121 vtvs 125
   |||||
Qy 136 VTVSS 140
```


Search completed: Tue Mar 18 10:03:53 1997
Job time : 45 secs.

PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR N-PSDB; Q83491.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.2; 97pp; English.
CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC chains were cloned into pGEM7f+ and transformed into E. coli
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for
CC antibody engineering.
SQ Sequence 140 AA;

Query Match 100.0%; Score 1018; DB 13; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.29e-71;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mnrllsslllllpayvlsqvtlkespgqilqpsqtlsltcfsfsgfslstsgmgswirq 60
|||||
Qy 1 MNRLLSSLLLLLPAYVLISQVTLKESPGILQPSQTLSTCSFSGFSLSTSGMGSWIRQ 60
|||||

Db 61 psgkglewlahiywdddkrynpelkrltskdtssnqvflktsvtdadtatyyccarre 120
|||||
Qy 61 PSKGLEWLAHIYWDKRYNPISKRLTISKDTSSNQVFLKITSVDYDTATYYCARRE 120
|||||

Db 121 tvfywyfdwagagtvtvss 140
|||||
Qy 121 TVFYWYFDWAGAGTTVTSS 140
|||||

RESULT 2

ID R70191 standard; Protein; 141 AA.
AC R70191;
DT 20-SEP-1995 (first entry)
DE Chimeric antibody 3B9 heavy chain.
KW Chimeric antibody; antibody engineering; monoclonal antibody;
KW Mab; interleukin-4; IL-4; allergy.
OS Homo sapiens; Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Sig_peptide
FT Region 51..57
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 72..87
FT /label= CDR
FT /note= "complementarity determining region"
FT Peptide 120..130
FT /label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR N-PSDB; Q83492.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions
PS Disclosure; Fig.3; 97pp; English.
CC A human/mouse chimeric antibody heavy chain variable region was
CC constructed (given in R70191) that contained the mouse anti-human
CC IL-4 Mab 3B9 variable region including 3 CDRs (R70198-200) and a
CC human antibody signal peptide (R70193). The construct was used
CC for humanized antibody production.
SQ Sequence 141 AA;

Query Match 88.8%; Score 904; DB 13; Length 141;
Best Local Similarity 95.5%; Pred. No. 2.48e-62;
Matches 128; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Db 10 sllllwisgay---gvltlkespgqilqpsqtlsltcfsfsgfslstsgmgswirqpsqkgl 67
|||||
Qy 7 SLLLLIYPAYVLISQVTLKESPGILQPSQTLSTCSFSGFSLSTSGMGSWIRQPSGKGL 66
|||||
Db 68 ewlahiywdddkrynpelkrltskdtssnqvflktsvtdadtatyyccarretvfywy 127
|||||
Qy 67 EWLAHIYWDKRYNPISKRLTISKDTSSNQVFLKITSVDYDTATYYCARRETVIFYWY 126
|||||
Db 128 fdwagagtvtvss 141
|||||
Qy 127 FDWAGAGTTVTSS 140
|||||

RESULT 3

ID R54092 standard; Protein; 143 AA.
AC R54092;
DT 29-DEC-1994 (first entry)
DE Sequence of mouse VH showing the sequences of recombinant
DE anti-FHV-1 antibody CDRs 1, 2 and 3.
KW Feline herpes virus; FHV-1; monoclonal antibody; CDR;
KW complementarity determining region.
OS Mus musculus.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= leader
FT Region 20..47
FT /label= FR1
FT Region 48..56
FT /label= CDR1
FT Region 57..70
FT /label= FR2
FT Region 71..86
FT /label= CDR2
FT Region 87..118
FT /label= FR3
FT Region 119..132
FT /label= CDR3
FT Region 133..143
FT /label= FR4
PN W09412661-A.
PD 09-JUN-1994.
PF 25-NOV-1993; J01724.
PR 28-NOV-1992; JP-341255.
PR (KAGA) CHEMO SERO THERAPEUTIC RES INST.
PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;
DR WPI; 94-200288/24.
DR N-PSDB; Q64166.
PT Feline monoclonal antibody and recombinant antibodies specific
PT for FHV-1 - for detection, treatment and prevention of FHV-1
PT infection.
PS Disclosure; Page 17-18; 53pp; Japanese.

CC The inventors claim a monoclonal antibody against feline herpes
CC virus (FHV-1). They also claim a recombinant antibody against FHV-1
CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
CC used in the detection, treatment and prevention of FHV-1. The
CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
CC antibody are given in R54092. The sequences of the CDRs in the VL of
CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR
CC sequences are claimed.
SQ Sequence 143 AA;

Query Match	80.5%;	Score 819;	DB 10;	Length 143;
Best Local Similarity	81.9%;	Pred. No. 1.97e-55;		
Matches	118;	Conservative 8;	Mismatches 13;	Indels 5; Gaps 3;
Db	1	mgrltsflllipyavvlsvqlkespgqilqpseqlsltcfsfslsetsgmaqwirq	60	
Qy	1	MRLRSTSLILLIYPAYVLISQVTLKESGPGILQPSQTLSTLCFSFCFSLSGSGVSWIRQ	60	
Db	61	psqkglewlahiwdvdkrynpalkritskidsstssqvfkliaavdtadtatfcvrsq	120	
Qy	61	PSQKGLEWLAHIWDDDKRYNP SLKGRLTISKDTSSNQVFLKITSVDTAADTATTCARRE	120	
Db	121	iyfdydgaw-fpfwgqgatlvtvsa	143	
Qy	121	TVF-Y---WYFDVAGAGATTVTVSS	140	

RESULT	4
ID	R70192 standard; Protein; 141 AA.
AC	R70192;
DE	20-SEP-1995 (first entry)
DT	Humanized antibody 3B9 heavy chain.
KW	Humanized antibody; antibody engineering; monoclonal antibody;
KW	MAb; interleukin-4; IL-4; allergy.
OS	Homo sapiens.
FH	Key Location/Qualifiers
FT	Peptide 1..19
FT	/label= sig_peptide
FT	Region 51..57
FT	/label= CDR
FT	/note= "complementarity determining region"
FT	Region 72..87
FT	/label= CDR
FT	/note= "complementarity determining region"
FT	Region 120..130
FT	/label= CDR
FT	/note= "complementarity determining region"
PN	M09507301-A.
PD	16-MAR-1995.
PF	07-SEP-1994; V10308.
PR	07-SEP-1993; US-117366.
PR	14-OCT-1993; US-136783.
PA	(SMIK) SMITHKLINE BEECHAM CORP.
PA	(SMIK) SMITHKLINE BEECHAM PLC.
PI	Gross MS, Holmes SD, Sylvestre DR;
DI	WPI; 95-123387/16.
DR	N-PDSB; Q83493.
PT	Chimeric and humanised IL-4 monoclonal antibodies (mabs), deriv
PT	from high affinity mabs - useful in treatment of IL-4-mediated
PT	and IgE-mediated allergic conditions
PS	Disclosure; Fig.4; 9/pp; English.
CC	A humanized antibody heavy chain variable region and signal
CC	sequence is given in R70192. The signal sequence is also
CC	provided in R70193. The CDR sequences of the construct are

CC	identical to the native CDRs of mouse anti-human IL-4 MAb
CC	3B9 (R70198-200).
SQ	Sequence 141 AA;

Query Match 79.3%; Score 807; DB 13; Length 141;
Best Local Similarity 81.3%; Pred. No. 1.85e-54;
Matches 109; Conservative 12; Mismatches 11; Indels 2; Gaps 1;

Db	10	sllllwisay--qvtlrresgalvhtqtltctsfafstscmgvswirgppokql	67
		: : : : : :	
Qy	7	SLLLLIPAYVLSQVTLKESGPILOPQSLTSLTCSFSGSILSTSGMGVSWIROPSCKGL	66
		: : : : : :	
Db	68	ewlahiywdddkrynpksrlstskdternqvlvtmmdpvdttvyycarretvfywy	127
		: : : : : :	
Qy	67	EWLAHIYWDDEKRYNPSLKSLRTISKDTSNQVFLKITSVDTAATYTCARRETVFYWY	126
		: : : : : :	
Db	128	fdwgrgtprtvs	141
Ov	127	FDWGAGITTVTS	140

RESULT	5	
ID	R88107	standard; Protein; 139 AA.
AC	R88107;	
DE	25-JUL-1996	(first entry)
DT	Murine anti-Protein C MAb	HPC-4 VH gamma protein.
DD	Epitope; activation; heavy chain; protein C; vitamin K;	plasma protein;
KW	zymogen; cleavage; mouse; humanised antibody; variable region;	
KW	light chain; inhibition; anticoagulant; coagulation; tumour.	
OS	Mus musculus.	
Key	Location/Qualifiers	
FT	Peptide	1..19
FT	/note= "signal peptide"	
FT	Peptide	20..139
FT	/note= "mature peptide"	
PN	W09534652-A1.	
PD	21-DEC-1995.	
PF	09-JUN-1995; U07372.	
PR	10-JUN-1994; US-259321.	
PA	(OKLA-) OKLAHOMA MED RES FOUND.	

n-F50b, 102233.
 PT Calcium-binding monoclonal antibody immunoreactive with Protein C -
 PT inhibits Protein C anticoagulant activation by
 PT thrombin-thrombomodulin, e.g. for treating tumours
 PS Claim 2; Page 29; 41pp; English.
 CC This is the amino acid sequence of the heavy chain variable region from
 CC the murine anti-protein C monoclonal antibody HPC-4 which recognises
 CC the activation peptide region (R88106) of the heavy chain of protein C,
 CC a vitamin K-dependent plasma protein zymogen. Protein C is converted to
 CC activated protein C (APC) by cleavage between the Arg-Ileu amino acid
 CC contained within the activation peptide sequence. HPC-4 prevents protein
 CC C activation to APC by binding to this region. The DNA sequences encoding
 CC the variable regions of the heavy and light chains of the antibody
 CC (T09299-302) were used to construct humanised antibodies using the PCR
 CC primers T09303-9. The humanised antibodies are useful as inhibitors of
 CC coagulation and can be used for the treatment of tumours by inhibiting
 CC the anticoagulant activity of APC by preventing conversion of protein C
 CC to APC.

Query Match 78.8%; Score 802; DB 17; Length 139;
Best Local Similarity 81.4%; Pred. No. 4.69e-54;

Query Match 78.5%; Score 799; DB 13; Length 139;
Best Local Similarity 82.1%; Pred. No. 8.21e-54;
Matches 115; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

	Query Match	73.8%; Score 751; DB 7; Length 141;
	Best Local Similarity	78.0%; Pred. No. 6.27e-50;
	Matches	110; Conservative 11; Mismatches 19; Indels 1; Gaps 1;
D _b	1 mdrtsflllmvpayvlsvqlksgpgilqpsqtldtclcsfsqslstygmcvwirg	60
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Q _y	1 MNRUTSSLLLLLVPAYVLSVTIKESGCGILQPSTLSLTCSFSQSLSFGMGYSWIRQ	60
D _b	61 ssqkglewlanywsdskaynpelknritiskdtsmmqafkitnmdtadtaiyycagrg	120
	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Q _y	61 PSGRGLEWLHAHYMDKKRNPYSLKSRLLTISKDTSSNQFLKITSVDTAATYTCARR-	119
D _b	121 ategivsfdywghgmvtvss	141
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
O _v	120 ETVFYFYFDWGAGTTTVSS	140

RESULT	8
ID	R53339 standard; Protein; 141 AA.
AC	R53339;

DT	18-NOV-1994	(first entry)	
DE	KW50	cell-derived Ig H chain variable region.	
KW	Monoclonal antibody; Ab;	ganglioside GM2; chimera;	
KW	chimeric antibody;	expression vector; heavy; light; chain;	
KW	hypervariable region; CDR;	constant region; hybridoma;	
KW	Ig; immunoglobulin;	promoter; enhancer.	
OS	Rat rattus.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT	/label= sig_peptide		
PN	AU9346181-A.		
PD	17-MAR-1994.		
PF	07-SEP-1993;	046181.	
PR	07-SEP-1992;	JP-238452.	
PA	(KYOW) KYOWA HAKKO KOGYO KK.		
PI	Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;		
PI	Shitara K;		
DR	WPI; 94-126857/16.		
DR	N-PSDB; Q45437.		
PT	Humanised antibody specific for ganglioside GM2 - used for		
PT	producing a cytotoxic effect on cancers such as melanoma,		
PT	neuroblastoma and glioma.		
PS	Reference example 1; Page 114-115; 191pp; English.		
CC	Example 1 describes the construction of the vector pChIgLA1		
CC	for chimeric human antibody L chain expression.		
CC	Ig H chain promoter and enhancer genes were isolated from KM50		
CC	cells (anti-human serum albumin).		
CC	Sequence 141 AA;		

[illegible]

RESULT	9
ID	R92089 standard; Protein; 120 AA.
AC	R92089;
DT	16-MAY-1996 (first entry)
DE	Anti-RSV F glycoprotein MAb 1129 VH.
KW	Humanised antibody; chimeric antibody; antibody engineering;
KW	monoclonal antibody; WAB 1129; respiratory syncytial virus; RSV;
KW	heavy chain; complementarity determining region; CDR.
OS	Mus musculus.
FH	Key
FT	Region
FT	/label= CDR1
FT	Region
FT	/label= VDR2
FT	Region
FT	/label= CDR3
PN	W09605229-A1.
PD	22-FEB-1996.

PF	09-AUG-1995; U10053.
PR	15-AUG-1994; US-290592.
PA	(MEDI-) MEDIMMUNE INC.
PI	Johnson LS;
PT	WPI; 96-139646/14.
PT	New chimeric antibodies against respiratory syncytial virus -
PT	comprise human antibodies with CDR's from the variable heavy and
PT	light chains of a murine antibody
PS	Example 7; Fig 7A-7B; 55pp; English.
CC	A human-mouse chimeric antibody heavy chain has a human <i>Cos</i>
CC	framework contg. complementarity determining region (CDRs) from the
CC	variable heavy (VH) chain of a murine monoclonal antibody (MAB 1129)
CC	against respiratory syncytial virus (RSV) glycoprotein F antigenic
CC	site C. CDRs from MAB 1129 VH (see R92089) were grafted into the
CC	human Cor VH region (R92086) or Cess VH region (R92087) to produce
CC	CDR-grafted MEDI-493 VH (R92088). A similar procedure was used to
CC	obtain CDR-grafted VL (R92091). The humanised antibody is used to
CC	treat RSV infection.
SQ	Sequence 120 AA;

Query Match	73.0%;	Score 743;	DB 16;	Length 120;
Best Local Similarity	86.8%;	Pred. No. 2,78e-49;		
Matches 105;	Conservative 4;	Mismatches 11;	Indels 1;	Gaps 1;
Db	1	qvelqesgqilqpsqtllslctsfsgfslstsgmsvgwlrqpsgegglewladlwwddkkd	60	
Qy	20	QVTVKESGPGTLPQSTLSLCTSFSGFSLSTSGMGSWNRQPSGKGLEWLAHYHWDKKR	79	
Db	61	ynpslksrltiskdtsasngvfikitgvdktadtatyyccars-mitnwfydvwgagttvtvs	119	
Qy	80	YNPSLKSRLTISKDTSSNOVFLKITSVDLTADTATYYCARRETVFYHFDVWGAGTTVTVS	139	
Db	120	s 120		
Qy	140	s 140		

RESULT	10	
ID	R58612	standard; Protein; 246 AA.
AC	R58612;	
DT	28-APR-1995	(first entry)
DE	IL-6 binding inhibitor.	
KW	Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;	
DE	Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;	
KW	septic shock; multiple myeloma; ss.	
OS	Homo sapiens.	
PN	EP-617126-A.	
PD	28-SEP-1994.	
PF	16-FEB-1994; 102346.	
PR	17-FEB-1993; JP-028173.	
PA	(AJIN) AJINOMOTO KK.	
PI	Hamuro J, Nakazawa H, Shimamura T;	
PT	WPI; 94-295777/37.	
DR	N-PSDB; Q70612.	
PT	Polypeptide inhibiting binding of human interleukin-6 (IL-6) to	
PT	its receptor - useful for treating autoimmune disease induced	
PT	or aggravated by IL-6	
CS	Claim 5; Page 18; 26pp; English.	
CC	Q70612 codes for human interleukin-6 binding inhibitor, the	
CC	polypeptide described in R58612. This polypeptide inhibits the	
CC	binding of human IL-6 to its receptor, and can therefore be	
CC	useful in the treatment of a variety of autoimmune diseases;	
CC	specifically in the treatment of rheumatoid arthritis, septic	
CC	shock due to bacterial infection and multiple myeloma.	
SQ	Sequence	246 AA;

	Query Match	72.6%;	Score 739;	DB 11;	Length 246;
	Best Local Similarity	84.9%;	Pred. No. 5.84e-49;		
	Matches	107;	Conservative	8;	Mismatches 6;
				Indels	5;
				Gaps	4;
Db	122	tqvkleeqgpiqpqstlsltcfsqfslstsgmvsqirpsqgkglewlahiywddk	181		
		:::			
Qy	19	SQVTLKESGPIQLQPQSTLSLTCFSQFSLSTSGMVSQIRPSQGKGLEWLAHYWD	78		
		:::			
Db	182	hynpslksrltkiekdstnqvflkitstvdadtatycarr-slygnwgydamdywgggt	240		
		:::			
Qy	79	RYNPSLKSRLFTISKDTSSNQFLKITSTVDATATYCARRETVF-YW--Y-FDWMGAGT	134		
		:::			
Db	241	svtvss	246		
		:::			
Qy	135	TVTVS	140		
		:::			

RESULT 11

ID	R54101 standard; Protein; 122 AA.
AC	R54101;
DT	08-FEB-1995 (first entry)
DE	Humanised MAb H-chain.
KW	Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
KW	complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN.
OS	Chimeric - Mus musculus.
OS	Chimeric - Homo sapiens.
EH	Key
EH	Location/Qualifiers
FT	Region
FT	/label= CDR1
FT	Region
FT	/label= CDR2
FT	Region
FT	/label= CDR3
PN	J06141885-A.
PD	24-MAY-1994.
PD	05-NOV-1992; 322476.
PR	05-NOV-1992; JP-322476.
PR	(RAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
PA	WPI; 94-205040/25.
DR	N-PSDB; Q68709.
PT	Recombinant anti-HIV monoclonal antibody - capable of
PT	neutralising strains which can not be neutralised by anti-IIIB
PT	and IIIMN antibodies
PS	Disclosure; Page 13; 23pp; Japanese.
CC	The sequences given in R54101-02 represent the heavy and light chains
CC	respectively of the humanised monoclonal antibody (MAb) of the
CC	invention. The antibody has the ability to neutralise human
CC	immunodeficiency virus. The antibody is classified as IgG kappa and
CC	has the sequence RIGPCR or RVGPCR in the principal neutralising
CC	domain. The antibody may be used to neutralise the clinically
CC	separate strains which cannot be neutralised by the neutralising
CC	antibodies against IIIB and IIIMN strains.
SQ	Sequence 122 AA;

Query Match 70.9%; Score 722; DB 11; Length 122;
Best Local Similarity 86.3%; Pred. No. 1.38e-47;
Matches 107; Conservative 5; Mismatches 7; Indels 5; Gaps 3;

```

Db      1 qvtlkespgilqpsqtlsltcfsfsgfslsfmgvswirqpqskvlewlahiywddkdh 60
        |||||
Qv     20 QVTLKESGPGILQPSQVTLTLCTCFSEGSFSLTSCGMGVSWIRQPSGKGLEWLAHYWDDDKR 79
        |||||

```

61 vnpslksr|tisedtsnnavflkittvtdadtatvycarr--vfvansdfmdhwgaatsv 118

QY	80	YNPSLKSRLTISKDTSNQVELKITSVDTAOTATYCARRETFY--W-YFDWCAGTTV	136
Db	119	tvag	122
QY	137	TVSS	140

RESULT 12

ID	R92088	standard; Protein; 120 AA.
AC	R92088;	
DT	16-MAY-1996	(first entry)
DE	CDR-grafted anti-RSV F glycoprotein MEDI-493 VH.	
KW	Humanised antibody; chimeric antibody; antibody engineering;	
KW	monoclonal antibody; MAb 1129; respiratory syncytial virus; RSV;	
KW	heavy chain; complementarity determining region; CDR.	
OS	Chimeric Homo sapiens;	
OS	Chimeric Mus musculus.	
FH	Key	Location/Qualifiers
FT	Region	31..36
FT	/Label= CDR1	
FT	Region	52..67
FT	/Label= VDR2	
FT	Region	100..109
FT	/Label= CDR3	
PN	W09605229-A1.	
PD	22-FEB-1996.	
PR	09-AUG-1995; U10053.	
PR	15-AUG-1994; US-290592.	
PA	(MEDI-) MEDIMUNE INC.	
PI	Johnson LS;	
DI	WPI; 96-139646/14.	
PT	New chimeric antibodies against respiratory syncytial virus -	
PT	comprise human antibodies with CDR's from the variable heavy and	
PT	light chains of a murine antibody	
PS	Example 7; Fig 7A-7B; 55pp; English.	
CC	A human-mouse chimeric antibody heavy chain has a human Cos	
CC	framework contg. complementarity determining region (CDR) from the	
CC	variable heavy (VH) chain of a murine monoclonal antibody (MAb 1129)	
CC	against respiratory syncytial virus (RSV) glycoprotein F antigenic	
CC	site C. CDRs from MAb 1129 VH (see R92089) were grafted into the	
CC	human Cor VH region (R92086) or Cess VH region (R92087) to produce	
CC	CDR-grafted MEDI-493 VH (R92088). A similar procedure was used to	
CC	obtain CDR-grafted VL (R92091). The humanised antibody is used to	
CC	treat RSV infection.	
SQ	Sequence	120 AA;

Query Match	68.4%;	Score 696;	DB 16;	Length 120;
Best Local Similarity	77.7%;	Pred. No. 1.72e-45;		
Matches	94;	Conservative 15;	Mismatches 11;	Indels 1; Gaps 1;

Db	1	qvtlresgpaivkptqtlitctfsgfslstsgmsvgwirppgkalewladiwddk	60
	:::	:::	:::
Qy	20	QVTLKESGFGIILAPSQLLSLTCFSGFSLSTSGMGVSWIRQPSGKGLELAHIYVDDDKR	79

Db	61	ynp	lks	rlt	isk	tds	snq	vlk	vtn	md	pad	at	yy	car	s-mit	wny	fd	vw	gag	tt	vt	vs	119	
Ov <td>80</td> <td>YNP</td> <td>LKS</td> <td>RLT</td> <td>ISK</td> <td>TD</td> <td>SNQ</td> <td>VLK</td> <td>VTN</td> <td>MD</td> <td>PAD</td> <td>AT</td> <td>YY</td> <td>CAR</td> <td>S</td> <td>MIT</td> <td>WNY</td> <td>FD</td> <td>VW</td> <td>GAG</td> <td>TT</td> <td>VT</td> <td>VS</td> <td>139</td>	80	YNP	LKS	RLT	ISK	TD	SNQ	VLK	VTN	MD	PAD	AT	YY	CAR	S	MIT	WNY	FD	VW	GAG	TT	VT	VS	139

Db 120 s 120
Qy 140 s 140

RESULT 13

ID R88109 standard; peptide; 120 AA.
AC R88109;
DE 25-JUL-1996 (first entry)
DT Murine anti-Protein C MAB HPC-4 VH gamma mature peptide.
KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
KW zymogen; cleavage; mouse; humanised antibody; variable region;
KW light chain; inhibition; anticoagulant; coagulation; tumour.
OS Mus musculus.
PN W09534652-A1.
PD 21-DEC-1995.
PF 09-JUN-1995; U07372.
PR 10-JUN-1994; US-259321.
PA (OKLA-) OKLAHOMA MED RES FOUND.
PI Esmon CT, Rezaie A;
DR WF1; 96-049681/05.
DR N-PSDB; T09300.
PT Calcium-binding monoclonal antibody immunoreactive with Protein C -
PT inhibits Protein C anticoagulant activation by
PT thrombin-thrombomodulin, e.g. for treating tumours
PS Claim 2; Page 29; 41pp; English.
CC This is the amino acid sequence of the mature peptide from the murine
CC anti-protein C monoclonal antibody HPC-4 heavy chain variable region.
CC HPC-4 recognises the activation peptide region (R88106) of the heavy
CC chain of protein C, a vitamin K-dependent plasma protein zymogen.
CC Protein C is converted to activated protein C (APC) by cleavage between
CC the Arg-Leu amino acid contained within the activation peptide sequence.
CC HPC-4 prevents protein C activation to APC by binding to this region.
CC The DNA sequences encoding the variable regions of the heavy and light
CC chains of the antibody (T09299-302) were used to construct humanised
CC antibodies using the PCR primers T09303-9. The humanised antibodies are
CC useful as inhibitors of coagulation and can be used for the treatment of
CC tumours by inhibiting the anticoagulant activity of APC by preventing
CC conversion of protein C to APC.
SQ Sequence 120 AA;

Query Match 67.7%; Score 689; DB 17; Length 120;

Best Local Similarity 81.8%; Pred. No. 6.31e-45;
Matches 99; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

Db 1 qvtlkesqpilqpsqtlitlctslgfsalrtsgmgvgtwqpsgkglewlahiwdddkr 60

Qy 20 QVTLKESGPIQLQPSQTLSLTCFSFGSLSTSGMGVSWIRQPSRGLEWLAHYWDDDKR 79

Db 61 ynpvlkerliiekdtsrkqvfikiasvdtadtatyycvrmdd-ydandygggtvts 119

Qy 80 YNPSIKSLRTISKDTSSNQVFLKITSVDTADTATYTCARRETVFYWFDVWGAGTTVTS 139

Db 120 s 120

Qy 140 S 140

RESULT 14

ID R66299 standard; Protein; 119 AA.

AC R66299;

DT 07-AUG-1995 (first entry)

DE Human immunoglobulin variable heavy chain #5.

KW Primer; PCR; amplifi; human; immunoglobulin; variable; heavy chain;

KW cosmid; placenta; vector; pJB81; E.coli; mammalian.

OS Homo sapiens.

PN W09476895-A.

PD 24-NOV-1994.

PF 10-MAY-1993; J00603.

PR 10-MAY-1993; W0-J00603.

PA (NISR) JAPAN TOBACCO INC.

PI Honjo T, Matsuda F;

DR WF1; 95-006791/01.

DR N-PSDB; Q78943.

PT DNA fragment comprising human immunoglobulin Vh genes - for the

PT production of human immunoglobulin in mammalian hosts

PS Disclosure; Page 36-37; 130pp; Japanese.

CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain

CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were

CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;

CC Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using primers

CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The

CC fragments cover a region of 800 kb. The DNA fragments were isolated from

CC high molecular weight DNA from human placenta. The DNA was partially

CC digested with TaqI restriction enzyme. The fragments were separated by

CC gel electrophoresis and 35-45 kb fractions were collected. The fragments

CC were ligated with ClaI-digested cosmid vector pJB81. The ligation

CC products were in vitro packed and infected into E.coli 490A. The

CC fragments were then subcloned by colony hybridisation. The Vh genes and

CC the DNA fragments encoding them are useful in producing human

CC immunoglobulin in mammalian hosts.

SQ Sequence 119 AA;

Query Match 65.8%; Score 670; DB 12; Length 119;

Best Local Similarity 72.3%; Pred. No. 2.14e-43;

Matches 86; Conservative 21; Mismatches 12; Indels 0; Gaps 0;

Db 1 mdltcstlllltipwlsqitlkesgtlivtqtltlctcfsgfslstsgvqvgtir 60

Qy 1 MNRITSSLLILVPAVLQVTLKESGPIQLQPSQTLSLTCFSFGSLSTSGMGVSWIRQ 60

Db 61 ppqkalewlllywmddkryspelskrltitktdeknvgvltmtmdpvdtycahr 119

Qy 61 PSRGLEWLAHYWDDDKRYPNPSIKSLRTISKDTSSNQVFLKITSVDTADTATYTCARR 119

RESULT 15

ID R38315 standard; Protein; 139 AA.

AC R38315;

DT 04-DEC-1993 (first entry)

DE Sequence of the Vh of antibody B17X2

KW Variable heavy antibody chain; human subgroup 4 germline.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 50..56

FT /label= CDR1

FT Region 71..86

FT /label= CDR2

FT Region 119..126

FT /label= CDR3

PN W09312231-A.

PD 24-JUN-1993.

PF 13-DEC-1991; AU0583.

PR 13-DEC-1991; W0-AU0583.

PA (DOMC) DOW CHEM AUSTRALIA LTD.

PI Johnson KS, Mezes PS, Richard RA;

DR WF1; 93-214173/26.

DR N-PSDB; Q45597.

PT New composite antibody binding to tumour associated TAG-72

PT antigen - includes light chain variable region from human

PT subgroup 4 germline gene, useful, opt. as conjugate, for

PT diagnosis or treatment of cancer

PS Disclosure; Figure 4; 150pp; English.

Search completed: Tue Mar 18 10:05:00 1997
Job time : 51 secs.

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(TM)

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MPsrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

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Run on: Wed Mar 19 07:56:44 1997; MasPar time 215.27 Seconds
866.589 Million cell updates/sec
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Tabular output not generated.

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Title:
Description:
Perfect Score:
N.A. Sequence:
Comp:

```

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

EST-ST5

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
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51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98
99:EST99

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7
136:STS8 137:STS9 138:STS10 139:enEST1 140:enEST1
141:enEST2 142:enEST3 143:enEST4 144:enEST5 145:enEST6
146:enEST7 147:enEST8 148:enEST9 149:enEST10 150:enEST11
151:enEST12 152:enEST13 153:enEST14 154:enEST15
155:enEST16 156:enSTS 157:enEST1 158:enEST2 159:enEST3
160:enEST4 161:enEST5 162:enEST6 163:enEST7 164:enEST8
165:enEST9 166:enEST10 167:enEST11 168:enEST12
169:enEST13 170:enEST14 171:enEST15 172:enEST16
173:enEST1 174:enSTS2

Statistics: Mean 9.626; Variance 1.694; scale 5.682

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	65	15.4	228	14	H24604	y140b06.r1 Homo sapie	6.17e-88
2	58	13.7	390	14	H26580	y113f10.r1 Homo sapie	2.61e-73
3	50	11.8	364	108	T27579	EST100049 Homo sapien	5.13e-57
4	43	10.2	125	11	H15753	y127d09.r1 Homo sapie	3.05e-43
5	32	7.6	331	108	T27715	EST13381 Homo sapiens	6.06e-23
6	30	7.1	180	108	T27730	EST13989 Homo sapiens	1.68e-19
7	30	7.1	299	108	T27727	EST13874 Homo sapiens	1.68e-19
8	28	6.6	325	109	T27916	EST91759 Homo sapiens	3.68e-16
9	27	6.4	418	118	T61697	yb6ef08.r1 Homo sapie	1.56e-14
10	26	6.1	410	15	H30111	y59b04.r1 Homo sapie	6.17e-13
11	26	6.1	485	87	RS4774	yj75f04.r1 Homo sapie	6.17e-13
12	25	5.9	169	85	R48619	yj68a01.r1 Homo sapie	2.25e-11
13	24	5.7	346	154	HSU53085	Human clone 7/24 mRNA	7.58e-10
14	24	5.7	346	163	HS530851	Human clone 7/24 mRNA	7.58e-10
15	23	5.4	318	43	HSC2NR041	H. sapiens partial cD	2.33e-08
16	23	5.4	478	19	H43753	yp21g01.r1 Homo sapie	2.33e-08
17	22	5.2	234	109	T28164	EST30734 Homo sapiens	6.47e-07
18	22	5.2	297	108	T27868	EST18962 Homo sapiens	6.47e-07
19	22	5.2	330	103	SSC1D10	S.scrofa mRNA; expres	6.47e-07
20	22	5.2	428	119	T65452	yc73a07.r1 Homo sapie	6.47e-07
21	22	5.2	672	11	H15870	ym22b10.r1 Homo sapie	6.47e-07
c 22	21	5.0	287	108	T27609	EST101034 Homo sapien	1.62e-05
23	21	5.0	334	5	CELK087GYR	C.elegans cDNA clone	1.62e-05
24	21	5.0	340	6	CELK11722R	C.elegans cDNA clone	1.62e-05
c 25	21	5.0	360	5	CELK102HIF	C.elegans cDNA clone	1.62e-05
c 26	21	5.0	360	5	CELK087GYF	C.elegans cDNA clone	1.62e-05
27	21	5.0	490	56	N31150	yx52g08.r1 Homo sapie	1.62e-05
c 28	20	4.7	106	130	G03791	human SFS WI-91.	3.60e-04
29	20	4.7	245	110	T33317	EST57414 Homo sapiens	3.60e-04
30	20	4.7	377	43	HSC31A071	H. sapiens partial cD	3.60e-04
31	20	4.7	409	102	R1C51A950A	Rice cDNA, partial se	3.60e-04
32	20	4.7	419	142	N82396	TgESTy52g06.r1 Toxop	3.60e-04
33	20	4.7	419	29	T73816	yell1b01.r1 Homo sapie	3.60e-04
34	20	4.7	419	172	TC3964	TgESTzy52g06.r1 Toxop	3.60e-04
35	20	4.7	437	154	HSU53086	Human clone 8/24 mRNA	3.60e-04
36	20	4.7	437	163	HS530861	Human clone 8/24 mRNA	3.60e-04
37	20	4.7	484	21	H48330	yq77q02.r1 Homo sapie	3.60e-04
c 38	19	4.5	313	100	R97700	yq61b08.s1 Homo sapie	7.04e-03
39	19	4.5	360	6	CELK119C5F	C.elegans cDNA clone	7.04e-03
40	19	4.5	405	70	N77176	yy42b06.r1 Homo sapie	7.04e-03
41	19	4.5	405	159	HS716311	yy42b06.r1 Homo sapie	7.04e-03
42	19	4.5	405	141	N71776	yy42b06.r1 Homo sapie	7.04e-03

Db 9 atgtgttcagaccaggtcttcattctctgttctgtctgtggtctctgggacctacggg 68
 |||||
 Qy 1 ATGTGTTGCAGACCCAGGCTTCATTCTCTGTTGCTCTGGATCTCTGGTCCCTACGGG 60

RESULT 3 T27579 364 bp mRNA EST 06-SEP-1995
 LOCUS EST100049 Homo sapiens cDNA 5' end similar to immunoglobulin light
 DEFINITION chain, V region (Ht:3078).

ACCESSION T27579
 NID g609677

KEYWORDS EST.

SOURCE human primer=M13 Reverse library=Human Pancreas.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 364)

AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
 Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
 Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
 Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, J.F., P.S.,
 Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
 Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T.,
 Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
 Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
 Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A.,
 Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,
 Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
 Gruber, P., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
 Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
 Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
 Haseltine, W.A., Fields, C., Frazer, C.M. and Venter, J.C.
 Initial Assessment of Human Gene Diversity and Expression Patterns
 Based Upon 52 Million Basepairs of cDNA Sequence
 Unpublished (1995)

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
 JOURNAL Based Upon 52 Million Basepairs of cDNA Sequence
 COMMENT Unpublished (1995)

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 The Institute for Genomic Research
 932 Clopper Rd, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423

Email: tdbinfo@tdb.tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please contact the TIGR Database
 (tdbinfo@tdb.tigr.org).

FEATURES Location/Qualifiers
 source 1..364

/organism="Homo sapiens"
 /note="human"
 <1..>364

BASE COUNT 80 a 98 c 87 g 93 t 6 others
 ORIGIN
 Query Match 11.8%; Score 50; DB 108; Length 364;
 Best Local Similarity 98.0%; Pred. No. 5.13e-57;
 Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 cagaccaggtcttcattctctgttctgtctgtggtctctgggacctacggg 51
 |||||
 Qy 10 CAGACCCAGGCTTCATTCTCTGTTGCTCTGGATCTCTGGTCCCTACGGG 60

RESULT 4 H15753 125 bp mRNA EST 27-JUN-1995
 LOCUS Y127d09_r1 Homo sapiens cDNA clone 159473 5' similar to
 DEFINITION gb:123238_cds1 IG HEAVY CHAIN V-II REGION (HUMAN);.

ACCESSION H15753

NID g880573

KEYWORDS EST.

SOURCE human clone=159473 library=Soares breast 3NbHbEst vector=p7T73D
 (Pharmacia) with a modified polylinker host=DH10B (ampicillin
 resistant) primer=M13RP1 Reitel=Not I Reite2=Eco RI Adult human.
 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGCCGCCCTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptore (Pharmacia),
 digested with Not I and cloned into the Not I and Eco RI sites of a
 modified pT73 vector (Pharmacia). Library went through one round
 of normalization to a Cot = 20. Library constructed by Bento Soares
 and M.Fatima Bonaldo.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 125)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)

TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT

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 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@wustl.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality.

FEATURES Location/Qualifiers

source 1..125

/organism="Homo sapiens"

/clone="159473"

/note="human"

BASE COUNT 35 a 40 c 28 g 22 t
 ORIGIN

Query Match 10.2%; Score 43; DB 11; Length 125;
 Best Local Similarity 68.1%; Pred. No. 3.05e-43;
 Matches 81; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Db 2 cgcacagtcacatctctggagagaggtccaccatccacagcagcctccaaagtcgg 61
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Qy 238 CGTTACAAACCGCCTGAAATCCCGTCTCAGCATATCCAAAGACACCTCCCGTACACAG 297
 |||||

Db 62 gtagctctacaatgaccacacatggacctgtggacacagccacacatattactgtcagc 120
 |||||

QY 298 GTTGTTCGACCATGACTAACATGGACCGGTTGACACCGCTACCTACTACTGGCTCG 356

RESULT	5				
LOCUS		331 bp	mRNA	EST	06-SEP-1995
DEFINITION		EST13381 Homo sapiens cDNA 5' end similar to immunoglobulin gamma heavy chain V region (GB:M97921) (Ht:3789).			
ACCESSION		T27715			
NID		9609813			
KEYWORDS		EST.			
SOURCE		human primer=M13 Reverse library=Human Testis.			

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Frichman, J.L., Geodhagen, N.S.M.,
Glodek, A., Gnehm, L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S.,
Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Fertie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, C., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Meissner, P., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Haellinckx, W.A., Fields, C., Fraser, C.M. and Venter, J.J.

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For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tigr.org).

FEATURES

```

1.331
/organism="Homo sapiens"
/note="human"
<1..2331
mRNA

```

BASE COUNT	62 a	90 c	91 g	80 t	8 others
ORIGIN					

Query Match 7.6%; Score 32; DB 108; Length 331;
Best Local Similarity 60.9%; Pred. No. 6.06e-23;
Matches 84; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

D_b 89 ctgcaggatcgggccccaggactggtgaaqccttcggagacctgtccctcacttgcact 148

Qv 70 CTGCGTGAATCCGGTCCGGCACTAGTTAAACCGACCCAGACCTGACGTTAAACCTGCACC 129

Db 149 qtctctqqtatntccqctctacadtqacaatttttactggggctgggtccgccaggcccca 208

130 TTCTCCGGTTCTCCCTGTCGACCTCCGGTATGGGTGTTTCTCGATCCGTAGCCGCCG 189

Db 209 qaaaqqqctqgaqtqq 226

RESULT	6					
LOCUS		T27730	180 bp	mRNA	EST	06-SEP-1995
DEFINITION		EST13989 Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain, V region (GB:212364) (HT:3115).				

1274306
 NID
 9609828
 EST.
 human primer=M13 Reverse library=Human Testis.
 Homo sapiens
 ORGANISM
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Chonata; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE AUTHORS	TITLE
Adams,M.D., Lerlage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.L., Georhagen,N.S.M., Glodak,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S., Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R., Small,K.V., Springs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferlie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greener,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.	Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence
	Unpublished (1995)
	JOURNAL.

Contact: Venter, JC
The Institute for Genomic Research
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Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR database
(tdbinfo@db.tigr.org).

FEATURES	Location/Qualifiers
source	1..180

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/organism="Homo sapiens"
/note="human"
<1..>180
mRNA

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BASE COUNT	33 a	49 c	54 g	39 t	5 others
ORIGIN					

Query Match 7.1%; Score 30; DB 108; Length 180;
Best Local Similarity 60.9%; Pred. No. 1.68e-19;
Matches 78; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Db 6 ctgcaggagtcaggagctggaagcctcnaagaccctgcctccacctgcncct 65
||||| || ||||| || ||||| || || ||||| || || ||||| || || ||||| ||
Qy 70 CTGCGTGAATCCGCTCGCGCACTAGTTAAACGACGACCGCTGTAACCTGCACC 129
||||| || ||||| || ||||| || || ||||| || || ||||| || || ||||| ||
Db 66 gtctctgggtccatccagcagtggtggtactcctcctggagctggaatccggcagccacca 125
||||| || ||||| || || || || || ||||| || ||||| || || ||||| ||
Qy 130 TTCTCCGGTTTCTCCCTGTCTGACCTCCGGTATGCGTGTTCCTGATCCGTGAGCGCGC 189
||||| || ||||| || || || || || ||||| || ||||| || || ||||| ||
Db 126 gggaaaggg 133
|| || ||
Qy 190 GGTAAAGG 197

RESULT 7
LOCUS T77727 299 bp mRNA EST 06-SEP-1995
DEFINITION EST13874 Homo sapiens cDNA 5' end similar to immunoglobulin mu
(gamma) heavy chain, V(IV)DJC regions (HT:3057).
ACCESSION T77727
NID g609825
KEYWORDS EST.
SOURCE human primer=M13 Reverse library=Human Testis.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 299)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,
Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S.,
Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T.,
Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
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Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,
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Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,
Haseeltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
JOURNAL Unpublished (1995)
COMMENT

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Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@db.tigr.org).

FEATURES
source
Location/Qualifiers
1..299
/organism="Homo sapiens"
/note="human"
mRNA <1..>299
BASE COUNT 61 a 84 c 82 g 68 t 4 others
ORIGIN

Query Match 7.1%; Score 30; DB 108; Length 299;
Best Local Similarity 67.9%; Pred. No. 1.68e-19;
Matches 57; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
Db 79 caggtgcagctgcaggatcggggccaggagctggtgaagccttcggagacccctgtccctc 138
||||| ||||| || ||||| || ||||| || || ||||| || || ||||| || || ||||| ||
Qy 61 CAGGTACCTCGCTGAATCCGGTCCGGCACTAGTTAAACGACCGACCGCTGACGTTA 120
||||| ||||| || ||||| || || ||||| || || ||||| || || ||||| ||
Db 139 acctgcactgtctctcgtgggtctcc 162
||||| ||||| ||||| ||||| |||||
Qy 121 ACCTGCACCTCTCCGCTTCTCC 144

RESULT 8
LOCUS T29716 325 bp mRNA EST 06-SEP-1995
DEFINITION EST91759 Homo sapiens cDNA 5' end similar to immunoglobulin heavy
chain V,D,J regions (GB:M34029) (HT:3782).
ACCESSION T29716
NID g61814
KEYWORDS EST.
SOURCE human primer=M13 Reverse library=Human Synovial membrane.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 325)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,
Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S.,
Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T.,
Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,
Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,
Haseeltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
JOURNAL Unpublished (1995)
COMMENT

Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@db.tigr.org).

FEATURES
source
Location/Qualifiers
1..325
/organism="Homo sapiens"
/note="human"
mRNA <1..>325
BASE COUNT 72 a 92 c 81 g 80 t

ORIGIN

Query Match 6.1%; Score 26; DB 15; Length 410;
Best Local Similarity 59.8%; Pred. No. 6.17e-13;
Matches 79; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Db 70 gactcgccgcgaactggtgaagccttcgagaccctgtccctcaactgcagtctctct 129

||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 76 GAATCGCGTCGGCAGCTAGTTAAACCGACCGACCTGACGTTAACTGCACCTTCTCC 135

||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 130 aatggttcacagcaactccacttactactggtcgctggatccgcagctcccccggaag 189

||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 136 GCTTTCCTCCCTGCACCTCCGGATGGGTGTTCTCGATCCGTACGCCCGGGTAAA 195

||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 190 ggcctggaatgg 201

||||| ||| ||| |||

Qy 196 GGTCTAGAAATGG 207

RESULT 11

LOCUS R54774 485 bp mRNA EST 22-MAY-1995
DEFINITION YJ75504.r1 Homo sapiens cDNA clone 154591 5' similar to gb:X17115
IG MU CHAIN C REGION (HUMAN);.

ACCESSION R54774

NID g819296

KEYWORDS EST.

SOURCE human clone=154591 library=Soares breast 2NbHBst vector=pt7T3D

(Pharmacia) with a modified polylinker host=DH10B (ampicillin

resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Adult female.

1st strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCGAAGTGGAGCGCGCCGCTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),

digested with Not I and cloned into the Not I and Eco RI sites of a

modified pT7T3 vector (Pharmacia). Library went through one round

of normalization to a Cot = 230. Library constructed by Bento

Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 485)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 291

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

1..485

/organism="Homo sapiens"

/clone="154591"

/note="human"

BASE COUNT 101 a 137 c 132 g 112 t 3 others
ORIGIN

Query Match 6.1%; Score 26; DB 87; Length 485;
Best Local Similarity 76.0%; Pred. No. 6.17e-13;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 143 actgtgacttcgattctggcgctggcaccctgtgcactgtctctctca 192

||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 374 ACTGGTACTTCGACGCTTTGGGGTGTGGTACCCAGTACCGTGAGCTCA 423

||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12

LOCUS R48619 169 bp mRNA EST 18-MAY-1995
DEFINITION YJ68a01.r1 Homo sapiens cDNA clone 153864 5' similar to gb:U23556
IG HEAVY CHAIN V-II REGION (HUMAN);.

ACCESSION R48619

NID g810645

KEYWORDS EST.

SOURCE human clone=153864 library=Soares breast 2NbHBst vector=pt7T3D

(Pharmacia) with a modified polylinker host=DH10B (ampicillin

resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Adult female.

1st strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCGAAGTGGAGCGCGCCGCTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),

digested with Not I and cloned into the Not I and Eco RI sites of a

modified pT7T3 vector (Pharmacia). Library went through one round

of normalization to a Cot = 230. Library constructed by Bento

Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 169)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality.

FEATURES

source

1..169

/organism="Homo sapiens"

/clone="153864"

/note="human"

BASE COUNT 26 a 56 c 47 g 40 t

Mar 19 07:59

US-08-612-929-11.rst

17

Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabakchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
and its expression

C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

JOURNAL
MEDLINE
95277534

Cloning method: total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA
vector;

Sequencing method: single read, full automatic;

Primer: M13_reverse

cDNA sequence colinear to mRNA

Stretch removed: nothing

Normalization method: Bento Soares, P.N.A.S. 91:9228-9232 (1994);

Genexpress_library_id: C;

Genexpress_sequence_id: ylc-2nh04.

FEATURES

source

1..318
/organism="Homo sapiens"
/isolate="muscular atrophy patient"
/clone_lib="normalized infant brain cDNA from B.Soures,
Psychiatry Dept. Columbia University USA"
/sex="female"

/issue_type="total brain"
/dev_stage="3 months old"

BASE COUNT 58 a 104 c 84 g 68 t 4 others

ORIGIN

Query Match 5.4%; Score 23; DB 43; Length 318;

Best Local Similarity 74.5%; Pred.No. 2.33e-08;

Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 54 ggtacttcgatctctggggccgtggcaccctggcactgtctctca 100

||||| | | | | | | | | | | | | | | | | | | | |

Qy 377 GGTACTTCGACGTTGGCGTCGTGGTACCCACGTTACCGTGAGCTCA 423

Search completed: Wed Mar 19 08:01:27 1997

Job time : 283 secs.

WATERMAN

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 07:55:10 1997; MaePar time 41.64 Seconds
Tabular output not generated. 885.965 Million cell updates/sec

Title: >US-08-612-929-11

Description: (1-423) from US08612929.seq

Perfect Score: 423

N.A. Sequence: 1 ATGGTGTTCAGACCCAGGT.....CCCCAGTACGGTGAGCTCA 423

Comp: TACCACACGCTGGGTGCTCA.....GGGCTCAATGGCAGCTCGACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneeq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 8.172; Variance 4.663; scale 1.753

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	421	99.5	423	14	Q83493	Humanized antibody 3B 8.96e-288
2	259	61.2	6285	22	T34109	Anti-IL-5 humanised a 2.88e-167
3	215	50.8	423	14	Q83492	Chimeric antibody 3B9 7.54e-135
4	199	47.0	357	22	T34093	Humanised 2B6 antibody 4.08e-123
5	153	36.2	483	14	Q83491	Mouse MAB 3B9 heavy c 1.29e-89
6	127	30.0	613	13	Q78943	Human immunoglobulin 6.72e-71
7	124	29.3	546	13	Q78964	Human immunoglobulin 9.40e-69
8	121	28.6	423	7	Q45597	Sequence encoding the 1.30e-66

9	120	28.4	120	14	Q83499	Heavy chain variable	6.75e-66
10	117	27.7	117	14	Q83498	Heavy chain variable	9.26e-64
11	115	27.2	360	19	T09300	Murine anti-Protein C	2.45e-62
12	115	27.2	417	19	T09299	Murine anti-Protein C	2.45e-62
13	114	27.0	418	13	Q75917	Anti-human IL-6 chimera	1.26e-61
14	114	27.0	418	13	Q75916	Anti-human IL-6 chimera	1.26e-61
15	112	26.5	738	12	Q70612	IL-6 binding inhibitor	3.32e-60
16	111	26.2	366	11	Q68709	Humanised MAB H-chain	1.70e-59
17	107	25.3	429	11	Q64166	Sequence of mouse VH	1.16e-56
18	107	25.3	630	13	Q78948	Human immunoglobulin	1.16e-56
19	103	24.3	120	14	Q83500	Heavy chain variable	7.77e-54
20	103	24.3	418	13	Q75889	Mouse heavy chain var	7.77e-54
21	96	22.7	812	6	Q37056	Rat immunoglobulin H	6.51e-49
22	94	22.2	812	11	Q45437	RMSO cell-derived Ig	1.64e-47
23	68	16.1	84	14	Q83518	Signal sequence 3' pr	1.40e-29
24	63	14.9	83	14	Q83517	Signal sequence 5' pr	3.28e-26
25	60	14.2	60	22	T34108	Signal peptide coding	3.31e-24
26	60	14.2	60	14	Q83494	Human antibody signal	3.31e-24
27	60	14.2	400	1	N80499	Encodes V region of L	3.31e-24
28	60	14.2	407	4	Q26047	V-region of L-chain o	3.31e-24
29	60	14.2	5703	22	T34110	Anti-IL-5 humanised a	3.31e-24
30	58	13.7	1047	2	Q10572	Human Natriuretic Pep	7.05e-23
31	57	13.5	57	10	Q44851	Signal sequence for p	3.23e-22
32	54	12.8	3314	10	Q58896	Humanised anti-CEA sF	3.05e-20
33	52	12.3	619	1	N80498	Encodes V region of L	6.18e-19
34	52	12.3	1088	10	Q56735	Sequence of HumAVL ge	6.18e-19
35	52	12.3	1097	7	Q45602	Sequence of the Humd	6.18e-19
36	52	12.3	1373	1	N80941	Encodes Vchi region o	6.18e-19
37	49	11.6	351	1	Q06214	VH domain of antibody	5.43e-17
38	49	11.6	354	4	Q26757	431/26 VH hum.	5.43e-17
39	49	11.6	357	6	Q38670	MAB GAH variable regi	5.43e-17
40	49	11.6	799	13	Q78977	Human immunoglobulin	5.43e-17
41	49	11.6	1288	17	T04181	Plasmid pFv-PF fragme	5.43e-17
42	48	11.3	1047	2	Q10572	Human Natriuretic Pep	2.39e-16
43	47	11.1	923	17	T04171	Plasmid pSW1VHD1.3VKD	1.05e-15
44	47	11.1	1615	12	Q70667	ScFv-DNaseI fusion DN	1.05e-15
45	47	11.1	1952	15	Q91987	Fv restriction fragme	1.05e-15

ALIGNMENTS

RESULT 1
ID Q83493 standard; cDNA; 423 BP.
AC Q83493;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 heavy chain.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW MAb; interleukin-4; IL-4; allergy; da.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..423
FT /*tag= a
FT sig_peptide 1..57
FT /*tag= b
FT mat_peptide 58..423
FT /*tag= c
PN WO9507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;

DR WP1; 95-123387/16.
DR P-PSDB; R70192.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.4; 97pp; English.
CC A humanized antibody heavy chain variable region and signal
CC sequence is given in R70192. The signal sequence is also
CC provided in R70193. The CDR sequences of the construct are
CC identical to the native CDRs of mouse anti-human IL-4 mAb
CC 389 (R70198-200).
SQ Sequence 423 BP; 84 A; 131 C; 102 G; 106 T;

Query Match 99.5%; Score 421; DB 14; Length 423;
Best Local Similarity 99.8%; Pred. No. 8,96e-288;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 atgggtgtgcagaccaggtcttcattctctgttctgtggtatctctggctacggg 60
|||||
Qy 1 ATGGGTGTGCAGACCCAGGCTTCATTCTCTGTGCTGTGATCTCTGGTGCTACGGG 60
|||||
Db 61 caggttacctcgtgaatccggtccggcactagttaaaccgaccagaccctgacgtta 120
|||||
Qy 61 CAGGTTACCTCGCTGGAATCCGGTCCGGCACTAGTTAAACCGACCCAGACCTTGACGTTA 120
|||||

Db 121 acctgcacctctccggtttctccctgtgcacctccggtatgggtgttctcgtacgt 180
|||||
Qy 121 ACCTGCACCTCTCCGGTTTCTCCCTGTGCACTCCGGTATGGGTGTTCTCGATCCGT 180
|||||

Db 181 cagccgcgggttaagaggtctagaatggctgtcactatctactgggacgacgacaaact 240
|||||
Qy 181 CAGCGCGCGGTTAAGAGGTCTAGAAATGGCTGGCTGCATCTACTGGGACGACGAAAGCT 240
|||||

Db 241 tacaaccgagcctgaatccgctgaccatatacgaagacacacctccgtaccaggtt 300
|||||
Qy 241 TACAACCGGAGCCTGAATCCCGCTCTGACGATATCCAAAGACACCTCCCGTACCAGGTT 300
|||||

Db 301 gttctgacacatacgaatgacccggttgacaccgctactactactcgtcgcgcagc 360
|||||
Qy 301 GTTCTGACCATGACTTAACATGGACCGGTTTGACACCGCTACCTACTACTGCGCTCAGCG 360
|||||

Db 361 gaaaccgttttctactcgtactcgcagcttgggtcgtggtaccaccagttaccgtgagc 420
|||||
Qy 361 GAACCGTTTTTCTACTGTTACTTCGACGTTTGGGTCGTGTTACCCAGTTACCGTGAGC 420
|||||

Db 421 tca 423
|||
Qy 421 TCA 423
|||

RESULT 2
AC T34109 standard; DNA; 6285 BP.

DE Anti-IL-5 humanised antibody heavy chain plasmid pCDIL5HZH1.0.
KW Antibody engineering; humanised antibody; chimeric antibody; Fab;
KW Interleukin-5; IL-5; eosinophil; asthma; allergic rhinitis;
KW atopic dermatitis; therapy; diagnosis; heavy chain; VH;
KW monoclonal antibody; mAb; plasmid pCDIL5HZH1.0; ds; cyclic.
OS Synthetic.
PN WO9621000-A2.
PD 11-JUL-1996.
PF 22-DEC-1995; UI7082.
PR 23-DEC-1994; US-363131.

PR 06-JUN-1995; US-470110.
PR 06-JUN-1995; US-467420.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PIC.
PI Ames RS, Appelbaum ER, Chaiken IM, Cook RM, Gross MS;
PI Holmes SD, McMillan LJ, Theisen TW;
PI WP1; 96-333976/33.
PT New monoclonal antibody to human interleukin-5 - used to produce
PT products for the treatment and diagnosis of conditions associated
PT with excess eosinophil prodn., e.g asthma etc.
PS Example 4; Page 70-75; 120pp; English.
CC pCDIL5HZH1.0 (T34109) is a pUC19-based plasmid that incorporates
CC a DNA sequence (see also T34093) coding for a humanised heavy chain
CC (R9488) of murine anti-human interleukin-5 (IL-5) monoclonal
CC antibody 2B6 as well as a beta-lactamase gene, an SV40 replication
CC origin, a cytomegalovirus promoter, a signal sequence (see also
CC T34108), a polyA signal from bovine growth hormone (BGH), a
CC beta-globin promoter, a dihydrofolate-reductase gene and another
CC BGH polyA signal. pCDIL5HZH1.0 and pCNIL5HZL1.0 (T34110) coding
CC for the humanised light chain were co-transfected into COS cells
CC for prodn. of humanised 2B6 antibody. This can be used for the
CC diagnosis and treatment of IL-5-mediated conditions, e.g. asthma,
CC allergic rhinitis and atopic dermatitis.
SQ Sequence 6285 BP; 1544 A; 1637 C; 1611 G; 1493 T;

Query Match 61.2%; Score 259; DB 22; Length 6285;
Best Local Similarity 84.2%; Pred. No. 2.88e-167;
Matches 356; Conservative 0; Mismatches 61; Indels 6; Gaps 2;

Db 1010 atgggtgtgcagaccaggtcttcattctctgttctgtggtatctctgtggtacggg 1069
|||||
Qy 1 ATGGGTGTGCAGACCCAGGCTTCTCTCTCTGTGCTCTGATCTCTGGTGCTACGGG 60
|||||

Db 1070 caggttacctcgtgaatccggtccggcactagttaaaccgaccagaccctgacgtta 1129
|||||
Qy 61 CAGGTTACCTCGCTGGAATCCGGTCCGGCACTAGTTAAACCGACCCAGACCTTGACGTTA 120
|||||

Db 1130 acctgcacgtctccggtttctccctgacgagcta---ta---gtgtacactgggtccgt 1183
|||||
Qy 121 ACCTGCACCTTCTCCGGTTTCTCCCTGTGCACTCCGGTATGGGTGTTCTCGATCCGT 180
|||||

Db 1184 cagccgcgggttaaggtctagaatggctgggtgtaatatgggctagtgaggacacagat 1243
|||||
Qy 181 CAGCGCGCGGTTAAGGCTTAGAATGGCTGGCTGCATCTACTGGGACGACGACAAAGCT 240
|||||

Db 1244 tataattcgggtctcatgtccggtctgtcgatatacgaagacacctccgtaaccaggtt 1303
|||||
Qy 241 TACAACCGGAGCCTGAAATCCCGCTTGACGATATCCAAAGACACACCTCCCGTACCAGGTT 300
|||||

Db 1304 gttctgaccatgactaacatggaccggttgacaccgctactactactcgtcgtcgagat 1363
|||||
Qy 301 GTTCTGACCATGACTTAACATGGACCCGGTTTGACACCGGTACTACTTACTGGGCTCAGCGC 360
|||||

Db 1364 cccctcttcttactcaaggcttgactactcgtgggtcgtgtaccacagttaccgtgagc 1423
|||||
Qy 361 GAACCGGTTTTCTACTGGTACTTTCGACGTTTGGGTCGTGTTACCCCACTTACCCGTGAGC 420
|||||

Db 1424 tca 1426
|||
Qy 421 TCA 423
|||

RESULT 3
ID Q83492 standard; cDNA; 423 BP.

QY	361	GAACACGGTTTCTACTGCTACTTCGACGTTTGGGGTGGTGGTACCCCGTAGCC	420
Db	421	tca 423	
QY	421	TCA 423	
RESULT	4		
ID	T34093	standard; DNA; 357 BP.	
AC	T34093;		
DE	12-OCT-1996	(first entry)	
DT	Humanised 2B6 antibody heavy chain variable region DNA.		
KW	Antibody engineering; humanised antibody; chimeric antibody; tab;		
KW	interleukin-5; IL-5; eosinophil; asthma; allergic rhinitis;		
KW	atopic dermatitis; therapy; diagnosis; heavy chain; VH;		
KW	monoclonal antibody; Mab; ss.		
OS	Synthetic.		
FH	Key	Location/Qualifiers	
FT	CDS	70..72	
FT	/*tag= a		
FT	/transl_except= (70..72, aa:Phe)		
FT	/note= "bases 70-72 (GTC) are given in TTC		
FT	encoding Phe in Fig 8"		
FT	CDS	109..111	
FT	/*tag= b		
FT	/transl_except= (109..111, aa:Ile)		
FT	/note= "bases 109-111 (GTC) are given as ATC		
FT	encoding Ile in Fig 8"		
PN	W09621000-A2.		
PD	11-JUL-1996.		
PR	22-DEC-1995; U17082.		
PR	23-DEC-1994; US-363131.		
PR	06-JUN-1995; US-470110.		

(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
Ames RS, Appelbaum ER, Chaiken IM, Cook RM, Gross MS;
Holmes SD, McMillan LJ, Theisen TW;
WPI; 96-333976/33.
p-P5DB; R98488.

New monoclonal antibody to human interleukin-5 - used to produce
PT products for the treatment and diagnosis of conditions associated
PT with excess eosinophil produ., e.g asthma etc.

PS Example 4; Page 53; 120pp; English.

CC A DNA sequence (T34093) codes for the heavy chain variable region
CC (R98488) of humanised antibody ZB6, comprising complementarity
CC determining regions (see also R98480-82) derived from murine
CC monoclonal antibody ZB6 VH (see also R98478) and framework regions
CC from human myeloma immunoglobulin COR. Murine ZB6 is specific for
CC human interleukin-5 (IL-5). The construct, in vector pCDIL5HZHC1.0
CC (T34109), was used to produce humanised ZB6 VH in COS cells.
CC Humanised ZB6 VL was also produced (see also T34094). Humanised
CC ZB6 can be used for the diagnosis and treatment of IL-5-mediated
CC conditions, e.g. asthma, allergic rhinitis and atopic dermatitis.

SQ Sequence 357 BP; 74 A; 108 C; 87 G; 88 T;

Query Match 47.0%; Score 199; DB 22; Length 357;
Best Local Similarity 81.5%; Pred. No. 4.08e-123;
Matches 296; Conservative 0; Mismatches 61; Indels 6; Gaps 2;

Ddb 1 caggttaccctgcgtgaatccggtccggcactagttaaacgccagacctgcagtta 60
|||||
61 CAGGTTCACCTGCGTGAAATCCGGTCCGGCACTAGTTAACCAGCACCCCTGCAGTTA 120

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Query Match      47.0%; Score 199; DB 22; Length 357;
Best Local Similarity 81.5%; Pred. No. 4, 08e-123;
Matches 296; Conservative 0; Mismatches 61; Indels 6; Gaps 2;

Db 1 caggttacctcgctgaatccggtccggcactagttaaaccgacccagacctgacgtta 60
Qy 61 CAGGTTACCTTCGCTGAATCCGGTCCGGCACTAGTTAAACCCAGCCAGCCCTGCAGTTA 120

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Mar 19:07:54

US-08-612-929-11.rmg

7

Db 61 acctgacacgtctccgtttctccctgacagcta---ta---gtgtacacgtgggtcgt 114
|||||
Qy 121 ACCTGACACCTTCTCCGCTTCTCCCTCTCGACCTCCGCTATGGGTGTTCTCGATCCGT 180
Db 115 cagccgcgggttaaggtcctaagatggctgggtgtaataatgggtcagtggagcacagat 174
|||||
Qy 181 CAGCCGCGGGTAAAGGCTAGAAATGGCTGGCTCACATCTACTGGGACGACGACAAAGCT 240
Db 175 tataattcggctctcatgctccgctgtcgtatgataccaaagacacacccctccgtacacaggtt 234
|||||
Qy 241 TACAAACCCGAGCGCTGAAATCCCGCTCTGACGATATCCAAAGACACCTCCGCTAACCAAGTT 300
Db 235 gtctgaccatgactaacatgacccggttgacaccgctactactactactcgtcgtcagat 294
|||||
Qy 301 GTTCTGACCATGACTAACATGGACCCGGTTGACACCCGCTACCTACTACTGCGGTGACGCC 360
Db 295 ccccttctctactacggttgactactgggtcgtggtggtaccagttaccgtgagc 354
|||||
Qy 361 GAAACCGTTTCTACTGCTACTTCCACGTTTGGGGTGGTGGTACCCCGAGTTACCGGTGAGC 420
Db 355 tea 357
|||
Qy 421 TCA 423

RESULT 5

ID Q83491 standard; cDNA; 483 BP.
AC Q83491;
DT 20-SEP-1995 (first entry)
DE Mouse MAb 3B9 heavy chain.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 64..483
FT /tag= a
FT sig_peptide 64..120
FT /tag= b
FT mat_peptide 121..483
FT /tag= c
PN M09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI: 95-123387/16.
DR P-PSDB; R70190.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.2; 97pp; English.
CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC chains were cloned into pCEM7f+ and transformed into E. coli
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for
CC antibody engineering.
SQ Sequence 483 BP; 108 A; 130 C; 124 G; 121 T;

Query Match 36.2%; Score 153; DB 14; Length 483;
Best Local Similarity 71.1%; Pred. No. 1.29e-89;

Mar 19:07:54

US-08-612-929-11.rmg

8

Matches 258; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
Db 121 caggttactctgaaagagctggccctggggatattgagccctccagacacctcagtcgt 180
|||||
Qy 61 CAGGTTACCGTCCGCTGAATCCGCTCGGCTAGTAAACCGACCCGACCTGACGTTA 120
Db 181 acttggtttctctcgtggttttcaactgagcactctgtgtatgggtgagctggattcgt 240
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Qy 121 ACCTGACACCTTCTCCGCTTCTCCCTCTCGACCTCCGCTATGGGTGTTCTCGATCCGT 180
Db 241 cagccttcaggaaagggtctggagtggctgggcacacatttactgggatgatgacaagcgc 300
|||||
Qy 181 CAGCGCGCGGGTAAAGGCTTACAATGGCTGGCTCACATCTACTGGGACGACGACAAAGCT 240
Db 301 tataaccatccctgaagagcgggtctcaaatctccaagataacctccagacaccagta 360
|||||
Qy 241 TACAAACCCGAGCGCTGAAATCCCGCTCTGACGATATCCAAAGACACCTCCGCTAACCAAGTT 300
Db 361 ttctcgaagatcacagctgtggacacatgacatactgacacatactactgtgctgaaga 420
|||||
Qy 301 GTTCTGACCATGACTAACATGGACCCGGTTGACACCGCTACCTACTACTGCTGCTGACGC 360
Db 421 gagactgttctactggtactcgtcgtggtggcgaggagaccaggtcacgtctcc 480
|||||
Qy 361 GAAACCGTTTCTACTGCTACTTCCACGTTTGGGGTGGTGGTACCCCGAGTTACCGGTGAGC 420
Db 481 tca 483
|||
Qy 421 TCA 423

RESULT 6

ID Q78943 standard; DNA; 613 BP.
AC Q78943;
DT 07-AUG-1995 (first entry)
DE Human immunoglobulin variable heavy chain #5.
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 71..513
FT /tag= a
FT /product= human immunoglobulin variable heavy chain
FT intron 117..202
FT /tag= b
FT misc_signal 514..516
FT /tag= c
FT /note= "miscellaneous signal, does not conform to
FT terminator or splice site sequence"
PN M09426895-A.
PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PR 10-MAY-1993; M0-J00603.
PA (NIBS) JAPAN TOBACCO INC.
PA Honjo T, Matsuda F;
DR WPI: 95-006791/01.
DR P-PSDB; R66299.
PT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts
PT Disclosure; Page 36-37; 130pp; Japanese.
CC A series of genes (Q78939-79002) encoding human immunoglobulin variable
CC heavy chains. The genes were isolated and cloned from a series of cosmid
CC constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131, by PCR
CC amplification using primers Q78917-38. The genes are subdivided into 5

CC families of Vh genes. The fragments cover a region of 800 kb. The DNA
CC fragments were isolated from high molecular weight DNA from human
CC placenta. The DNA was partially digested with TaqI restriction enzyme.
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
CC were collected. The fragments were ligated with ClaI-digested cosmid
CC vector pJB81. The ligation products were in vitro packed and infected
CC into E.coli 490A. The fragments were then subcloned by colony
CC hybridisation. The Vh genes and the DNA fragments encoding them are
CC useful in producing human immunoglobulin in mammalian hosts.
SQ Sequence 613 BP; 139 A; 194 C; 139 G; 141 T;

Query Match 30.0%; Score 127; DB 13; Length 613;
Best Local Similarity 71.7%; Pred. No. 6.72e-71;
Matches 210; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

214 cagatcacctgaaggagctggtcctacgctggtgaaccacacagaccctcacgctg 273
||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 CAGGTTACCTCGGTGAATCCGGTCCGGCACTAGTTAAACCGACCACGCCCTCAGCGTTA 120

Ddb 274 acctgeacttctcgggttcacacgacctagtgaggtaggggtgtgggctggatccgt 333

334 cagccccaggaaagccctggagtgccttgcactcattattggaatgatgataagcgc 393

181 CAGCCGCCGGGTAAAGGCTCTAGAATGGCTGGCTCAGATCTACTGGGACGACGACAAACGT 240

241 TACAACCGAGCCTGAAATCCCGTCTGACGATATCCAAAGACACCTCCCGTAACCGTT 300

454 gtcctacaatgaccaacatgacccctggacacagccacatatattactgtgc 506

ID Q/8964 standard; DNA; 546 BP.
AC Q78964;
DT 03-AUG-1995 (first entry)

Human immunoglobulin Vh gene #26.
Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
cosmid; placenta; vector: pJ881; E. coli; mammalian; de

US	Homo sapiens.	Key	Location/Qualifiers
FT		CDS	21..463

FI	/tag= a
FT	/product= human immunoglobulin variable heavy chain
FT	intron 67..152

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FT /tag= D 204.206
FT misc_signal
FT /*tag= c
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FT terminator or splice site sequence*

PF 10-MAY-1993; J00603.
PR 10-MAY-1993; W0-J00603.

PI Honjo T, Matsuda F;
DR WPI; 95-006791/01.

PT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts

PS Claim 35; Page 64-65; 130pp; Japanese.

CC A series of genes (Q78939-79002) encoding human immunoglobulin variable

CC heavy chains. The genes were isolated and cloned from a series of cosmid

CC constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131, by PCR

CC amplification using primers Q78917-38. The genes are subdivided into 5

CC families of Vh genes. The fragments cover a region of 800 kb. The DNA

CC fragments were isolated from high molecular weight DNA from human

CC placenta. The DNA was partially digested with *TaqI* restriction enzyme.

CC The fragments were separated by gel electrophoresis and 35-45 kb fractions

CC were collected. The fragments were ligated with *Clai*-digested cosmid

CC vector pJ881. The ligation products were *in vitro* packed and infected

CC into E.coli 490A. The fragments were then subcloned by colony

CC hybridisation. The Vh genes and the DNA fragments encoding them are

CC useful in producing human immunoglobulin in mammalian hosts.

SO Sequence 546 BP: 124 A: 17C: 124 G: 127 T:

Query Match	29.3%	Score 124;	DB 13;	Length 546;
Best Local Similarity	70.9%	Pred. No. 9.40e-69;		
Matches 210.	Conservative	0.	Mismatches 86;	Indels 0;
			Gaps 0;	

Db 164 caggtcaccttgaaggagctctggtccttgctggtgaaacccacagagaccctcacgctg 223

61 CAGGTAACCCGCGTGAATCCGGTCCGGGACIAGTAAACCGGACCCCGACCCCTGACGCTTAT 120

D6 224 acctgcacgtctctgggttctcactcagcaatgctagaatgggtgtgagctggatcctt 283

Qy 121 ACCTGCACCTCTCCGGTTCTCCCTGTCCGACCTCCGGTATGGGTGTTTCTCGATCCGT 180

181 CACCCGCCGGTAAAGGCTCAAGTCTACAATGGCTGGCTCACATCTACTGGGACGACGACAAACGT 240

Db 344 t a c a g c a c a t c t c t a a g a g c a g g c t c a c c a t c t c c a a g g a c a c c t c a a a a g c a g g t g 403

Db 404 gtccttaccatgaccaacatggaccctgtggacacagccacatatattactgtgcacg 459

Qy 301 GTTCTGACCATGACTAACATGGACCCGGTTGACACCGCTACTACTACTGCGCTGG 356

RESULT 8
ID Q45597 standard; DNA; 423 BP.
QC Q45597.

DT 04-DEC-1993 (first entry)
DE Sequence encoding the VH of antibody B17X2
WV Variable heavy chain; chain; human subgroup 4 germ-line

OS	Homo sapiens.
FH	Key
FT	Location/Qualifiers 7 423

FT / *tag= a
PN W09312231-A,
PD 24-JUN-1993.

PR 13-DEC-1991; WO-AU583.
PA (DOWC) DOW CHEM AUSTRALIA LTD. PA

DR WPI; 93-214173/26.
DR P-PSDB; R38315.

PT antigen - includes light chain variable region from human subgroup 4 germline gene, useful, opt. as conjugate, for

PS Disclosure; Figure 4; 150pp; English.

[illegible]

RESULT	14
ID	Q75916 standard; DNA; 418 BP.
AC	Q75916;
DT	23-AUG-1995 (first entry)
DE	Anti-human IL-6 chimaeric Ab H chain V region in HEI-RVH-SK2a.
DD	Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;
EW	interleukin; antibody; hydridoma; CDR; framework; constant region;
KW	heavy chain; disorder; antigenicity; ds.

CC (R77201-3) inserted into several framework regions (FR) (R77204-7) and
CC (ii) a human light chain constant region and (b) a heavy chain with (i)
CC variable region containing 3 CDR (R77212-4) inserted into an FR
CC (R77215-8) and (ii) a human light chain constant region. The FR of the
CC light chain may be mouse derived (Q75888) or from the human antibody RE1
CC The heavy chain FR may also be mouse derived (Q75889) or from the human
CC antibody DAM. The antibodies can be used in the treatment of IL-6
CC related disorders. The antibodies are useful as they have low
CC antigenicity due to the use of human derived sequences and low
CC antigenicity mouse derived sequences.
CC sequence 418 BP; 94 A; 116 C; 110 G; 98 T;
SQ

CC light chain may be mouse derived (Q75888) or from the human antibody RE
CC antibody DMW. The antibodies can be used in the treatment of IL-6
CC The heavy chain FR may also be mouse derived (Q75889) or from the human
CC antibody DMW. The antibodies are useful as they have low
CC related disorders. The antibodies are useful as they have low
CC antigenicity due to the use of human derived sequences and low
CC antigenicity mouse derived sequences.
CC Sequence 418 BP; 94 A; 116 C; 110 G; 98 T;
SQ

Db 47 gtgctcactccccagtgactctgagggaagtctggacctgccttgtgagactacaga 106
|||||
Qy 50 GTGCTACGGGAGCTTACCCTGGCTCAATCCGGTCGGGCACTACTTAACCGCACCCGA 109

WATERMAN

(TM)

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 07:48:09 1997; MaePar time 286.77 Seconds
1214.896 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-11

Description: (1-423) from US08612929.seq

Perfect Score: 423

N.A. Sequence: 1 ATGGCTTTCAGACCCAGGT.....CCCCAGTTACGTCAGTCAC 423

Comp: TACCACAACTGCTGGTCCA.....GGGTCAATGGCAGCTGACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

embl-new5
1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI
10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

Database:

genbank94
16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7
23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5
30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2
37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLN1 43:PLN2
44:PLN3 45:PLN4 46:PLN5 47:PLN6 48:PLN7 49:PLN8 50:PRI1
51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8
58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1
64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8
71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4
78:VRL5 79:VRL6 80:VRL7 81:VRL8

Database:

genbank-new5
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89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL

Database:

u-embl46_94
96:part1

Statistics: Mean 10.141; Variance 4.217; scale 2.405

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	139	32.9	389	59	HUMIGHCXH	Human fetal Ig heavy	5.05e-104
2	135	31.9	363	62	U00575	Human immunoglobulin	3.84e-100
3	132	31.2	460	59	HUMIGHV2H	Human Ig germline hea	3.09e-97
4	131	31.0	417	56	HSVHRA10	H.sapiens mRNA for im	2.87e-96
5	131	31.0	461	59	HUMIGHV2J	Human Ig germline hea	2.87e-96
6	130	30.7	297	54	HSIGVHLI1	H.sapiens variable re	2.66e-95
7	130	30.7	432	56	HSVHIF3	H.sapiens mRNA for im	2.66e-95
8	130	30.7	445	59	HUMIGHV2F	Human Ig germline hea	2.66e-95
9	129	30.5	363	56	HSVHP46	H.sapiens mRNA P46 fo	2.46e-94
10	129	30.5	366	62	S73953	Ig VH-immunoglobulin	2.46e-94
11	129	30.5	460	59	HUMIGHV2K	Human Ig germline hea	2.46e-94
12	128	30.3	288	54	HSIGDP27	H.sapiens germline Ig	2.27e-93
13	128	30.3	406	59	HUMIGAMKB	Human Ig rearranged a	2.27e-93
14	128	30.3	433	54	HSIGVHC2B	H.sapiens germline im	2.27e-93
15	128	30.3	461	59	HUMIGHV2D	Human Ig germline hea	2.27e-93
16	127	30.0	296	62	S69331	IgVH2/JH6-anti-pyruva	2.09e-92
17	127	30.0	366	62	U00552	Human clone Anu43-3 Ig	2.09e-92
18	127	30.0	369	62	U00555	Human clone Anu43-2 I	2.09e-92
19	127	30.0	415	54	HSIGHC2B	H.sapiens Ig rearrang	2.09e-92
20	127	30.0	442	59	HUMIGHV2E	Human Ig germline hea	2.09e-92
21	127	30.0	448	59	HUMIGHV2I	Human Ig germline hea	2.09e-92
22	127	30.0	460	59	HUMIGHV2C	Human Ig germline hea	2.09e-92
23	127	30.0	580	59	HUMIGHV2X	Human immunoglobulin	2.09e-92
24	127	30.0	613	56	HSVII5	H.sapiens VII-5 gene	2.09e-92
25	126	29.8	288	54	HSIGDP28	H.sapiens germline Ig	1.93e-91
26	126	29.8	433	54	HSIGVHC2A	H.sapiens germline im	1.93e-91
27	126	29.8	433	54	HSIGVH2	H.sapiens germline im	1.93e-91
28	126	29.8	433	54	HSIGVHC2E	H.sapiens germline im	1.93e-91
29	126	29.8	433	54	HSIGVHC2	H.sapiens germline im	1.93e-91
30	126	29.8	433	54	HSIGVH1A	H.sapiens germline im	1.93e-91
31	126	29.8	438	56	HSWAD3VR	H.sapiens heavy chain	1.93e-91
32	125	29.6	356	55	HSU00507	Human immunoglobulin	1.77e-90
33	124	29.3	366	64	MMIGMSMJ	Mouse mRNA for variab	1.63e-89
34	124	29.3	433	54	HSIGVHC1	H.sapiens germline im	1.63e-89
35	124	29.3	433	54	HSIGVH1B	H.sapiens germline im	1.63e-89
36	124	29.3	433	54	HSIGVHC2D	H.sapiens germline im	1.63e-89
37	124	29.3	440	59	HUMIGHV2B	Human Ig germline hea	1.63e-89
38	124	29.3	444	59	HUMIGHV2G	Human Ig germline hea	1.63e-89
39	124	29.3	546	59	HUMIGH226X	Human immunoglobulin	1.63e-89
40	123	29.1	360	63	MMHCVR3	M.musculus (A.SW) mRN	1.49e-88
41	123	29.1	441	62	S67984	Ig VH1 JH5-anti-HIV	1.49e-88
42	122	28.8	440	59	HUMIGHV2A	Human Ig germline hea	1.37e-87
43	121	28.6	360	65	MMU22979	Mus musculus CBI7 SCI	1.25e-86
44	121	28.6	399	59	HUMIGHVAA	Human Ig rearranged h	1.25e-86
45	121	28.6	469	52	HSACVRA	H.sapiens DNA for mon	1.25e-86

ALIGNMENTS

RESULT 1
LOCUS HUMIGHCXH 389 bp mRNA PRI 11-JUL-1995
DEFINITION Human fetal Ig heavy chain variable region (clone M60) mRNA,
partial cds.
ACCESSION M34027
NID g185270
KEYWORDS D-region; J-region; V-region; immunoglobulin heavy chain;
processed gene.
SOURCE Homo sapiens (individual_isolate H8409) (clone: M60) 104 day foetus

Db	61	acctgaccccttctctgggttcttcaactcaagcactagtggatgtgtgtgagctggaccgtg	120
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Db	121	cagcccccagggaagccctggagcggttgcaactcattgattgggatgatataaac	180
Qy	181	CAGCGCGCGGGTAAAGGCTTAGAATGGCTGGCTCACATCTACTGGGAGCAGCACAAACGT	240
Db	181	tacagcacatctctgaagcaggctcaccatctccaagacacactccaaaaaccagtg	240
Qy	241	TACACCCGCGACCTGAATCCGCTCTGACGATATCCAAAGACACCTCCCGTACCACGGTT	300
Db	241	gtccttaacaatgaccaactggacccctgtggacacagccacgtattactgtgcaggacc	300
Qy	301	GTTCTGACCATGATACATACGACCGCGGTTCAGACCGCTACCTACTACTCGGCTCGAGCG	360
Db	301	cgctacgctgactacgggacttttgactactgggcacagagacccctgggtcacccgtctcc	360
Qy	361	GAAAACCGTTTCTACTGTGTACTTCGACGTTTGGGGTCGTGGTACCCAGCTTACCGTGAGC	420
Db	361	tea	363
Qy	421	TC	423

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3
RESULT
LOCUS HUMIGVH2H 460 bp DNA PRI 16-MAR-1994
DEFINITION Human Ig germline heavy-chain mRNA, subgroup VH2, V-region, 5' end.
ACCESSION L21969
NID 9405213
KEYWORDS immunoglobulin heavy chain; variable region subgroup VH2.
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.
REFERENCE 1 (bases 1 to 460)
AUTHORS Andris,J.S., Brodeur,B.R. and Capra,J.D.
TITLE Molecular characterization of human antibodies to bacterial
antigens: utilization of the less frequently expressed VH2 and VH6
heavy chain variable region gene families
JOURNAL Mol. Immunol. 30 (17), 1601-1616 (1993)
MEDLINE 94067179
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/codon_start=1
47..137
144..440
/product="immunoglobulin heavy chain"
441..460
/note="immunoglobulin heptamer/nonamer recombination
signal; putative"
BASE COUNT 108 a 134 c 104 g 114 t
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Query Match 31.2%; Score 132; DB 59; Length 460;
Best Local Similarity 72.3%; Pred. No. 3.09e-97;
Matches 214; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
Db 144 caggtcaccttgaggagctgtgctgcgtgcgtgcgtgcagaccacacagaccctcacactg 203

```

Qy	61	CAGGTTACCTTCGGTGAATCCGGTCGGCAGT	120
Db	204	acctgcaacctctctcgggtctcacaatcagcaactagt	263
Qy	121	ACCTGCACTTCTCCGGTTTCCTTCGACCTCGGTAT	180
Db	264	cagcccccaaggagccctggagtggctgcactcatgatt	323
Qy	181	CACCGCCGGGTAAAGTCTAGAAATGGCTGGCT	240
Db	324	tacagcacatctctgaagaccagcgctcaccatctc	383
Qy	241	TACAACCGGACGCTGAATCCGCTTGACGATAT	300
Db	384	gtccttaacaatgacacaatggacctgtggacacagcc	439
Qy	301	GTCTTGACCATGATCAACATGACCGCGGTTCAC	356

RESULT	4
LOCUS	HSVHHAL0 417 bp RNA PRI 15-FEB-1996
DEFINITION	H.sapiens mRNA for immunoglobulin heavy chain V-region (clone CDN3HA10).
ACCESSION	Z47237
NID	g1197309
KEYWORDS	immunoglobulin; immunoglobulin heavy chain; variable region.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 113) Demaïson,C., David,D., Letourneur,F., Zouali,M., Saragosti,S. and Theze,J. A cDNA/anchor-PCR approach to analyse the human VH gene repertoire expressed by peripheral CD19+ B cells reveals a strong bias usage Unpublished 2 (bases 1 to 417) Demaïson,C. Direct Submission Submitted (16-DEC-1994) Christophe Demaïson, Immunologie, Unite d'Immunogenetique Cellulaire-Institut Pasteur, 25, rue du Docteur Roux, Paris, 75015, FRANCE 3 (bases 1 to 417) Demaïson,C., David,D., Letourneur,F., Theze,J., Saragosti,S. and Zouali,M. Analysis of human VH gene repertoire expression in peripheral CD19+ B cells JOURNAL Immunogenetics 42 (5), 342-352 (1995)
MEDLINE	96006568
FEATURES	Location/Qualifiers 1..417 /organism="Homo sapiens" /clone="CDN3HA10" /dev stage="adult" /tissue_type="peripheral blood lymphocyte" cell_type="B-lymphocyte" 1..57 58..417 sig peptide V_region /product="immunoglobulin variable region"
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[illegible]

Query Match	30.7%	Score 130;	DB 59;	Length 445;
Best Local Similarity	72.1%;	Pred. No. 2.66e-95;		
Matches 212;	Conservative	0;	Mismatches 82;	Indels 0; Gaps 0;

Db	146	ggtcaaccttgaggagctcgtgcctcgctcgtgtgtaaacccacacagaccctcacactgac	205
Qy	63	GGTTACCTTCGCGTGAATCCGTCGGGACTAGTTAAACCGACCACGCCCTGCAGTTAAC	122
Db	206	ctgcacctctctgggtttctcatcscgaactadtggaatggtgtgagctggatccgcaca	265
Ov	123	CTGCACCTTTCGCGTTTTCTCCTGTCAACCTCCGATGCGTGTTTCTCGATCGGCTCA	182

Mar 19:07:53

US-08-612-929-1.lrg

11

Db 266 gcccccaggagcctgagtgcttcacgcattgattgattgattgataataacta 325
Qy 183 gccccgggtaagcttgaatggctggctcacatctcgaagacaccccaaacagggtggt 385
Db 326 cagcacatctctgaagaccaggctcaccatctccaagacacccctccaaacacagggtggt 385
Qy 243 caacccgagcctgaattcccgctgcagatatccaaagacacactcccgtaaccaggtgtg 302
Db 386 ccttaaatgaccaaactggaacccctggacacagccagcagctattactgtgcacg 439
Qy 303 tctgaccatgactaaatggacccggctgacacggctacctactactgacctgctcg 356

RESULT 9
LOCUS HSVVP46 363 bp RNA PRI 01-JUN-1993
DEFINITION H.sapiens mRNA P46 for IG heavy chain variable region.
ACCESSION X64147
NID g37827
KEYWORDS Ig heavy chain; immunoglobulin;
immunoglobulin heavy chain variable region; VH region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Carnivora; Hominidae; Homo.

REFERENCE 1 (bases 1 to 363)
AUTHORS Ebeling,S.B., Schutte,M.E., Akkermans-Koolhaas,K.E., Bloem,A.C.,
Gnelli-Meyling,F.H. and Logtenberg,T.

TITLE Expression of members of the Immunoglobulin VH3 gene families is
not restricted at the level of individual genes in human chronic
lymphocytic leukemia

JOURNAL Int. Immunol. 4 (3), 313-320 (1992)

MEDLINE 92232604

REFERENCE 2 (bases 1 to 363)

AUTHORS Ebeling,S.

TITLE Direct Submission

JOURNAL Submitted (23-DEC-1991) to the EMBL/GenBank/DBJ databases. S.

Heidelberglaan, 3584 CX Utrecht, THE NETHERLANDS

COMMENT See also X64234-43 & X64147.

FEATURES Location/Qualifiers

source 1..363

/organism="Homo sapiens"

/dev_stage="adult"

/tissue_type="peripheral blood"

/cell_type="B lymphocyte"

/cell_line="peripheral blood from CLL patient P46"

/isolate="P46"

/chromosome="14"

misc_feature 1..300

/note="VH2 gene"

misc_feature 301..327

/note="D segment"

misc_feature 328..363

/note="JH4 gene"

BASE COUNT 87 a 109 c 95 g 72 t

ORIGIN

Query Match 30.5%; Score 129; DB 56; Length 363;

Best Local Similarity 67.8%; Pred. No. 2.46e-94;

Matches 246; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Mar 19:07:53

US-08-612-929-1.lrg

12

Db 1 cagatcaccttgaagagctcctacgctgggtgaacccacacagacccctcagctg 60
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Db 61 acctgcaacctctcctgggtctcactcagcactagtgagtggtgggtgggtggatcgt 120
Qy 121 ACCTGCACCTTCTCCGGTTCTCCCTCTCGACCTCCGGTATGGGTGTTCTCTGGATCGGT 180
Db 121 cagccccaggaagccctcctgagtggtgctcactcatttattggatgatgaagcgc 180
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Qy 301 GTTCTGACCATCACTAACATGACCCGGTTGACACCCGCTACCTACTACTGCGGTGACGC 360
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Qy 361 GAAACCGTTTTCTACTGCTGCTTCGACGTTTGGGGTCTGGTACCCAGTTACCGTGAGC 420
Db 361 tca 363
Qy 421 TCA 423

RESULT 10
LOCUS S73953 366 bp mRNA PRI 28-APR-1995
DEFINITION Ig VH-immunoglobulin heavy chain VDJ region [human, chronic
lymphocytic leukemia patient ARN, mRNA Partial, 366 nt].

ACCESSION S73953

NID g786355

KEYWORDS human chronic lymphocytic leukemia patient ARN.

SOURCE Homo sapiens

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 366)

AUTHORS Korganow,A.S., Martin,T., Weber,J.C., Lioure,B., Lutz,P.,

Knapp,A.M. and Pasquali,J.L.

Molecular analysis of rearranged VH genes during B cell chronic

lymphocytic leukemia: intraclonal stability is frequent but not

constant

JOURNAL Leuk. Lymphoma 14 (1-2), 55-69 (1994)

MEDLINE 95004012

REMARK GenBank staff at the National Library of Medicine created this

entry [NCBI gibbsq 157305] from the original journal article.

This sequence comes from Fig. 2.

FEATURES Location/Qualifiers

source 1..366

/organism="Homo sapiens"

/note="human"

Join(1..296,324..366)

/partial

/gene="Ig VH"

/note="Method: conceptual translation supplied by author.

This sequence comes from Fig. 2."

/codon_start=1

/product="Immunoglobulin heavy chain VDJ region"

/db_xref="PID:g786356"

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ORIGIN					
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Best Local Similarity	72.0%; Pred. No. 2,46e-94;				
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Df	61	acctgcacctctctgggttcctcactcagcaactagtggagtgggttggtgatccgt	120		
Qy	121	ACCTGCACCTTCTCCGGTTTTCTCCCTCTGCACTCCGGATGGGTGTTCCTCGATCCGT	180		
Df	121	cagcccccaagaagcccctggagtgtttcgactcatttatggatgatataaacgc	180		
Qy	181	CAGCCCCGGGTAAAGCTAGAATTGGCTGGCTCACATCTACTTGGGACGACGAACAAGT	240		
Df	181	tacgcccatctctgaagcagagctcaccatcacccaaggacacctcaaaaaaccaggtg	240		
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RESULT	11	HUMIGHVH2K	460 bp	DNA	PRI 16-MAR-1994
LOCUS	Human Ig germline heavy-chain mRNA, subgroup VH2, V-region, 5' end.				
DEFINITION					
ACCESSION	L21972				
NID	9405216				
KEYWORDS	immunoglobulin heavy chain; variable region subgroup VH2.				
SOURCE	Homo sapiens DNA.				
ORGANISM	Homo sapiens Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homidae.				
REFERENCE	1	(bases 1 to 460)			
AUTHORS	Andris,J.S., Brodeur,B.R. and Capra,J.D.				
TITLE	Molecular characterization of human antibodies to bacterial antigens: utilization of the less frequently expressed VH2 and VH6 heavy chain variable region gene families				
JOURNAL	Mol. Immunol. 30 (17), 1601-1616 (1993)				
MEDLINE	94067179				
FEATURES	Location/Qualifiers				
source	1..460 /organism="Homo sapiens" /cell_type="B-cell" /germline /sequenced_mol="DNA" 47..132 144..440 /product="immunoglobulin heavy chain" 441..460 /notes="immunoglobulin heptamer/nonamer recombination signal; putative"				
intron					
V_region					
misc_signal					
BASE COUNT	108 a	136 c	105 g	111 t	
ORIGIN					
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Best Local Similarity	72.0%; Pred. No. 2,46e-94;				
Matches	211; Conservative 0; Mismatches 82; Indels 0; Gaps 0;				

Dn	144	caggtcacctgaagagtgctgtcctacgctggtagaacccacacagaccctcaagctg	203
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Dn	204	acctgcaactctctcggtttctcaactcagcactagtggagtggtggctggatccctg	263
Qy	121	ACCTGCACCTTCTCGGTTTTCTCCCTCTCGACTTCGGGTATGGGTGTTTCTCGATCCGT	180
Dn	264	cagccccagagaagcccctggagtggttgcactcatattattgggatgatgaagcgc	323
Qy	181	CAGCCCCGGGTAAAGGCTTAGAATGGCTGGCTCACATCTACTGGCAGCAGCACAAACGT	240
Dn	324	tacggcccatctctgaagcaggctcacccatcaccaagagcacctccaaaacacaggctg	383
Qy	241	TACACCCGAGCCTGAAATCCGCTTGACCATATCCAAGACACATCCCGTAACAGATT	300
Dn	384	gtccttaaatgaccaacatggaccctgtggacagcagccacatatattactgtcg	436
Qy	301	GTTCTGACCATGATAACATGGACCCGGTTGACACCGCTACCTACTACTGCCG	353
RESULT	12		
LOCUS	HSIGDP27	288 bp DNA	PRI 11-DEC-1992
DEFINITION	H.sapiens germline Ig H-chain V-region (DP-27).		
ACCESSION	Z12329		
NID	g32875		
KEYWORDS	immunoglobulin; immunoglobulin heavy chain; variable region.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;		
	Metazoa; Emetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;		
	Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;		
	Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;		
	Catarrhini; Homidae; Homo.		
REFERENCE	1 (bases 1 to 288)		
AUTHORS	Tomlinson,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-JUN-1992) to the EMBL/GenBank/DBJ databases. Ian Tomlinson, MRC Centre for Protein Engineering, Hills Road, Cambridge, CB2 2QH, U.K		
REFERENCE	2 (bases 1 to 288)		
AUTHORS	Tomlinson,I.M., Walter,G., Marks,J.D., Llewelyn,M.B. and Winter,G.		
TITLE	The repertoire of human germline VH sequences reveals about fifty groups of VH segments with different hypervariable loops		
JOURNAL	J. Mol. Biol. 227 (3), 776-798 (1992)		
MEDLINE	93021117		
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ORIGIN

Query Match	30.3%;	Score 128;	DB 59;	Length 406;
Best Local Similarity	71.6%;	Pred. No. 2,27e-93;		
Matches	212;	Conservative	0;	Mismatches 84;
			Indels	0;
			Gaps	0;

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Qy	61	CAGGTTACCTTCGGTCAATCCGGTCCGGCAGTATTAAACGCCACACCTGACGTTA 120
Db	92	acctgcaacctctctgggttctcactcagcactagtggaatctctgtaactggatccgct 151
Qy	121	ACCTGCACCTTCCTCGGTTTCTCCCTGCGACTCCGGTATGGGTGTTTCTCTGGATCCGT 180
Db	152	cagccccaggaagccctggagtggctgcactcgttgactgggatgatgataaat 211
Qy	181	CAGCCGCCGGGTAAAGCTTAGAATGGCTGGCTCAGATCTACTTGGGACGACGACAAAGCT 240
Db	212	tacagcacatctctgaagacagagactcaccatctccagggacacctcccaaaacccgggtg 271
Qy	241	TACAACGGAGCCTGAATTCGGCTCTGACGATATCCAAAGACACCTCCCGTAACCAAGTT 300
Db	272	gtccttaaatgaccacactgacctgtggacagaccacgctactctctgtgcacg 327
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[illegible]

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FEATURES             Location/Qualifiers
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BASE COUNT

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[illegible]

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DEFINITION		Human Ig germline heavy-chain mRNA, subaroup VH2, V-region, 5' end.			

KEYWORDS immunoglobulin heavy chain; variable region subgroup VH2.

ORGANISM	Homo sapiens
	Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates: Haplorhini; Catarrhini; Hominoidea.

AUTHORS Andris, J. S., Brodeur, B. R. and Capra, J. D.
TITLE Molecular characterization of human antibodies to bacterial antigens: utilization of the less frequently expressed VH2 and VH6 heavy chain variable region gene families
JOURNAL Mol. Immunol. 30 (17), 1601-1616 (1993)

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FEATURES
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ORIGIN				

Query Match 30.3%; Score 128; DB 59; Length 461;
Best Local Similarity 71.6%; Pred. No. 2.27e-93;
Matches 212; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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Ov 121 acctgcaccttctccggtttccctctgcacctccggatgggtgtttccctggatccgt 180
|||||

Db 264 cagccccagggaagccctggagtggattgcacgcattgattaggatgatgataaatac 323
||||| || | | | | | | | | | | | | | | | |
Ov 181 CAGCCGCGGGTAAAGSTCTACAATGCTGTGTACATCTACTGSCACGCACAAAAGT 240

Db 324 tacagcacatctctgaagaccagggtcaccatctccaaggacacctccaaaaaccaggtg 383

WVPSREH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:05:17 1997; MacPar time 4.30 Seconds
608.232 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-12
Description: (1-141) from US08612929.pgp
Perfect Score: 1068
Sequence: 1 MWLQTVFISLLWISGAYG.....TVFYVFDWGRGTPVTSS 141

Scoring table: PAM 150
Gap 11

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot33
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10

Statistics: Mean 43.081; Variance 80.072; scale 0.538

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	655	61.3	120	4	HV2B_HUMAN IG HEAVY CHAIN V-II R	7.85e-114
2	652	61.0	121	4	HV2E_HUMAN IG HEAVY CHAIN V-II R	3.56e-113
3	640	59.9	125	4	HV2D_HUMAN IG HEAVY CHAIN V-II R	1.50e-110
4	607	56.8	126	4	HV2A_HUMAN IG HEAVY CHAIN V-II R	2.40e-103
5	605	56.6	147	4	HV2H_HUMAN IG HEAVY CHAIN PRECUR	6.54e-103
6	563	52.7	119	4	HV2C_HUMAN IG HEAVY CHAIN V-II R	8.68e-94
7	479	44.9	144	4	HV43_MOUSE IG HEAVY CHAIN PRECUR	1.04e-75
8	456	42.7	137	4	HV46_MOUSE IG HEAVY CHAIN PRECUR	8.28e-71
9	447	41.9	115	4	HV44_MOUSE IG HEAVY CHAIN PRECUR	6.76e-69
10	431	40.4	135	4	HV02_XENLA IG HEAVY CHAIN PRECUR	1.66e-65
11	418	39.1	122	4	HV3G_HUMAN IG HEAVY CHAIN V-III	9.18e-63
12	416	39.0	116	4	HV45_MOUSE IG HEAVY CHAIN PRECUR	2.42e-62
13	412	38.6	116	4	HV61_MOUSE IG HEAVY CHAIN PRECUR	1.68e-61

14	407	38.1	116	4	HV60_MOUSE IG HEAVY CHAIN PRECUR	1.90e-60
15	403	37.7	119	4	HV38_MOUSE IG HEAVY CHAIN V REGI	1.31e-59
16	402	37.6	117	4	HV62_MOUSE IG HEAVY CHAIN PRECUR	2.13e-59
17	402	37.6	119	4	HV3I_HUMAN IG HEAVY CHAIN V-III	2.13e-59
18	397	37.2	129	4	HV2F_HUMAN IG HEAVY CHAIN V-II R	2.38e-58
19	394	36.9	136	4	HV01_XENLA IG HEAVY CHAIN PRECUR	1.01e-57
20	392	36.7	136	4	HV16_MOUSE IG HEAVY CHAIN PRECUR	2.65e-57
21	386	36.1	123	4	HV24_MOUSE IG HEAVY CHAIN V REGI	4.75e-56
22	384	36.0	122	4	HV21_MOUSE IG HEAVY CHAIN V REGI	1.24e-55
23	383	35.9	117	4	HV2G_HUMAN IG HEAVY CHAIN V-II R	2.01e-55
24	383	35.9	123	4	HV18_MOUSE IG HEAVY CHAIN V REGI	2.01e-55
25	382	35.8	121	4	HV3J_HUMAN IG HEAVY CHAIN V-III	3.25e-55
26	382	35.8	123	4	HV19_MOUSE IG HEAVY CHAIN V REGI	3.25e-55
27	381	35.7	117	4	HV30_HUMAN IG HEAVY CHAIN V-III	5.25e-55
28	381	35.7	146	4	HV2I_HUMAN IG HEAVY CHAIN PRECUR	5.25e-55
29	377	35.3	123	4	HV22_MOUSE IG HEAVY CHAIN V REGI	3.58e-54
30	377	35.3	123	4	HV23_MOUSE IG HEAVY CHAIN V REGI	3.58e-54
31	373	34.9	119	4	HV40_MOUSE IG HEAVY CHAIN V REGI	2.43e-53
32	372	34.8	122	4	HV3H_HUMAN IG HEAVY CHAIN V-III	3.93e-53
33	369	34.6	116	4	HV1A_RABIT IG HEAVY CHAIN V-A1 R	1.65e-52
34	369	34.6	119	4	HV37_MOUSE IG HEAVY CHAIN V REGI	1.65e-52
35	370	34.6	122	4	HV20_MOUSE IG HEAVY CHAIN V REGI	1.02e-52
36	368	34.5	119	4	HV3N_HUMAN IG HEAVY CHAIN V-III	2.66e-52
37	366	34.3	115	4	HV3F_HUMAN IG HEAVY CHAIN V-III	6.93e-52
38	364	34.1	126	4	HV3K_HUMAN IG HEAVY CHAIN V-III	1.80e-51
39	363	34.0	119	4	HV3M_HUMAN IG HEAVY CHAIN V-III	2.90e-51
40	361	33.8	115	4	HV3S_HUMAN IG HEAVY CHAIN V-III	7.53e-51
41	358	33.5	117	4	HV13_MOUSE IG HEAVY CHAIN V REGI	3.15e-50
42	358	33.5	117	4	HV2B_RABIT IG HEAVY CHAIN V-A2 R	3.15e-50
43	358	33.5	136	4	HV2C_RABIT IG HEAVY CHAIN PRECUR	3.15e-50
44	357	33.4	117	4	HV03_CAICR IG HEAVY CHAIN PRECUR	5.07e-50
45	357	33.4	123	4	HV25_MOUSE IG HEAVY CHAIN V REGI	5.07e-50

ALIGNMENTS

RESULT	1	HUMAN	STANDARD;	PRT;	120 AA.
ID	HV2B_HUMAN				
AC	P01815;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)				
DE	IG HEAVY CHAIN V-II REGION (COR).				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE; 70258837.				
RA	PRESS E.M., HOGG N.M.;				
RL	BIOCHEM. J. 117:641-660(1970).				
CC	-!- THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.				
DR	PIR; A02089; GHRUCO.				
DR	HSP; P01789; 2FGW.				
KW	IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.				
FT	MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.				
FT	DISULFID 22 94				
FT	CARBOHYD 62 62				
FT	NON TER 120 120				
SQ	SEQUENCE 120 AA; 13226 MW; D690F656 CRC32;				
Query Match		61.3%;	Score 655;	DB 4;	Length 120;
Best Local Similarity		81.3%;	Pred. No. 7.85e-114;		
Matches	100;	Conservative	6;	Mismatches	12; Indels 5; Gaps 3;

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Db 1 qvltresgpalvkptqtlitctfsgfslstgmcvgwvqirppgkalewlaridwdddky 60
 Qy 21 QVTLRESGALVKPTQTTLTCTFSGFSLSTGMCVGSWIRQPPKGLWLAHLYWDDDKR 80

Db 61 yntelettriskdtsnqvltm---dpvdtatycarivtvpapagymdwgrgtptv 117
 Qy 81 YNPSIKSLRITISKOTSRSNQVLTMTNMDPVDATYYCARRETTFY-W-YFDVWGRGTPTV 138

Db 118 vs 120
 Qy 139 VSS 141

RESULT 2
 ID HV2E HUMAN STANDARD; PRT; 121 AA.
 AC P01817;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V-II REGION (HE).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.

RX MEDLINE; 70114712.
 RA CUNNINGHAM B.A., PFLUM M.N., RUTISHAUSER U., EDELMAN G.M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 64:997-1003 (1969).
 CC -/- THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A02093; GIHUE.
 DR HSP; P01772; IFGV.
 KW IMMUNOGLOBULIN V REGION.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON TER 121 121
 SQ SEQUENCE 121 AA; 13483 MW; B91154F1 CRC32;

Query Match 61.08; Score 652; DB 4; Length 121;
 Best Local Similarity 71.3%; Pred. No. 3.56e-113;
 Matches 87; Conservative 22; Mismatches 11; Indels 2; Gaps 2;

Db 1 qvltkengplvkptetltctleglsltdgavgwirgpggalewllwydddk 60
 Qy 21 QVTLRESGALVKPTQTTLTCTFSGFSLSTGMCVGSWIRQPPKGLWLA-HLYWDDDK 79

Db 61 rfesplksrltvtctkngvltmmdpvdttatycvhrhrtl-afdwgqgtkvav 119
 Qy 80 RYNPSIKSLRITISKOTSRSNQVLTMTNMDPVDATYYCARRETTFYWFYFDVWGRGTPTV 139

Db 120 ss 121
 Qy 140 SS 141

RESULT 3
 ID HV2D HUMAN STANDARD; PRT; 125 AA.
 AC P01817;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V-II REGION (MCE).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.

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RN [1]
 RP SEQUENCE.
 RX MEDLINE; 81118242.
 RA GERBER-JENSON B., KAZIN A., KEHOE J.M., SCHEFFEL C., ERICKSON B.W.,
 RA LITMAN G.W.;
 RL J. IMMUNOL. 126:1212-1216 (1981).
 CC -/- THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM CRYOIMMUNOGLOBULIN.
 DR PIR; A02092; MHRUMC.
 DR HSP; P01772; IFGV.
 KW IMMUNOGLOBULIN V REGION.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON TER 125 125
 SQ SEQUENCE 125 AA; 13783 MW; 7F897793 CRC32;

Query Match 59.9%; Score 640; DB 4; Length 125;
 Best Local Similarity 73.6%; Pred. No. 1.50e-110;
 Matches 92; Conservative 17; Mismatches 12; Indels 4; Gaps 3;

Db 1 qitlkesgptlvkptetltctfsgfslstgmcvgwvqirppgkalewlaridwdddkr 60
 Qy 21 QVTLRESGALVKPTQTTLTCTFSGFSLSTGMCVGSWIRQPPKGLWLAHLYWDDDKR 80

Db 61 yepsrlsrilgtktdtsnqvltmmdpvdsgtyfcahrppwrfnlggfdwqggtl 120
 Qy 81 YNPSIKSLRITISKOTSRSNQVLTMTNMDPVDATYYCARRET-TFY-WY-FDVMGRGTP 136

Db 121 vtvas 125
 Qy 137 VTSS 141

RESULT 4
 ID HV2A HUMAN STANDARD; PRT; 126 AA.
 AC P01814;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V-II REGION (OU).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 74005511.
 RA PUTNAM F.W., FLORENT G., PAUL C., SHINODA T., SHIMIZU A.;
 RL SCIENCE 182:287-291 (1973).
 CC -/- THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
 DR PIR; A02088; MHRUO.
 DR HSP; P01607; IFGV.
 KW IMMUNOGLOBULIN V REGION.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 97
 FT NON TER 126 126
 SQ SEQUENCE 126 AA; 14276 MW; 459E1429 CRC32;

Query Match 56.8%; Score 607; DB 4; Length 126;
 Best Local Similarity 69.3%; Pred. No. 2.40e-103;
 Matches 88; Conservative 18; Mismatches 14; Indels 7; Gaps 5;

Db 1 qvltresgpalvkptqtlitctfsgfslstgmcvgwvqirppgkalewlarib-bbdkf 59
 Qy 21 QVTLRESGALVKPTQTTLTCTFSGFSLSTGMCVGSWIRQPPKGLWLAHLYWDDDKR 80

Db 60 ywstelttriskndeknqvlinvmpvdtatycarvsvmagyvvvymdvwqgk 119

RESULT 8
ID HV46 MOUSE STANDARD; PRT; 137 AA.
AC P01822;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (MOPC 315).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89238351.
RA RINFRET A., HORNE C., DORRINGTON K.J., KLEIN M.;
RL MOL. IMMUNOL. 26:431-434(1989).
RN [2]
RP SEQUENCE OF 1-31.
RX MEDLINE; 78094475.
RA JIJKA R.L., PESTKA S.;
RL PROC. NATL. ACAD. SCI. U.S.A. 74:5692-5696(1977).
RN [3]
RP SEQUENCE OF 1-21.
RX MEDLINE; 79148758.
RA SCHECHTER I., WOLF O., ZEMMEL R., BURSTEIN Y.;
RL FED. PROC. 38:1839-1845(1979).
RN [4]
RP SEQUENCE OF 19-136.
RX MEDLINE; 74170779.
RA FRANCIS S.H., LESLIE R.G.O., HOOD L., EISEN H.N.;
RL PROC. NATL. ACAD. SCI. U.S.A. 71:1123-1127(1974).
RN [5]
RP REVISION TO 53.
RX MEDLINE; 77244979.
RA HOOD L., MARGOLIES M.N., GIVOL D., ZAKUT R.;
RL UNPUBLISHED RESULTS, CITED BY:
RL PADLAN E.A., DAVIES D.R., PECHT I., GIVOL D., WRIGHT C.;
RL COLD SPRING HARB. SYMP. QUANT. BIOL. 41:627-637(1977).
CC -1- THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS
CC ANTI-DINITROPHENYL ACTIVITY.
DR ENBL; M27638; G602707; -.
DR ENBL; X07880; G295908; -.
DR PIR; P10102; AVMS35.
DR HSSP; P01789; 2FGW.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 18
FT CHAIN 19 137 IG HEAVY CHAIN V REGION (MOPC 315).
FT DOMAIN 19 48 FRAMEWORK 1.
FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 85 116 FRAMEWORK 3.
FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 127 137 FRAMEWORK 4.
FT DISULFID 40 114 BY SIMILARITY.
FT CONFLICT 15 15 G -> GG (IN G295908).
FT CONFLICT 15 15 G -> H (IN REF. 2).
FT CONFLICT 77 78 GY -> YG (IN REF. 4).
FT CONFLICT 102 102 N -> D (IN REF. 4).
FT CONFLICT 123 123 MISSING (IN REF. 4).
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15399 MW; 155A5E8D CRC32;

Query Match 42.7%; Score 456; DB 4; Length 137;
Best Local Similarity 53.4%; Pred. No. 8.28e-71;
Matches 70; Conservative 28; Mismatches 31; Indels 2; Gaps 2;
Db 9 lltalpgmsdvqlqespgqlvlpesqalsltcvtgysl-tagylfwnwlrqfpgnklew 67
|| || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 11 LLLMISGAYGVTLRESGPAVKPTQLTLTCTSGFSLSLTSGMGVSWIRPPGKLEWL 70
Db 68 gfikydsngynpslknrvaitrdteeqffliklnsvttdetatyccagndhly-yfdy 126
: | | : ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 71 AH1YDDDKRYNPSIKSLTISKDTSRNQVLTMNDPVDVDTATYTCARRETVFYVYFDV 130
Db 127 wggqgtlttves 137
|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 131 WGRGTPVTYSS 141
RESULT 9
ID HV44 MOUSE STANDARD; PRT; 115 AA.
AC P01820;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (PJ14).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81012133.
RA SAKANO H., MAKI R., KUROSAWA Y., ROEDER W., TONEGAWA S.;
RL NATURE 286:676-683(1980).
DR PIR; A02095; HVMS14.
DR HSSP; P01772; 1FDL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 115 IG HEAVY CHAIN V REGION (PJ14).
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12447 MW; 6E782F62 CRC32;
Query Match 41.9%; Score 447; DB 4; Length 115;
Best Local Similarity 55.5%; Pred. No. 6.76e-69;
Matches 66; Conservative 22; Mismatches 26; Indels 5; Gaps 5;
Db 1 mavlallf-clvtfpccilqsvqlkespglpvapeqlsictvsgfel-t-gygvnwvr 57
| : : | | : || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 1 MVLATQVFISLLLTWISGAYGVTLRESGPAVKPTQLTCTSGFSLSLTSGMGVSWIR 60
Db 58 qpqkglewlgmi-wgdstdynaalkrlsiskdnksqvlkmslqtdtdtaryca 115
||||||| : | | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 61 QPPCKGLEWLAHYWDDDKR-YNPSIKSLTISKDTSRNQVLTMNDPVDVDTATYCA 118
RESULT 10
ID HV02 XENLA STANDARD; PRT; 135 AA.
AC P20857;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (XIG14) (FRAGMENT).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN [1]
RP SEQUENCE FROM N.A.


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RX MEDLINE; 88176921.
RA SCHWAGER J., AKORYAK C.A., STEINER L.A.;
RL PROC. NATL. ACADEM. SCI. U.S.A. 85:2245-2249 (1988) .
DR ENBL; J03632; G214330; -.
DR PIR; B31933; B31933.
DR HSP; P01607; IFGV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT NON TER      1
FT STGNAL      <1
FT CHAIN       19 135
FT NON TER     135 135
SQ SEQUENCE    135 AA; 15080 MW; D8327985 CRC32;

Query Match          40.4%; Score 431; DB 4; Length 135;
Best Local Similarity 51.5%; Pred.No. 1.66e-65;
Matches 69; Conservative 22; Mismatches 39; Indels 4; Gaps

Db 6 f5lffspscisq-tlcespgtvkpselrlctcvsfelssylm--hwirppqkg1 121
   || : :: : | : |||||:: ||::|| |||| |||| ||| : | ||||| ||||
Qy 8 F5LLIIMISGAYQVTLRESGPALVPQTQTLTCTFSGSFSLSTSGMGVSWIROPKGL 67

Db 63 ewigviatggsgaiadlnrvitkdngkkqvylgmnmekvkt amycareyasg-n 121
   ||:: | ||||::||::|| ::|| | | : || ||||| : |
Qy 68 EWLAIHYDDDKRYNP SLKSRLTSISKDTSRNQVVLTMNDPVTATYYCARETVFY 127

Db 122 fdwagqgtmtvtls 135
Qy 128 FDWGRGTPVTSS 141
```

RESULT	11
ID	HV3G HUMAN STANDARD; PRT; 122 AA.
AC	P01768;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE	IG HEAVY CHAIN V-II REGION (CAM).
OS	O homo sapiens (human).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; PRIMATES.
RN	[1]
RP	SEQUENCE.
RX	MEDLINE; 81013859.
RA	LEHMAN D.W.; PUTNAM F.W.;
RL	PROC. NATL. ACAD. SCI. U.S.A. 77:3239-3243(1980).
CC	-!- THIS MJ CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH MACROGLOBULINEMIA.
DR	PIR; A02051; M3HUAM.
DR	HSPP; P01607; ZEGW.
KW	IMMUNOGLOBULIN V REGION.
FT	MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	NON TER 122 122
SQ	SEQUENCE 122 AA; 13668 MW; 4AF2E3D8 CRC32;

Query Match	39.1%	Score 418;	DB 4;	Length 122;
Best Local Similarity	48.4%	Pred. No. 9,18e-63;		
Matches	60;	Conservative	29;	Mismatches 30;
			Indels	5;
			Gaps	3;

Db	1	qvelvsggvvzpgsrllrscasgftfenvam--hwrqppgkglwvavisygbgbk	58
		: : : : : : : : : : : : :	
Qy	21	QVTLRESGFALVPTQTTLTCTESGSLTSGMGSVIRQPPKGLEWLAHI-YWDDCK	79
		: : : : : : : : : : : : :	

Db	59	yyabsvkgrftlsrdbskbtlylqmnslraebtavvycardrplygbfraynwgagtlv	118
		: : : : : : : : : : : : : :	

QY	80 RYNSPKSRLLTISKOTSRNQVULTMTNMDPVDITATYCARRETVE--YNYFDWGRGTPV 13
Db	119 tvss 122
QY	138 TVSS 141
RESULT	12
ID	HV45 MOUSE STANDARD; PRT; 116 AA.
AC	P01821;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE	IG HEAVY CHAIN PRECURSOR V REGION (MC101).
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
RN	(1)
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 82075900.
RA	KATAOKA T., MIKAIKO T., MIYATA T., MORIWAKI K., HONJO T.;
RL	J. BIOL. CHEM. 257:277-285(1982).
DR	PIR; A02096; GLMS10.
DR	HSSP; P01772; IFDL.
KW	IMMUNOGLOBULIN V REGION; SIGNAL.
FT	SIGNAL 1 19
FT	CHAIN 20 116 IG HEAVY CHAIN V REGION (MC101).
FT	NON TER 116 116
SO	SEQUENCE 116 AA; 12593 MW; 982C2581 CRC32;

		Query Match	39.0%;	Score 416;	DB 4; Length 116;
		Best Local Similarity	50.4%;	Pred. No. 2,47e-62;	
		Matches	60;	Mismatches 31; Indels 3; Gaps 3;	
Db	1 mavlgllf-clvtfpcvlsqvklkgqgplvpssqlcttcvtsgfs-l-tg-ygvhvvr 57				
	: : :	:	:	:	:
	: : :	:	:	:	:
Qy	1 MVLQTQVFTSLLIWISGAYGVQWTLRESGPALMKGTQLTLLTCFSGFLSTSGMSVMIR 60				
Db	58 qsqpgkglewlgwsqgstcdynaafierlslskdnksqvffkmalslqsndatlyycar 116				
	: : : : : :	:	:	:	:
	: : : : : :	:	:	:	:
Qv	61 oppckglfwLAHIVDDDKRKNPSSLSKSLITTSKOTSRNOVLTMNDPVDYATYYCAR 119				
	: : : : : :	:	:	:	:
	: : : : : :	:	:	:	:

RESULT	13
ID	HV61 MOUSE STANDARD; PRT; 116 AA.
AC	P1853Z;
DT	01-NOV-1990 (REL. 16, CREATED)
DT	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE	IG HEAVY CHAIN PRECURSOR V REGION (I843).
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC	EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/CJ;
RX	MEDLINE; 89279149.
RA	LEVY N.S., MALPIERO U.V., LEBEQUE S.G., GEARHART P.J.;
RL	J. EXP. MED. 169:2007-2019(1989).
CC	-!- THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR	PIR; JTO508; HWS1B.
DR	HSSP; PO1825; 1BAF.
KW	IMMUNOGLOBULIN V REGION; SIGNAL.
FT	SIGNAL 1 FT

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FT CHAIN 19 116 IG HEAVY CHAIN V REGION (1B43).
FT DOMAIN 19 48 FRAMEWORK 1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 54 67 FRAMEWORK 2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 85 116 FRAMEWORK 3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13158 MW; 10E4EE67 CRC32;

Query Match 38.6%; Score 412; DB 4; Length 116;
Best Local Similarity 48.7%; Pred. No. 1.68e-61;
Matches 57; Conservative 30; Mismatches 29; Indels 1; Gaps 1;
Db 1 mrvlllclftafgiledvqlqesgplvkpsqslctctvtgysl-tsqywhwlrqf 59
Qy 3 lqtqvflslwlllgagvgqvtlresgpalvkptqltltctsfslstsgmvgswirqp 62
Db 60 pnnklewmyihygsntsynpalkaristrdtsknqfllqlnsvttedtatyycar 116
Qy 63 pckglemlahiywddrrynpslksrltiskotsrnqovlwtmndpvdvtatyycar 119

RESULT 14
ID RV60 MOUSE STANDARD; PRT; 116 AA.
AC P18531;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (M315).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CJ;
RX MEDLINE; 89279149.
RA LEVY N.S., MALPIERO U.V., LEBECQUE S.G., GEARHART P.J.;
RL J. EXP. MED. 169:2007-2019 (1989).
DR PIR; JT0509; HVMS31.
DR HSP; P01825; IBAF.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION (M315).
FT DOMAIN 19 48 FRAMEWORK 1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 54 67 FRAMEWORK 2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 85 116 FRAMEWORK 3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13095 MW; 810F3E97 CRC32;

Query Match 38.1%; Score 407; DB 4; Length 116;
Best Local Similarity 53.2%; Pred. No. 1.90e-60;
Matches 58; Conservative 26; Mismatches 24; Indels 1; Gaps 1;

Db 9 lltaipgiledvqlqesgplvkpsqslctctvtgysl-tsqywmwlrqfpgnklewm 67
Qy 11 lllwtsagvgvtlresgpalvkptqltltctsfslstsgmvgswirqpckglewl 70
Db 68 gvisydgennpnslnkriidtrdtsknqfllklnsvttedtatyycar 116
Qy 71 ahlywddrrynpslksrltiskotsrnqovlwtmndpvdvtatyycar 119

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RESULT 15
ID HV38 MOUSE STANDARD; PRT; 119 AA.
AC P01808;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (T601).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79223895.
RA RAO D.N., RUDIKOFF S., KRUTZSCH H., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 76:2890-2894 (1979).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN THAT BINDS GALACTAN.
DR PIR; A02078; AVMST6.
DR HSP; P01810; IFVM.
KW IMMUNOGLOBULIN V REGION.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13169 MW; EEE850E1 CRC32;

Query Match 37.7%; Score 403; DB 4; Length 119;
Best Local Similarity 50.8%; Pred. No. 1.31e-59;
Matches 62; Conservative 21; Mismatches 34; Indels 5; Gaps 3;
Db 1 evkllesgglvpggslklscaasgdfsfrywm--swvzqpgkglewigeinpsdetsi 58
Qy 21 qvtlresgpalvkptqltltctsfslstsgmvgswirqpckglemlahiywddk- 79
Db 59 nytpslkdkfiisrdnakntlylqmskvrseatalyycarl--yygyfdwaggtvtv 116
Qy 80 rrvnslksrltiskotsrnqovlwtmndpvdvtatyycarretvfywfdwgrctpttv 139
Db 117 ss 118
Qy 140 SS 141

Search completed: Tue Mar 18 10:05:26 1997
Job time : 9 secs.

mpsrch no protein - protein database search. using Smith-Waterman algorithm

```
Run on: Tue Mar 18 10:05:44 1997; MasPar time 6.09 Seconds
595.430 Million cell updates/sec
Tabular output not generated.
```

Title: >IIS-08-612-929-12

Description: (1-141) from US08612929.pep

Perfect Score:

Sequence: 1 MVLQTQVFISLLWISGAYG.....TFEYWFYFDVWGRGTPVTVSS 141

Scoring table: PAM 150

Gap II

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database:
pir48
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unann
14:unrev
```

Statistics:
Mean 42.379: Variance 131.338: scale 0.323

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query		Length	DB	ID	Description	Pred. No.
			Match	Length					
1	713	66.8	124	5	A49002	rheumatoid factor he	3.39e-75		
2	713	66.8	138	5	S31513	Ig heavy chain - hum	3.39e-75		
3	686	64.2	119	5	S18555	Ig heavy chain - hum	1.27e-71		
4	685	64.1	122	5	S11740	Ig heavy chain precu	1.72e-71		
5	683	64.0	121	5	A36005	Ig heavy chain v reg	3.16e-71		
6	658	61.6	143	5	P01074	Ig heavy chain precu	6.28e-68		
7	655	61.3	120	2	G1HUCO	Ig heavy chain V-II	1.56e-67		
8	652	61.0	121	2	G1HHEH	Ig heavy chain V-II	3.88e-67		
9	641	60.0	113	5	S26465	Ig heavy chain v reg	1.09e-65		
10	640	59.9	125	2	MHHUMC	Ig heavy chain V-II	1.47e-65		
11	619	58.0	116	12	S2328	Ig heavy chain v reg	8.49e-63		
12	618	57.9	96	11	S26924	Ig heavy chain v reg	1.15e-62		


```
G.M.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1969) 64:997-1003
#title        Subgroups of amino acid sequences in the variable regions of
              immunoglobulin heavy chains.
#cross-references MUID:70114712
#accession     A02093
#molecule_type protein
##residues     1-121 ##label CUN
COMMENT       This gamma-1 chain was isolated from a myeloma protein.
GENETICS
#gene          GDB:IGHV8
##cross-references GDB:G00-128-528
#map_position  14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
1             #modified site blocked amino end (Gln) (probably
              pyroliodone carboxylic acid) #status experimental
SUMMARY       #length 121 #molecular-weight 13483 #checksum 9601

Query Match      61.0%; Score 652; DB 2; Length 121;
Best Local Similarity 71.3%; Pred. No. 3.88e-67;
Matches 87; Conservative 22; Mismatches 11; Indels 2; Gaps 2;

Db 1 qvtlkegptlvkptetltcttctglsalttdgavqgwgqgralewlawllywdddk 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 QVTLRESGALVKPTQTTLCTCTSGFSLSTSGMGVSWIRQPPGKLEWLA-HIYDDDK 79
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 rfspeklrktvtctekngvltmtmdpvdtdatyvchrrptl-afdwgggtkvav 119
      |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 80 RYNPSLSRLTISKOTSRNQVLTMTNMDPVDATYYCARRET-VFY-FDVMGRGTPTV 139

Db 120 ss 121
      ||
Qy 140 ss 141

RESULT 9
ENTRY   S26465 #type complete
TITLE   Ig heavy chain V region - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
              12-Apr-1995
ACCESSIONS S26465
REFERENCE  S26459
#authors   Kavalier, J.
#submission submitted to the EMBL Data Library, April 1991
#accession S26465
#status    preliminary
#molecule_type mRNA
##residues 1-113 ##label KAV
##cross-references EMBL:X59115
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY       #length 113 #molecular-weight 12508 #checksum 2993

Query Match      60.0%; Score 641; DB 5; Length 113;
Best Local Similarity 76.1%; Pred. No. 1.09e-65;
Matches 86; Conservative 13; Mismatches 11; Indels 3; Gaps 2;

Db 1 gilkpsqtlstcsfegfslstgmgvqgwgirgpgskglwlahiwdddkyynpslksql 60
      ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 30 ALVPTQTTLCTCTSGFSLSTSGMGVSWIRQPPGKLEWLAHIYDDDKRKNPSLSRL 89
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 tiskdtnqvfllkltvadtatycarraagymygyvfdwgagttvtv 113
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
Qy 90 TISKOTSRNQVLTMTNMDPVDATYYCARRETVE--Y-WYFDVMGRGTPTVT 139

RESULT 10
ENTRY   MHHUMC #type complete
TITLE   Ig heavy chain V-II region (McE) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     14-Nov-1983 #sequence_revision 22-Nov-1983 #text_change
              16-Feb-1996
ACCESSIONS A02092
REFERENCE  A02092
#authors   Gerber-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.;
              Erickson, B.W.; Litman, G.W.
#journal    J. Immunol. (1981) 126:1212-1216
#title      Molecular basis for the temperature-dependent insolubility of
              cryoglobulins. X. The amino acid sequence of the heavy
              chain variable region of McE.
#cross-references MUID:81118242
#accession  A02092
#molecule_type protein
##residues 1-125 ##label GER
#note       this chain was derived from a monoclonal IgM
              cryoimmunoglobulin
GENETICS
#gene       GDB:IGHV8
##cross-references GDB:G00-128-528
#map_position 14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS     pyrogutamic acid
FEATURE
1             #modified site pyroliodone carboxylic acid (Gln) #status
              experimental
SUMMARY       #length 125 #molecular-weight 13783 #checksum 9697

Query Match      59.9%; Score 640; DB 2; Length 125;
Best Local Similarity 73.6%; Pred. No. 1.47e-65;
Matches 92; Conservative 17; Mismatches 12; Indels 4; Gaps 3;

Db 1 qitlkegptlvkptetltcttctgfsfslstgmgvqgwgirgpgkalewlaflnwdndr 60
      |::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 QVTLRESGALVKPTQTTLCTCTSGFSLSTSGMGVSWIRQPPGKLEWLAHIYDDDKR 80
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ypslrirltgktstnqvlitmdpvdsgtyfcahrppwrfnlgfdxwggql 120
      |::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 YNPSLSRLTISKOTSRNQVLTMTNMDPVDATYYCARRET-VFY-WY--FDVMGRGTP 136
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 vtvas 125
      |||||
Qy 137 VTSS 141

RESULT 11
ENTRY   S26328 #type complete
TITLE   Ig heavy chain V region - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
              13-Jan-1995
ACCESSIONS S26328
REFERENCE  S26309
#authors   Stark, S.E.; Caton, A.J.
#journal    J. Exp. Med. (1991) 174:613-624
#title      Antibodies that are specific for a single amino acid
              interchange in a protein epitope use structurally distinct
              variable regions.
```



```
#accession S26328
##status preliminary
##molecule_type mRNA
##residues 1-116 ##label STA
##cross-references EMBL:X59198
SUMMARY
#length 116 #molecular-weight 12895 #checksum 8145
```

```
Query Match 58.0%; Score 619; DB 12; Length 116;
Best Local Similarity 71.6%; Pred. No. 8.49e-63;
Matches 83; Conservative 13; Mismatches 19; Indels 1; Gaps 1;
```

```
Db 2 eesggilqpsqtlsctsfsgfslstsmgvsqirpsqgkglewllhlwndskypnal 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 26 ESGPALVKPTQTTLTCTSGFSLTSGMGVSWIRPPGKGLEWLAHIYWDKRYNPSL 85
```

```
Db 62 krltiskdtnymqvflikianvdtatdyccarian-wdwyfdwsgagtvtvs 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 86 KSRLTISKOTSRNQVLTMTNMDPVDATYTCARRETVFWYFDWGRGTPVTSS 141
```

```
RESULT 12
ENTRY S26924 #type fragment
TITLE Ig heavy chain V region (DP-28) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
10-Nov-1995
ACCESSIONS S26924
REFERENCE S26885
authors Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.;
Winter, G.
#journal J. Mol. Biol. (1992) 227:776-798
#title The repertoire of human germline V(H) sequences reveals about
fifty groups of V(H) segments with different hypervariable
loops.
#accession S26924
##status preliminary
##molecule_type DNA
##residues 1-96 ##label TOM
##cross-references EMBL:212330
SUMMARY #length 96 #checksum 9197
```

```
Query Match 57.9%; Score 618; DB 11; Length 96;
Best Local Similarity 89.6%; Pred. No. 1.15e-62;
Matches 86; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
```

```
Db 1 qvtlresgalvkptqtlctctfsgfslstsmgvsqirpsqgkalewlaridwddkf 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 QVTRESGALVKPTQTTLTCTSGFSLTSGMGVSWIRPPGKGLEWLAHIYWDKDKR 80
```

```
Db 61 ystelkrltiskdtsknqvltmtndpvdttatyy 96
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 YNPSIKSRLTISKOTSRNQVLTMTNMDPVDATYTY 116
```

```
RESULT 13
ENTRY S26923 #type fragment
TITLE Ig heavy chain V region (DP-27) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
10-Nov-1995
ACCESSIONS S26923
REFERENCE S26885
authors Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.;
Winter, G.
```

```
#journal J. Mol. Biol. (1992) 227:776-798
#title The repertoire of human germline V(H) sequences reveals about
fifty groups of V(H) segments with different hypervariable
loops.
```

```
#accession S26923
##status preliminary
##molecule_type DNA
##residues 1-96 ##label TOM
##cross-references EMBL:212329
SUMMARY #length 96 #checksum 8452
```

```
Query Match 57.6%; Score 615; DB 11; Length 96;
Best Local Similarity 90.8%; Pred. No. 2.84e-62;
Matches 87; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

```
Db 1 qvtlresgalvkptqtlctctfsgfslstsmgvsqirpsqgkalewlaridwdddky 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 QVTRESGALVKPTQTTLTCTSGFSLTSGMGVSWIRPPGKGLEWLAHIYWDKDKR 80
```

```
Db 61 ystelkrltiskdtsknqvltmtndpvdttatyy 96
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 YNPSIKSRLTISKOTSRNQVLTMTNMDPVDATYTY 116
```

```
RESULT 14
ENTRY MHU000 #type complete
TITLE Ig heavy chain V-II region (Ou) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE #sequence_revision 13-Jul-1981 #text_change 16-Feb-1996
ACCESSIONS A02088
REFERENCE A02088
authors Putnam, F.W.; Florent, G.; Paul, C.; Shinoda, T.; Shimizu, A.
#journal Science (1973) 182:287-291
#title Complete amino acid sequence of the mu heavy chain of a human
IgM immunoglobulin.
#cross-references M01D:74005511
#accession A02088
##molecule_type protein
##residues 1-126 ##label PUT
COMMENT This mu chain was isolated from a Waldenström's macroglobulin.
GENETICS
#gene GDB:IGHV8
##cross-references GDB:G00-128-528
#map_position 14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS pyroglutamic acid
FEATURE
1 #modified_site pyrrolidone carboxylic acid (Gln) #status
experimental
22-97 #disulfide_bonds #status experimental
SUMMARY #length 126 #molecular-weight 14276 #checksum 4310
```

```
Query Match 56.8%; Score 607; DB 2; Length 126;
Best Local Similarity 69.3%; Pred. No. 3.19e-61;
Matches 88; Conservative 18; Mismatches 14; Indels 7; Gaps 5;
```

```
Db 1 qvtlresgalvkptqtlctctfsgfslstsmgvsqirpsqgkalewlarib-bbdkf 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 QVTRESGALVKPTQTTLTCTSGFSLTSGMGVSWIRPPGKGLEWLAHIYWDKDKR 80
```

```
Db 60 ywstelsrltiskdtsknqvltminpvdttatyyccarvmsmagyyyyymdvwkg 119
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 Y-YNPSIKSRLTISKOTSRNQVLTMTNMDPVDATYTCARR-ETV---FYWYF-DWVGGR 134
```


Mar 18 10:04

US-08-612-929-12.rpr

11

Db 120 ttvtvss 126

| | | | |

Qy 135 TPTVTSS 141

RESULT 15

ENTRY

GZHUCS #type complete

TITLE Ig heavy chain precursor V-II region (Cess) - human

ORGANISM #formal name Homo sapiens #common name nan

DATE 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change

16-Feb-1996

ACCESSIONS

A02090

REFERENCE

A02090

#authors Takahashi, N.; Noma, T.; Honjo, T.

#journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:5194-5198

#title Rearranged immunoglobulin heavy chain variable region (V-H)

pseudogene that deletes the second

complementarity-determining region.

#cross-references MUID:84298107

#accession A02090

#molecule_type mRNA

##residues 1-147 ##label TAK

##note the sequence was determined from the differentiated gene

##note the authors translated the codon GCG for residue 16 as

Trp, TGG for residue 142 as Met, TCA for residue 143

as Val, CCG for residue 144 as Thr, TCT for residue

145 as Val, CTT for residue 146 as Ser, and CAG for

residue 147 as Ser

GENETICS

#gene GDB:ICHV8

##cross-references GDB:G00-128-528

#map_position 14q32.33

#introns 15/3

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS immunoglobulin

FEATURE

1-19

20-147

#domain signal sequence #status predicted #label SIG\

#product Ig heavy chain V-II region (Cess) #status

predicted #label MAT\

#domain V segment #status predicted #label VAR\

#domain D segment #status predicted #label DIV\

#domain J segment #status predicted #label J01

#length 147 #molecular-weight 16323 #checksum 3237

SUMMARY

Query Match 56.6%; Score 605; DB 2; Length 147;

Best Local Similarity 75.0%; Pred. No. 5.83e-61;

Matches 84; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

Db 9 llltvsqvlsgvlnresgaivkathtlctfsglsvntgrmsvswirgpgkalew 68

||| : || :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 11 LLLMI-SGAYGVTLRESGALVKEQTLLCTSGESLSTSGVSWIRQPPCKGLEW 69

||| : ||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 69 lardwddkvygtetrltiketkngvklvtnmdpdtatyyccarmq 120

||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 70 LAHIYDDDKRYNPLKSRLLTISKDTSRQNVLTMTNMDPDTATYYCARRE 121

Search completed: Tue Mar 18 10:06:26 1997

Job time : 42 secs.

PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR N-PSDB; Q83493.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.4; 97pp; English.
CC A humanized antibody heavy chain variable region and signal
sequence is given in R70192. The signal sequence is also
CC provided in R70193. The CDR sequences of the construct are
CC identical to the native CDRs of mouse anti-human IL-4 MAb
CC 389 (R70198-200).
SQ Sequence 141 AA;

Query Match 100.0%; Score 1068; DB 13; Length 141;
Best Local Similarity 100.0%; Pred. No. 2.02e-79;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 mvltqtqvfiislllwisagayqvrtlresgpalkvptqtlitctfagfslstsgmgsuir 60
|||||
Qy 1 MVLTQTVFISLLWISAGAYQVTLRESGPALKVPTQTLITCTFSGFSLSTSGMGSWIR 60
|||||
Db 61 qpqgkglewlahiywdddkrynpkslkerltiskdtsrnqvltmtndpvdttatycarr 120
|||||
Qy 61 QPPGKGLEWLAHIYWDKRYNPSLKSRLTISKDTSRNQVVLTMNMDPVDVTATYTCARR 120
|||||
Db 121 etvfywyfdwgrgtpvtvss 141
Qy 121 ETVFYWFEDWGRGTPVTVSS 141
|||||

RESULT 2

ID R70191 standard; Protein; 141 AA.
AC R70191;
DT 20-SEP-1995 (first entry)
DE Chimeric antibody 389 heavy chain.
KW Chimeric antibody; antibody engineering; monoclonal antibody;
KW MAb; interleukin-4; IL-4; allergy.
OS Homo sapiens; Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Sig_peptide
FT Region 51..57
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 72..87
FT /label= CDR
FT /note= "complementarity determining region"
FT Peptide 120..130
FT /label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.
PD 16-MAR-1995.
PE 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR N-PSDB; Q83492.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions

PS Disclosure; Fig.3; 97pp; English.
CC A human/mouse chimeric antibody heavy chain variable region was
CC constructed (given in R70191) that contained the mouse anti-human
CC IL-4 MAb 389 variable region including 3 CDRs (R70198-200) and a
CC human antibody signal peptide (R70193). The construct was used
CC for humanized antibody production.
SQ Sequence 141 AA;

Query Match 88.3%; Score 943; DB 13; Length 141;
Best Local Similarity 86.5%; Pred. No. 9.59e-69;
Matches 122; Conservative 11; Mismatches 8; Indels 0; Gaps 0;
Db 1 mvltqtqvfiislllwisagayqvrtlresgpalkvptqtlitctfagfslstsgmgsuir 60
|||||
Qy 1 MVLTQTVFISLLWISAGAYQVTLRESGPALKVPTQTLITCTFSGFSLSTSGMGSWIR 60
|||||
Db 61 qpqgkglewlahiywdddkrynpkslkerltiskdtsrnqvltkitedtadtatycarr 120
|||||
Qy 61 QPPGKGLEWLAHIYWDKRYNPSLKSRLTISKDTSRNQVVLTMNMDPVDVTATYTCARR 120
|||||
Db 121 etvfywyfdwgrgtpvtvss 141
Qy 121 ETVFYWFEDWGRGTPVTVSS 141
|||||

RESULT 3

ID R70190 standard; Protein; 140 AA.
AC R70190;
DT 20-SEP-1995 (first entry)
DE Mouse MAb 389 heavy chain.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.
OS Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Sig_peptide
FT Region 50..56
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 71..86
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 119..129
FT /label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.
PD 16-MAR-1995.
PE 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR N-PSDB; Q83491.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.2; 97pp; English.
CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only
CC clone 389 was positive. cDNA clones of the 389 light and heavy
CC chains were cloned into pGEM7f+ and transformed into E. coli
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for

CC	antibody engineering.
SQ	Sequence 140 AA;

Query Match	75.6%	Score 807;	DB 13;	Length 140;
Best Local Similarity	81.3%;	Pred. No. 3.57e-57;		
Matches 109;	Conservative 12;	Mismatches 11;	Indels 2;	Gaps 1;

```

7 sllllivpaylvlsqvtlkespgilqpsqtlslctsfslstsgmgvswirpqsqgl 66
||||| || :|||||::: :||||:|||||:|||||:|||||:|||||
10 SLLLWISGAY--QGVTLRESGPALVKPQTTLTLCTSEFSLSLTCMGVSWIRQPPKGL 67

```

```

67 ewlahiywdddkrynpelkerltiekdtssnqvlkitesvtdadtatyycarretvfyw 126
   |||||
68 ewlahiywdddkrynpelksrlttskdtSRNQVLTWNMDPVDtATYYCARRETvfyw 127
   |||||

```

Db	127	fdvwgagttvtvss	140
Qv	128	FDVWGRGTPVTVSS	141

RESULT

ID	R92088	standard; Protein; 120 AA.
AC	R92088;	
DT	16-MAY-1996	(first entry)
DE	CDR-grafted anti-RSV F glycoprotein MEDI-493 VH.	
KW	Humanized antibody; chimeric antibody; antibody engineering;	
KK	monoclonal antibody; MAb 1129; respiratory syncytial virus; RSV;	
KK	heavy chain; complementarity determining region; CDR.	
OS	Chimeric Homo sapiens;	
OS	Chimeric Mus musculus.	
FT	Key	Location/Qualifiers
FT	Region	31..36
FT	/label= CDR1	
FT	Region	52..67
FT	/label= VDR2	
FT	Region	100..109
FT	/label= CDR3	
FT	/label= WO9605229-A1.	
PD	22-FEB-1996.	
PP	09-AUG-1995; U10053.	
PR	15-AUG-1994; US-290592.	
PA	(MEDI-) MEDIMMUNE INC.	
PI	Johnson JS;	
DR	WPI; 96-139646/14.	

New chimeric antibodies against respiratory syncytial virus - comprise human antibodies with CDR's from the variable heavy and light chains of a murine antibody
Example 7; Fig 7A-7B; 55pp; English.
A human-mouse chimeric antibody heavy chain has a human C₁ framework contg. complementarity determining region (CDR₁) from the variable heavy (VH) chain of a murine monoclonal antibody (MAB 1129) against respiratory syncytial virus (RSV) glycoprotein F antigenic site C. CDR₁ from MAB 1129 VH (see R92089) were grafted into the human Cor VH region (R92086) or Cess VH region (R92087) to produce CDR-grafted MED1-493 VH (R92088). A similar procedure was used to obtain CDR-grafted VL (R92091). The humanised antibody is used to treat RSV infection.
Sequence 120 AA.

Query Match 69.2%; Score 739; DB 16; Length 120;
Best Local Similarity 84.3%; Pred. No. 2.07e-51;
Matches 102; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

Db 1 qvtllresqpalvkptqtltltctfsqfslstsqmsvqwirqpqqkalewladlwddkdd 60

[illegible]

		61	y n p s l k e r l t i s k d t e a n q v l k v t n m d p a d t a y y c a r s - m l t n w y f d w g a g t t v t s	119
Db				
			:	:
				:
				:
		81	y n p s l k r l t i s k d t s r n o v l t w t n m d p v d t a y c a r r e t v y w f y d w g r c t p t v t s	140
Qy				

Db	120	s	120
		—	
Qy	141	S	141

RESULT

ID R66299 standard; Protein; 119 AA.
 ID AC R66299;
 DT 07-AUG-1995 (first entry)
 DE Human immunoglobulin variable heavy chain #5.
 KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pJB81; E.coli; mammalian.
 OS Homo sapiens.
 PN W09426895-A.
 PD 24-NOV-1994.
 PF 10-MAY-1993; J00603.
 PR 10-MAY-1993; WO-J00603.
 PA (NISB) JAPAN TOBACCO INC.
 PI Honjo T, Matsuda F;
 DR WPI; 95-006791/01.
 DR N-PSDB; Q78943.
 PT DNA fragment comprising human immunoglobulin Vh genes - for the
 PT production of human immunoglobulin in mammalian hosts
 PS Disclosure; Page 36-37; 130pp; Japanese.
 CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
 CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were
 CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;
 CC Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using primers
 CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The
 CC fragments cover a region of 800 Kb. The DNA fragments were isolated from
 CC high molecular weight DNA from human placenta. The DNA was partially
 CC digested with TaqI restriction enzyme. The fragments were separated by
 CC gel electrophoresis and 35-45 Kb fractions were collected. The fragments
 CC were ligated with ClaI-digested cosmid vector pJB81. The ligation
 CC products were in vitro packed and infected into E.coli 490A. The
 CC fragments were then subcloned by colony hybridisation. The Vh genes and
 CC the DNA fragments encoding them are useful in producing human
 CC immunoglobulin in mammalian hosts.
 SQ Sequence 119 AA;

Query Match 64.2%; Score 686; DB 12; Length 119;
Best Local Similarity 82.9%; Pred. No. 6.22e-47;
Matches 92; Conservative 14; Mismatches 4; Indels 1; Gaps 1;

```

9  lllt!pswvlsq!tlkesgptlvkptqtl!tctfsgfslstsgvgvgw!rqpbgkalew 68
   |||  ::  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
11 ll!w!sg-aygovt!r!sggalvkp!tot!t!tctfsgfslstsgm!cvsh!r!oppk!glew 69

```

Db 69 laliywnddkryspslksrltktdktsknqvlmtmndpvdttatyycahr 119
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
QV 70 LAHIYWDDBKRYNPSLKSRLTISKOTSRNQVLMTMNDPVDTTATYYCARR 120

RESULTS

ID	R38315 standard; Protein; 139 AA.
AC	R38315;
DT	04-DEC-1993 (first entry)

FT	/label= CDR2
FT	Domain 87..118
FT	/label= Framework region 3
FT	Domain 119...128
FT	/label= CDR3
FT	Domain 129..139
FN	/label= Framework region 4
PN	W09428159-A.
PD	08-DEC-1994.
PPI	30-MAY-1994; J00859.
PPF	31-MAY-1993; JP-129787.
PR	(CHUS) CHUGAI SEIYAKO KK.
PA	(CHUS) CHUGAI PHARM CO LTD.
PI	Hirata Y, Sato K, Tsuchiya M;
PPI	WPI; 95-022828/03.
DR	N-PDSB; Q75916.
DR	Antibody against IL-6 - useful for the therapy and treatment of
PT	IL-6 related disorders.
PS	Claim 21; Page 60-61; 82pp; Japanese.
CC	The sequence of the heavy chain variable region of a chimaeric antibody
CC	against human interleukin-6 (IL-6). The sequence is found on the plasmid
CC	HEL-RVH-SK2a. This vector and vectors Q75914, -5 and -7 express
CC	constructs encoding fragments of a chimaeric antibody to the human IL-6
CC	comprising (a) a light chain with (i) a variable region containing 3
CC	complementary determining regions (CDR) (R77201-3) inserted into
CC	several framework regions (FR) (r77204-7) and (ii) a human light chain
CC	constant region and (b) a heavy chain with (i) a variable region
CC	containing 3 CDR (R77212-4) inserted into an FR (r77215-8) and (ii) a
CC	human light chain constant region. The CDR region are derived from the
CC	mouse anti-human IL-6 antibody SK2. The FR of the light chain may be
CC	mouse derived (Q75898) or from the human antibody REI. The heavy chain FR
CC	may also be mouse derived (Q75899) or from the human antibody DAW. The
CC	antibodies can be used in the treatment of IL-6 related disorders. The
CC	antibodies are useful as they have low antigenicity due to the use of
CC	human derived sequences and low antigenicity mouse derived sequences.
SQ	Sequence 139 AA;
Query Match 61.8%; Score 660; DB 13; Length 139;	
Best Local Similarity 69.9%; Pred.No. 9.68e-45;	
Matches 95; Conservative 17; Mismatches 22; Indels 2; Gaps 2;	
Db	6 rvff-llavaprahsgvltresgpalvrptgtlrlctcfagfslstegmtvgwlrqpqge 64 :: : : : ::
Qy	6 QVFISLLIHLSGAYGVQLRESGPALVRPOTLTLCFSGFSLSTSGCWVSWIRPPGK 65 :
Db	65 alewhlahwnddkynypalkgrlavskdtknqvlsmtvpqgdttatycarmed-yd 123 : : : :
Qy	66 GLEWLAHLYWDKKRNPKSLSRILTISKDTSRNQVLITNDMPDVTATTCARRETFY 125 :
Db	124 eandwyggqlivrtves 139 :
Qy	126 WYFDVNGRGTPTVSS 141 :
RESULT	8
ID	R67659 standard; Protein; 139 AA.
AC	R67659;
DC	23-AUG-1995 (first entry)
DE	Anti-human IL-6 chimaeric Ab H chain V region in HEL-RVH-SK2b.
KW	Primer; PCR; amplif; kappa; light chain; variable region; mouse; human;
KX	interleukin; antibody; hybridoma; CDR; framework; constant region;
KW	heavy chain; disorder; antigenicity.
OS	Synthetic.
HF	Key
SH	Location/Qualifiers

PA (MEDI-) MEDIMUNE INC.
PI Johnson JS;
DR WPI; 96-139646/14.
PT New chimeric antibodies against respiratory syncytial virus -
PT comprise human antibodies with CDR's from the variable heavy and
PT light chains of a murine antibody
PS Example 7; Fig 7A-7B; 55pp; English.
CC A human-mouse chimeric antibody heavy chain has a human C₁
CC framework contg. complementarity determining region (CDRs) from the
CC variable heavy (VH) chain of a murine monoclonal antibody (Mab 1129)
CC against respiratory syncytial virus (RSV) glycoprotein F antigenic
CC site C. CDRs from Mab 1129 VH (see R92089) were grafted into the
CC human Cor VH region (R92086) or C₁ VH region (R92087) to produce
CC CDR-grafted MEDI-493 VH (R92088). A similar procedure was used to
CC obtain CDR-grafted VL (R92091). The humanised antibody is used to
CC treat RSV infection.
SQ Sequence 120 AA;

Query Match 61.0%; Score 652; DB 16; Length 120;
Best Local Similarity 72.7%; Pred. No. 4.57e-44;
Matches 88; Conservative 13; Mismatches 19; Indels 1; Gaps 1;
Db 1 qvelqesgpgilqpsqtltscsfsgslstsgmvgvwrqsgglewldkddk 60
||:||||:|:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Qy 21 QVTLRESGPAIVKPTQTTLTCTGFSGLSTSGMVGWIRQPPCKGLELAHIYWDKDR 80
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 61 ynpslkarltiaktsgnqvlkltgtdaktatyyccars-mitnwyfdwaggtvtvs 119
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Qy 81 YNPSLKSRLTISKOTSRSQVLTMTNMDPVDATYTCARRETVFYWFDWAGGTPVTVS 140

Db 120 s 120
Qy 141 S 141

RESULT 11
ID R88107 standard; Protein; 139 AA.
AC R88107;
DT 25-JUL-1996 (first entry)
DE Murine anti-Protein C MAb HPC-4 VH gamma protein.
KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
KW zymogen; cleavage; mouse; humanised antibody; variable region;
KW light chain; inhibition; anticoagulant; coagulation; tumour.
OS Mus musculus.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "signal peptide"
FT Peptide 20..139
FT /note= "mature peptide"
PN W09534652-A1.
PD 21-DEC-1995.
PF 09-JUN-1995; U07372.
PR 10-JUN-1994; US-259321.
PA (OKLA-) OKLAHOMA MED RES FOUND.
PI Eamon CT, Rezaie A;
DR WPI; 96-049681/05.
DR N-PSDB; T09299.
PT Calcium-binding monoclonal antibody immunoreactive with Protein C -
PT inhibits Protein C anticoagulant activation by
PT thrombin-thrombomodulin, e.g. for treating tumours
PS Claim 2; Page 29; 41pp; English.
CC This is the amino acid sequence of the heavy chain variable region from
CC the murine anti-protein C monoclonal antibody HPC-4 which recognises
CC the activation peptide region (R88106) of the heavy chain of protein C,

CC a vitamin K-dependent plasma protein zymogen. Protein C is converted to
CC activated protein C (APC) by cleavage between the Arg-Leu amino acid
CC contained within the activation peptide sequence. HPC-4 prevents protein
CC C activation to APC by binding to this region. The DNA sequences encoding
CC the variable regions of the heavy and light chains of the antibody
CC (T09299-302) were used to construct humanised antibodies using the PCR
CC primers T09303-9. The humanised antibodies are useful as inhibitors of
CC coagulation and can be used for the treatment of tumours by inhibiting
CC the anticoagulant activity of APC by preventing conversion of protein C
CC to APC.
SQ Sequence 139 AA;

Query Match 60.2%; Score 643; DB 17; Length 139;
Best Local Similarity 68.7%; Pred. No. 2.61e-43;
Matches 92; Conservative 19; Mismatches 20; Indels 3; Gaps 2;

Db 7 sfllliapaylsgvtlkesgpgilqpsqtltscsfsgslstsgmvgvwrqsgkgk 66
||:||||:|:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Qy 10 SLLLIWISGAY--GQVTLRESGPAIVKPTQTTLTCTGFSGLSTSGMVGWIRQPPCKGL 67
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 67 ewlahiwdddkrynpvlkerliiskdtsrkqvlkiasvtdaktatyyccvrmdd-yda 125
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Qy 68 EMLAHYWDKDRNPSLSKRLTISKOTSRSQVLTMTNMDPVDATYTCARRETVFYWY 127
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 126 mdywqggtvtvs 139
| ||:||||:|
Qy 128 FDMWGRGTPVTVS 141

RESULT 12
ID R54101 standard; Protein; 122 AA.
AC R54101;
DT 08-FEB-1995 (first entry)
DE Humanised MAb H-chain.
KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN.
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..37
FT /label= CDR1
FT Region 52..67
FT /label= CDR2
FT Region 100..111
FT /label= CDR3
PN J06141885-A.
PD 24-MAY-1994.
PF 05-NOV-1992; 322476.
PR 05-NOV-1992; JP-322476.
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
DR WPI; 94-205040/25.
DR N-PSDB; Q68709.
PT Recombinant anti-HIV monoclonal antibody - capable of
PT neutralising strains which can not be neutralised by anti-IIIB
PT and IIIMN antibodies
PS Disclosure; Page 13; 23pp; Japanese.
CC The sequences given in R54101-02 represent the heavy and light chains
CC respectively of the humanised monoclonal antibody (Mab) of the
CC invention. The antibody has the ability to neutralise human
CC immunodeficiency virus. The antibody is classified as IgG kappa and
CC has the sequence RIGPCR or RIVPCR in the principal neutralising
CC domain. The antibody may be used to neutralise the clinically
CC separate strains which cannot be neutralised by the neutralising
CC antibodies against IIIB and IIIMN strains.

Mar 18 10:05

US-08-612-929-12.rag

I5

Db 61 ynpvklrllskdtrskvfkiasvtdadtatycvrrmdd-ydamdywgqtsvtvs 119
||||| ||||| ||||| ||| :||| ||||| | | |||:|||||
Qy 81 YNPSLKSRLTTSKOTSRNQVLTMTNMDPVDTATYCARRETVFYWFDVWGRGTPVTS 140

Db 120 s 120

Qy 141 s 141

RESULT 15

ID R66318 standard; Protein; 119 AA.
AC R66318;
DT 03-AUG-1995 (first entry)
DE Human immunoglobulin variable heavy chain #24.
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW cosmid; placenta; vector; pJB81; E.coli; mammalian.
OS Homo sapiens.
PN W09426895-A.
PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PR 10-MAY-1993; W0-J00603.
PA (NLSB) JAPAN TOBACCO INC.
PI Honjo T, Matsuda F;
DR WPI; 95-006791/01.
DR N-PSDB; Q78964.
PT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts
PS Claim 35; Page 64-65; 130pp; Japanese.
CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were
CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;
CC Y6; Y24; 3-31; M84; M18 and M131, by PCR amplification using primers
CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The
CC fragments cover a region of 800 kb. The DNA fragments were isolated from
CC high molecular weight DNA from human placenta. The DNA was partially
CC digested with TagI restriction enzyme. The fragments were separated by
CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
CC were ligated with ClaI-digested cosmid vector pJB81. The ligation
CC products were in vitro packed and infected into E.coli 490A. The
CC fragments were then subcloned by colony hybridisation. The Vh genes and
CC the DNA fragments encoding them are useful in producing human
CC immunoglobulin in mammalian hosts.
SQ Sequence 119 AA;

Query Match 58.4%; Score 624; DB 12; Length 119;
Best Local Similarity 72.9%; Pred. No. 1.04e-41;
Matches 86; Conservative 16; Mismatches 15; Indels 1; Gaps 1;

Db 1 mdtlcytlilllttspwlsqsvlvtksqplvkvptetltlctctvsfslsnarmgvsuirq 60
::| : ||| : : ||||| ||||| ||||| ||||| : |||||
Qy 3 lqtqvffsllwmisc-aygqvltresgpalvkrptqtlrlctfsgfslstsgmgvswirq 61

Db 61 ppgkalewlahifendekystelkerltiskdskqvltatmdpvdtdatycar 118
||||| ||||| : ||| : ||||| ||||| : ||||| ||||| ||||| |||||
Qy 62 PPGKLEWLAHYWDDKRYNPSLKSRLTTSKOTSRNQVLTMTNMDPVDTATYCAR 119

Search completed: Tue Mar 18 10:07:12 1997
Job time : 29 secs.

WATERMAN

(TM)

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MPearch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:08:10 1997; MasPar time 208.67 Seconds
830.598 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-13
Description: (1-393) from US08612929.seq
Perfect Score: 393
N.A. Sequence: 1 ATGGGATGACCTCTATCAT.....CCAAAGTGGACATCAACGT 393
Comp: TACCTACTCGACAGTAGTA.....GGTTCACCTCTAGTTTGA

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

EST-STS
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98
99:EST99
EST-STS-TWO
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124
125:EST125 126:EST126 127:EST127 128:EST128 129:STS1

Database:

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7
136:STS8 137:STS9 138:STS10 139:ueEST 140:gnEST1
141:gnEST2 142:gnEST3 143:gnEST4 144:gnEST5 145:gnEST6
146:gnEST7 147:gnEST8 148:gnEST9 149:gnEST10 150:gnEST11
151:gnEST12 152:gnEST13 153:gnEST14 154:gnEST15
155:gnEST16 156:gnSTS 157:enEST1 158:enEST2 159:enEST3
160:enEST4 161:enEST5 162:enEST6 163:enEST7 164:enEST8
165:enEST9 166:enEST10 167:enEST11 168:enEST12
169:enEST13 170:enEST14 171:enEST15 172:enEST16
173:enSTS1 174:enSTS2

Statistics: Mean 9.913; Variance 1.988; scale 4.987

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	146	37.2	364	108	EST10049 Homo sapien	5.40e-234
2	114	29.0	210	91	y83c03.r1 Homo sapie	6.94e-170
3	112	28.5	393	108	EST100653 Homo sapien	6.33e-166
4	109	27.7	488	14	y148g05.r1 Homo sapie	5.33e-160
5	107	27.2	470	25	yu40h01.r1 Homo sapie	4.69e-156
6	100	25.4	463	91	yj82d09.r1 Homo sapie	2.58e-142
7	96	24.4	516	91	y142h11.r1 Homo sapie	1.65e-134
8	93	23.7	381	109	EST69430 Homo sapiens	1.12e-128
9	92	23.4	434	127	ye24e07.r1 Homo sapie	9.72e-127
10	92	23.4	503	79	yh57e08.r1 Homo sapie	9.72e-127
11	91	23.2	279	109	EST89211 Homo sapiens	8.40e-125
12	90	22.9	383	109	EST99871 Homo sapiens	7.21e-123
13	89	22.6	467	14	y165d05.r1 Homo sapie	6.16e-121
14	84	21.4	438	90	y122f09.r1 Homo sapie	2.54e-111
15	83	21.1	390	20	yp22b04.r1 Homo sapie	2.09e-109
16	79	20.1	397	85	yj55c03.r1 Homo sapie	8.84e-102
17	78	19.8	261	85	yj54h03.r1 Homo sapie	7.00e-100
18	78	19.8	383	108	EST19007 Homo sapiens	7.00e-100
19	76	19.3	387	92	yj81e03.r1 Homo sapie	4.28e-96
20	76	19.3	395	109	EST69384 Homo sapiens	4.28e-96
21	75	19.1	332	109	EST77181 Homo sapiens	3.31e-94
22	74	18.8	366	14	y165f06.r1 Homo sapie	2.54e-92
23	72	18.3	359	108	EST100475 Homo sapien	1.45e-88
24	72	18.3	408	96	yp12g07.r1 Homo sapie	1.42e-88
25	71	18.1	359	14	y161g07.r1 Homo sapie	1.08e-86
26	71	18.1	367	117	yc01b07.r1 Homo sapie	1.08e-86
27	70	17.8	132	118	yb98g11.r1 Homo sapie	7.98e-85
28	70	17.8	438	91	yj82d12.r1 Homo sapie	7.98e-85
29	69	17.6	570	92	yj81d08.r1 Homo sapie	5.83e-83
30	68	17.3	390	14	y113f10.r1 Homo sapie	4.22e-81
31	67	17.0	430	27	yr86f06.r1 Homo sapie	3.03e-79
32	65	16.5	405	85	yj65f10.r1 Homo sapie	1.50e-75
33	65	16.5	451	126	ye15d10.r1 Homo sapie	1.50e-75
34	65	16.5	464	118	yc16e03.r1 Homo sapie	1.50e-75
35	64	16.3	203	18	yo53d07.r1 Homo sapie	1.04e-73
36	63	16.0	213	14	y147d10.r1 Homo sapie	7.14e-72
37	62	15.8	357	109	EST69270 Homo sapiens	4.83e-70
38	62	15.8	445	85	yj66c09.r1 Homo sapie	4.83e-70
39	59	15.0	257	86	yj71a07.r1 Homo sapie	1.39e-64
40	59	15.0	288	108	EST100107 Homo sapien	1.39e-64
41	58	14.8	141	18	y167h12.r1 Homo sapie	8.91e-63
42	57	14.5	443	85	yj56g05.r1 Homo sapie	5.64e-61

43 55 14.0 288 108 T77721 EST13641 Homo sapiens 2.16e-57
 44 55 14.0 385 14 H26475 yL51q05.r1 Homo sapie 2.16e-57
 45 55 14.0 399 19 H44798 yp24a10.r1 Homo sapie 2.16e-57

ALIGNMENTS

RESULT 1
 LOCUS T77579 364 bp mRNA EST 06-SEP-1995
 DEFINITION EST100049 Homo sapiens cDNA 5' end similar to immunoglobulin light chain, V region (HT:3078).
 ACCESSION T77579
 NID g609677
 KEYWORDS EST.
 SOURCE human primer=M13 Reverse Library=Human Pancreas.
 ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 364)

ADAMS, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., Kelley, J.M., Klinek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bedharik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
 Initial Assessment of Human Gene Diversity and Expression Patterns
 Based Upon 52 Million Basepairs of cDNA Sequence
 Unpublished (1995)

CONTACT: Venter, J.C.
 The Institute for Genomic Research
 932 Clopper Rd, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).
 FEATURES
 source Location/Qualifiers
 1..364
 /organism="Homo sapiens"
 /note="human"
 <1..>364

BASE COUNT 80 a 98 c 87 g 93 t 6 others
 ORIGIN
 Query Match 37.2%; Score 146; DB 108; Length 364;
 Best Local Similarity 79.4%; Pred. No. 5.40e-234;
 Matches 239; Conservative 0; Mismatches 55; Indels 7; Gaps 6;

Db 40 gdtgctacgggagcaccgtgatgaccagctccagactccctggtgtctctgggc 99

Qy 46 GGTGTCCACTCCGATATCGTATGACCCAGCTCCAGACTCGTGTCTCTGGGC 105
 Db 100 gagagggccaccatcaactgcagggtccagccagagtggttttagacagctccacaatacg 159
 Qy 106 GAGAGGGCCACCATCAACTGCCAAGGCTCCCAAAGCTGTGATTAT-GATGGTG--ATAGT 162

Db 160 aactactagcttggtaccactgaaccaggagcagctcctaagctgctcattactgg 219
 Qy 163 TA-FA-TGAACCT-GGTATACAGAGAAACCCGGGAGGCTCTCTAAGTTCTCATTTACGCT 219
 Db 220 gnatctaccgggaatccgggtccctgaccgattcagtgccagcggtctcnggacana 279
 Qy 220 GCATCCAATCTAGAACTCTGGGTACCTCACCGATTCACTGGCAGCGGCTCT-GGGACAGA 278
 Db 280 ttctantctcaacctcagcgctcaggttgagatgagtgaggtttattactgtcagca 339
 Qy 279 TTTCACTCTCCACATCAGCAGGCTCGAGGCTGAGAGTGGCAGGTACTACTGTCTCAGCA 338
 Db 340 a 340
 Qy 339 A 339

RESULT 2
 LOCUS R69482 210 bp mRNA EST 01-JUN-1995
 DEFINITION yJ83c03.r1 Homo sapiens cDNA clone 155332 5' similar to gb:L09085 IG KAPPA CHAIN V-I REGION (HUMAN);.

ACCESSION R69482
 NID g842999
 KEYWORDS EST.

SOURCE human clone=155332 library=Soares breast 2NbHBst vector=pf7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite=Not I Rsite2=Eco RI Adult female.
 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTCAAGTGGGAGCGGCCCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pf7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 210)

REFERENCE Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1

Qy 389 AACG 392

RESULT 6 R69532 463 bp mRNA EST 01-JUN-1995
LOCUS yj32d09.r1 Homo sapiens cDNA clone 155249 5' similar to gb:M63438
DEFINITION IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);.
ACCESSION R69532
NID g843049
KEYWORDS EST.
SOURCE human clones-155249 library=Soares breast 2NbHBst vector=pT73D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13RP1 Reitel=Not I Reite2=Eco RI Adult female.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTCAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 230. Library constructed by Bento
Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 463)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 394
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source
1..463
/organism="Homo sapiens"
/clone="155249"
/notes="human"

BASE COUNT 103 a 125 c 115 g 114 t 6 others
ORIGIN

Query Match 25.4%; Score 100; DB 91; Length 463;
Best Local Similarity 78.3%; Pred. No. 2.58e-142;
Matches 137; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Db 171 ctggtaccagcaaacctggccaggtcccagntctctcatctatgtgtgaccaccag 230
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 171 CTGGTATCAGCAGAAACCCGGGAGCCCTCTAGTTCGTCATTTCGTCATCCACT 230

Db 231 ggcactggatccagcaggttcagtgccagtggtggtgggacagaggtctttctcac 290
| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Qy 231 AGAATCTGGGGTACCTGACCGATTAGTGGCGCCGGGCTGGGACAGATTTCTACT 290

Db 291 catcagcagctgcagcctgaagatttgcagtttattattgttcagcaataat 345
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 291 CATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTATACTACTGTCTCAGCAAGTAA 345

RESULT 7 R67559 516 bp mRNA EST 30-MAY-1995
LOCUS y142h11.r1 Homo sapiens cDNA clone 141957 5' similar to
DEFINITION gb:X00965_cds1 IG KAPPA CHAIN PRECURSOR V-I REGION (HUMAN);.
ACCESSION R67559
NID g840197
KEYWORDS EST.
SOURCE human clones-141957 library=Soares placenta Nb2HP vector=pT73D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13RP1 Reitel=Not I Reite2=Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5'
AACTGAGAGTAATCCGGCGCGCAGCAATTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 516)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 313
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source
1..516
/organism="Homo sapiens"
/clone="141957"
/notes="human"

BASE COUNT 118 a 137 c 120 g 134 t 7 others
ORIGIN

Query Match 24.4%; Score 96; DB 91; Length 516;
Best Local Similarity 73.3%; Pred. No. 1.65e-134;
Matches 173; Conservative 0; Mismatches 60; Indels 3; Gaps 2;

Db 170 acctatttaattggtatcatcaaaaaccagggaagccctaaactctatccaggct 229
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 160 AGTTATATGAATGCTATCAGCAAAACCCGGGAGGCTCTTAAGTTCCTATTTCAGCT 219

and M. Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

REFERENCE 1 (bases 1 to 390)
AUTHORS Hillier, L.; Clark, N.

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasaki, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Tel: 314 286 1800

Fax: 314 286 1810

Fax: 514 200 1010
Email: est@watson.wustl.edu

Small, estewatson.wustl.edu
High quality sequence stons: 19A

High quality sequence stops: 11
Source: IMAGE Consortium, 11/11

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

FEATURES

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1..390
/organism="Homo sapiens"
/clone="188143"
/note="human"
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BASE COUNT	93 a	81 c	99 g	107 t	10 others
ORIGIN					

Query Match 21.1%; Score 83; DB 20; Length 390;
Best Local Similarity 73.9%; Pred. No. 2.09e-109;
Matches 136; Conservative 0; Mismatches 47; Indels 1; Gaps 1;

Ddb

5 t g a c c t g g t t g g c c t g g t a t c a g c a g a a c c a g g a a a a g c c c t a g c c t c c t a a t c t a 64
||||| | ||| ||||| ||||| ||||| | | |||| | ||| |||

Oy

156 T G A T A G T T A T A T G A C T G T P A T C A C A G A A A C C G G G C A G C C T F C C T A G T T G C T C A T T A 215

65 **tgaggcatctactttagaagatgggggtcccatcaagattcagcggcagtggtatctggga** 124
 216 **CGGTGCATCCCAATCTAGAACTGGGGTACTGACCGATTAGTGGCAGCGGGTCTTGGGA** 274

125 ccgaattcaccctcaccatcagcagccgcgacctgatgatttgcactttactgcc 184
| | | | | | | | | | | | | | | | | | | | | |
275 CAGATTTCACTCTCACCACAGCGAGCCGCGGGTGAAGATGGCGGACTACTACTGTC 334

185 *acca* 188

105	agca	100
106		
QV	335 AGCA	338

Search completed: Wed Mar 19 08:11:47 1997
Job time : 217 secs.

WATERMAN

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:06:58 1997; MasPar time 41.85 Seconds
819.095 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-13

Description: (1-393) from US08612929.seq

Perfect Score: 393

N.A. Sequence: 1 ATGGGATGAGCTCTATCAT.....CCAAAGTGAGATCAACCT 393
Comp: TACCCTACTCGACATAGTA.....GGTTCACCTCTAGTTGCA

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 8.325; Variance 5.169; scale 1.611

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	389	99.0	393	14	Q83520 Humanized antibody 3B	7.09e-242
2	389	99.0	393	14	Q73986 Humanized antibody 3B	7.09e-242
3	223	56.7	339	10	Q44828 Humanised light chain	9.30e-129
4	221	56.2	339	10	Q44827 Humanised light chain	2.08e-127
5	218	55.5	5703	22	T34110 Anti-IL-5 humanised a	2.21e-125
6	215	54.7	396	14	Q83490 Mouse MAb 3B9 light c	2.33e-123
7	213	54.2	339	22	T34094 Humanised 2B6 antibod	5.20e-122
8	207	52.7	333	12	Q70372 Anti HIV antibody lig	5.75e-118

	9	10	207	52.7	333	11	Q65554	Mouse anti-HIV mu5.5	5.75e-118
1	205	52.2	393	6	Q36609		Anti-CD4 antibody MT	1.28e-116	
11	205	52.2	619	1	N80498		Encodes V region of L	1.28e-116	
12	205	52.2	1088	10	Q36735		Sequence of Hum4VL ge	1.28e-116	
13	205	52.2	1373	1	N80941		Encodes Vchi region o	1.28e-116	
14	202	51.4	900	1	Q04039		Anti-Leu 3a light cha	1.34e-114	
15	200	50.9	733	4	Q25658		Mouse 0.5beta anti-HI	2.96e-113	
16	200	50.9	780	1	N90495		A V chi region gene.	2.96e-113	
17	200	50.9	1028	7	Q45606		Sequence of pATDFLAG	2.96e-113	
18	200	50.9	1330	7	Q45605		Sequence of Hum4 VL-C	2.96e-113	
19	200	50.9	1359	7	Q45607		Sequence of pSC49FLAG	2.96e-113	
20	198	50.4	334	1	N90492		Gene fragment of immu	6.54e-112	
21	198	50.4	400	1	N80499		Encodes V region of L	6.54e-112	
22	198	50.4	1361	10	Q36740		Sequence of plasmid p	6.54e-112	
23	197	50.1	1097	7	Q45602		Sequence of the Hum4	3.08e-111	
24	195	49.6	342	6	Q33032		MAb GAH variable regi	6.80e-110	
25	194	49.4	7305	18	T15933		Anti-IgE VL expressio	3.19e-109	
26	191	48.6	336	2	Q12684		Murine IB4 light chai	3.30e-107	
27	191	48.6	360	12	Q71718		Monoclonal antibody L	3.30e-107	
28	190	48.3	334	9	Q55002		Murine anti-CD18 Ab 6	1.55e-106	
29	187	47.6	393	5	Q30757		p64-k4.	1.60e-104	
30	187	47.6	836	7	Q45604		Sequence of single ch	1.60e-104	
31	185	47.1	333	9	Q55917		Humanised light chain	3.50e-103	
32	185	47.1	407	4	Q26047		V-region of L-chain o	3.50e-103	
33	184	46.8	334	11	Q73749		Light chain variable	1.64e-102	
34	183	46.6	333	14	Q82818		Murine NM-01 variable	7.67e-102	
35	183	46.6	336	16	Q96285		Human IgE receptor-bi	7.67e-102	
36	179	45.5	333	12	Q70376		Chimeric anti HIV ant	3.66e-99	
37	179	45.5	333	11	Q85558		Mouse-human chimeric	3.66e-99	
38	179	45.5	336	16	Q96283		Human IgE receptor-bi	3.66e-99	
39	179	45.5	783	17	T08490		Anti-G5 MAb N19/8 scF	3.66e-99	
40	177	45.0	363	10	Q56686		Sequence of the monoc	7.99e-98	
41	176	44.8	336	2	Q10379		Chimeric MAb 9.2.27 l	3.73e-97	
42	176	44.8	451	1	Q04694		Light chain variable	3.73e-97	
43	176	44.8	717	18	T04019		Anti-EGFR single chai	3.73e-97	
44	175	44.5	363	10	Q56688		Sequence of the monoc	1.74e-96	
45	173	44.0	363	6	Q37472		Sequence encoding the	3.78e-95	

ALIGNMENTS

RESULT	1
ID	Q83520 standard; cDNA; 393 BP.
AC	Q83520;
DT	20-SEP-1995 (first entry)
DE	Humanized antibody 3B9 light chain.
KW	Humanized antibody; antibody engineering; monoclonal antibody;
KW	MAb; interleukin-4; IL-4; allergy; ds.
OS	Homo sapiens.
FH	Key
FT	Key
FT	CDS
FT	/*tag= a
PN	W09507301-A.
PD	16-MAR-1995.
PF	07-SEP-1994; U10308.
PR	07-SEP-1993; US-117366.
PR	14-OCT-1993; US-136783.
PA	(SMIK) SMITHKLINE BEECHAM CORP.
PA	(SMIK) SMITHKLINE BEECHAM PLC.
PI	Gross MS, Holmes SD, Sylvester DR;
DR	WPI; 95-123387/16.
DR	P-PSDB; R70202.
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions
 PS Disclosure; Page 71-72; 9pp; English.
 CC A humanized antibody light chain variable region and signal
 CC sequence is given in R75355. The signal sequence is also
 CC provided in R70194. The sequences of the 3 CDRs
 CC are identical to mouse anti-human IL-4 MAb 3B9 light chain
 CC CDRs (given in R70195-97) .
 SQ Sequence 393 BP; 98 C; 105 G; 93 T;

Query Match 99.0%; Score 389; DB 14; Length 393;
Best Local Similarity 99.5%; Pred. No. 7.09e-242;
Matches 391; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

[illegible]

Db 121 aactgcaaggctcccaagtgttgattatgatgggtgatagttatatgaactggtatcag 180

Db 181 cagaacccggcagcctcctaagttgctcattacgctgcacccaatctagaatctggg 240

Qy 181 CAGAAACCCGGGCAGCCCTCCTAAGTTGCTCATTTACGCTGCATCCAAATCTAGAATCTGGG 240

Qy 241 GTACCTGACCGATTTCAGTGGCAGCGGGTCTGGACAGATTTCACTCTCACCATCAGCAGC 300

Db 301 ctgcaggctgaagatgtggcagtatatactactgtcagcaagtaatgaggatcctccgacg 360

Db 361 ttcggcgaggagaccaaagtggagatcaaacgt 393

Qy 361 TTCGCGGAGGACCAAGCTGGAGATCAACGT 393

RESULT	2
ID	Q73986 standard; cDNA; 393 BP.

DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain.

KW MAb; interleukin-4; IL-4; allergy; ds.
 OS Homo sapiens.

FT	CDS	1.393
FT	/*tag= a	
FT	cin rest/de	1.60

FT	mat_peptide	61..393
FT	mat_peptide	61..393

PN W0950/301-A.
PD 16-MAR-1995.
PF 07-SEP-1994: 1110308.

PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.

FA (SMITH) SMITHLINE BEECHAM FLO.

PI	Cross MS, Holmes SD, Sylvester DR;
DR	WPI; 95-123387/16.
DR	p-PSDB; R75355.
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT	from high affinity mAbs - useful in treatment of IL-4-mediated
PT	and IGE-mediated allergic conditions
PS	Disclosure; Fig.5; 97pp; English.
CC	A humanized antibody light chain variable region and signal
CC	sequence is given in R75355. The signal sequence is also
CC	provided in R70194. The sequences of the first 2 CDRs
CC	are identical to mouse anti-human IL-4 MAb 389 light chain
CC	CDRs (given in R70195-96), but the third (R70201) differs
CC	by a single amino acid from the native mouse CDR (R70197).
SO	Sequence 393 BP; 97 A; 96 C; 108 G; 92 T.

Query Match	99.0%;	Score 389;	DB 14;	Length 393;
Best Local Similarity	99.5%;	Pred. No. 7.09e-242;		
Matches	391;	Conservative	0;	Mismatches 2;
		Indels	0;	Gaps 0;

Db 1 atgggatggagctgtatcatcctcttcttggtagcaacagctacaggtgtccactccgat 60

QY 1 ATGGGATGGAGGATGATCATCCCTCTTCCTGGTACCTACATCAGCTACAGGCTGCTCCAGTCCGCT 30

Dbb 61 atcgtgaatgaccagactctccagactcactagctatctctctgtggcagagagggccaccacc 120

Qy 61 ATCGTGATGACCGAGTCTCCAGACTCGCTAGCTGTCTCTGGCGAGAGGGCCACCATC 120

121 AACTGCAAGGCGCTCCCAACTGTTGATTATGATGGTGATAGTTATATGCAACTGGTATTCAG 180

Db 181 cagaaacccggcagccctcctaagttgctcattacgtgcacccaatctagaatctggg 240

Db 241 gtacctgaccgattcagtggcagcgggtctggacagatttcactctcaccatcagcagc 300

241 GTACCTGACCGATTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCAATCAGCAGC 300

QY 301 CTGCAGCTGAACATGTGCAGTATCTACTCTCAGCAAGTAATGAGGATCTCTCCGAGG 360

D_b 361 ttccggaggagaccacgaatgagatcaaacgt 393
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O_a 361 TTCCGCCACGACCAAGATCCTCAAACT 393

ID Q44828 standard; DNA; 339 BP.
AC Q44828;

DE Humanised light chain variable region PfHzLc1-2.
KW Monoclonal antibody; Plasmodium falciparum; CDR;
173 complementarity determining region; fusion protein.

KW	murine; variable; light; heavy; chain; malaria; ds.
OS	Synthetic.
PU	Reaction/Qualifiers

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FT /*tag= a
FT /!bol= cnp!
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FT misc feature 166..186
FT /*tag= b
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Qy	298	AGCCTCGAGGTGAAGATCGCGATATCTACTCTAGCAAAAGTAATGAGGATCCTCCG	357
Db	849	acattcgctgaggcgaccacaacctggaaatcaagcgt	884
Qy	358	AGGTTTCGGCGAGGACCAAGGTGAGATCAAAAGCT	393

RESULT 15

ID	Q25658	standard; DNA; 733 BP.
AC	Q25658;	
DT	08-DEC-1992	(first entry)
DE	Mouse 0.5beta anti-HIV antibody Light chain.	
OS	Heavy; light; CDR; HIV; AIDS; FR; framework region; ds.	
KW	Synthetic.	
FH	Key	Location/Qualifiers
FT	primer_bind	
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FT	/note= "binding site for the primer	
FT	represented Q30550"	
FT	primer_bind	709..730
FT	/*tag= b	
FT	/note= "binding site for the primer	
FT	represented Q30551"	
PN	J04141095-A.	
PD	14-MAY-1992.	
PF	02-OCT-1990; 266091.	
PR	02-OCT-1990; JP-266091.	
PA	(KAGA) KAGAKU OYOBI KESSEI RYOHU.	
DR	WPI; 92-212765/26.	
PT	New recombinant modified anti-HIV antibodies - comprise human x	
PT	mouse modified antibody H and L chains	
PS	Discloure; Fig 4; 15pp; Japanese.	
CC	Recombinant modified anti-HIV antibodies comprise framework regions	
CC	derived from human antibody and CDRs derived from mouse monoclonal	
CC	antibody 0.5beta. The anti-HIV modified antibody can be used for	
CC	the prophylaxis and treatment of AIDS.	
SQ	Sequence	733 BP; 194 A; 162 C; 161 G; 216 T;

Query Match 50.9%; Score 200; DB 4; Length 733;
Best Local Similarity 79.8%; Pred. No. 2.96e-113;
Matches 268; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Db	382	gacatttgctgaccacaatctccagctcttggctgctctctaggcagagggccacc	441
Qy	58	CATATCGTCATGACCCAGTCTCCAGACTCGCTAGCTGTCTCTGGCGGAGAGGGCCACC	117
Db	442	atctctgccaaggccagccaaagtgttgattgatggtgatagttatgaactgggtac	501
Qy	118	ATCACTGCGAGGCGCTCCCAAGTGTTCATTATGATGGTGATAGTTATATGAACACTGGTAT	177
Db	502	caacagaaacaggacagcagccaccaactcctcatctatgctgcataccaatctagaatct	561
Qy	178	CACAGAAACCGGGCAGCGCTCCTAAGTGTGCTCATTTACGCTGCATCCAACTAGAAATCT	237
Db	562	gggattccagccaggttttagtgagcgtgggtctagacagaacttcacccctcaacatccat	621
Qy	238	GGGTACCTGACCGATTCACTGGCGAGGGGTCTGGGACAGATTTCACTCTCACCATCAGC	297
Db	622	cctgtggagaggaggatgctgcaacctattactgcagcaaatgaatgaggatccattc	681
Qy	298	AGCCTGCAGGCTGAGATCTGGCAGCTATACTACTCTCAGCAAAAGTAATGAGGATCTCCG	357
Db	682	acgttcggctcggggacaaagtctggaataaaaact	717

QY 358 AGGTTGGCGGAGCGGACCAAGGTGGAGATCAACGT 393

Search completed: Wed Mar 19 08:07:45 1997
Job time : 47 secs.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1
Locus	MMU07207
DEFINITION	Mus musculus clone 31 anti-C5a Ig light chain V region mRNA, partial cds.
ACCESSION	U07207
NID	g459212
KEYWORDS	.
SOURCE	mouse.
ORGANISM	Mus musculus
	333 bp
	mRNA
	ROD
	08-OCT-1994

REFERENCE 1 (bases 1 to 333)
AUTHORS Ames, R.S., Tornetta, M.A., Jones, C.S. and Teui, P.
TITLE Isolation of neutralizing anti-C5a monoclonal antibodies from a filamentous phage monovalent Fab display library [published erratum appears in J Immunol 1994 Jul 15;153(2):910]
JOURNAL J. Immunol. 152 (9), 4572-4581 (1994)
MEDLINE 94209678
REFERENCE 2 (bases 1 to 333)
AUTHORS Ames, R.S.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-1994) Robert S. Ames, Molecular Genetics, SmithKline Beecham Pharmaceuticals, 709 Swedeland Road, PO Box 1539, King of Prussia, PA 19406-0939, USA

FEATURES
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/clone="31"
/clone_lib="Combinatorial Fab library constructed in phage display vector pKTFabGene3"
/organism="Mus musculus"
/tissue type="spleen"
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GOPPKLLIYAASNLSEGPAPFSGSRDTFLINPVETDDVATYYCQSHEDPYTF
GGGTKLEIK"

BASE COUNT 89 a 86 c 81 g 77 t
ORIGIN

Query Match 53.2%; Score 209; DB 64; Length 333;
Best Local Similarity 82.2%; Pred. No. 9.26e-174;
Matches 267; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Db 9 gatgaccagctccagctctttgtgtctctaggcagagggccaccatctctg 68
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Qy 66 GATGACCAAGTCTCCAGACTCGCTAGCTGTGTCTCTGGCGAGCGCCACCACATCACTG 125
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Db 69 caaggccagccaaagtgtgaattatgatgtgatgtattatgaactgttaccacagaa 128
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Qy 126 CAAGGCCCTCCAAAGCTTGTATTATGCTGTGATGTTATGAACTGGTATCAGCAGAA 185
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Db 129 accaggacagcccccacccatctcatctatgtgtcatccaaacctagaactctggatccc 188
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Qy 186 ACCGGGGCAGCCTCTAAGTTGCTCTATTAGCGTGCATCCCAATCTAGAACTCTGGGGTACC 245
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Db 189 tgccaggttcagtgccagtggtgttagacagacttcacctcaccattaatcctgtgga 248
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Qy 246 TGACCGGATTGCTGGCAGCGGGCTGGGACAGATTTTCACTCTCACCATCAGCAGCCTGCA 305
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Db 249 gactgatgtgtgaacctattactgtcagcaaaagtcaggtacgtacctacacgttcgg 308
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Qy 306 GCGTGAAGATGTGGCAGTACTACTGTGCAGCAAGTAATAGGATTCCTCGAGGTTCGG 365
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Db 309 aggggggaccagctggaataaaa 333
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Qy 366 CGGAGGACCAAGGTCGAGATCAAA 390

RESULT 2
LOCUS MUSL93IGKV 363 bp mRNA ROD 29-OCT-1994
DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial

cds.
ACCESSION M97879
NID g198681
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.

ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 363)
AUTHORS Lohman, K.L., Buck, D.W., Carrillo, M.A. and Kennedy, R.C.

TITLE Characterization of murine monoclonal anti-CD4; epitope recognition, idiotope expression, and variable gene sequence
JOURNAL Unpublished (1992)

FEATURES
Location/Qualifiers
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/standard_name="L93; monoclonal antibody (CD4 antigen specificity)"
/map="6"

BASE COUNT 94 a 97 c 89 g 83 t
ORIGIN

Query Match 53.2%; Score 209; DB 67; Length 363;
Best Local Similarity 81.2%; Pred. No. 9.26e-174;
Matches 272; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Db 1 gacattgtgtaccacaaatccagctcttggctgtgtctctaggcagagggccacc 60
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Qy 58 GATATCGTATGACCCAGTCTCCAGACTCGCTAGCTGTGTCTCTGGCGAGAGGCCACC 117
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Db 61 atctctgtcaaggccagccaaagtgttgattgatgtgatgtatataaactggtac 120
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Qy 118 ATCAACTGCAGAGGCTCCCAAGTCTTGATGATGATGATGATGATGATGATGATGATGAT 177
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Db 121 caacagaaaccaggacagtcacccaaactctcatctatgtgtcatccaatctagaatct 180
|||||

Qy 178 CAGCAGAAACCCGGGAGGCTCTTAAGTCTCTCATTTACGCTGCATCCATCTAGANTCT 237
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Db 181 gggatccacagccaggtttagtgagtggtgtggagcagacttcacctcaacatccat 240
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Qy 238 GGGGTACTTCACCGATTACCTGGCAGCGGGCTCTGGGACAGATTTCACTCTCACCACAC 297
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Db 241 cctgtggaggaggaggtgctgcaacctattactgtcagcaagcaaatcaggatctccg 300
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Qy 298 AGCCTGCGGCTGAAGATGTGGCAGTACTACTGTGCGAAGTAATAGGATCTCTCCG 357
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Db 301 acgttcggtggggcaccagctggaatcaaacg 335
|||||

Qy 358 AGGTTCCGGCGAGGACCAAGGTGGAGATCAACG 392

RESULT 3
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).
ACCESSION X65091
NID g52288

KEYWORDS	ig light chain; VJ domain.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcophytii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 336)
AUTHORS	Weissenhorn,W.
TITLE	Direct Submission
JOURNAL	Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W. Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000 Muenchen 2, FRG
REFERENCE	2 (bases 1 to 336)
AUTHORS	Weissenhorn,W., Riethmueller,G., Weiss,E.M. and Rieber,E.P.
JOURNAL	Structural characterization of CD4 mAb
FEATURES	Unpublished
source	Location/Qualifiers
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	/product="alpha CD4 mAb immunoglobulin light chain VJ region"
	/db_xref="PID:g52289"
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BASE COUNT	89 a 90 c 81 g 76 t
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Query Match	52.9%; Score 208; DB 64; Length 336;
Best Local Similarity	81.0%; Pred. No. 9.32e-173;
Matches	272; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
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Db	61 atctctgcaaggcagccaaagtcttgattgatgdtgatgttatgaactggtac 120
Qy	118 ATCACTGCAAGGCTCCAAAGCTTGATTATGATGCTGATAGTATATGCACTGGTAT 177
Db	121 caacgaaacaggacagccaccacaaactcctcatctatgtctgcaccaatctagaatct 180
Qy	178 CAGGAGAAACCCGGCGCCTCTAGTGTGCTATTACGCTGCATCAATCTAGAACTCT 237
Db	181 gggatccacaggcagatttagtggcagtggttcgggagcagacttcacccctcaacatccat 240
Qy	238 GGGGTACTTCAGCGATTTCAGTGGCAGCGGGCTCTGGGACAGATTTCACTCTCACAATCAGC 297
Db	241 cctgtgaggaggagatgctgcaacctattactgtcagcaaatagtgaggaatcctccg 300
Qy	298 AGCGTCGAGGCTCAGAGTGTGGCAGTGTACTGTCTGACAGAAAGTAATGAGGATCTCCG 357
Db	301 agcttcggtgagcaccacagctggaaatcaaacgt 336
Qy	358 AGGTTCCGGCGAGGACCAAGGTTGGAGATCAAACTG 393

[illegible]


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Qy 358 AGTTTCGGCGGAGGACCAAGTGCAGATCAAA 390

RESULT 9 HUMIGKAW 405 bp mRNA PRI 04-JAN-1995
LOCUS Human Ig rearranged kappa-chain mRNA V-JI-region, hybridoma AE6-5,
DEFINITION 5' end.
ACCESSION M29467
NID g185920
KEYWORDS J-region; V-region; immunoglobulin-kappa; processed gene;
variable region subgroup VK-IV.
SOURCE Human (patient POP) hybridoma AE6-5 DNA, clone phiUCVK, derived
from B-CLL cell line UC729-5.
ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
REFERENCE 1 (bases 1 to 405)
AUTHORS Spatz,L.A., Wong,K.K., Williams,M., Desai,R., Golier,J.,
Berman,J.E., Alt,F.W. and Latov,N.
TITLE Cloning and sequence analysis of the VH and VL regions of an
anti-myelin/DNA antibody from a patient with peripheral neuropathy
and chronic lymphocytic leukemia
JOURNAL J. Immunol. 144 (7), 2821-2828 (1990)
MEDLINE 90203623
COMMENT Draft entry and printed sequence for [1] kindly submitted by
L.A.Spatz, 26-Oct-1989, for release after publication. Columbia
University, Department of Neurology BB-322, 630 W. 168th street,
New York, NY 10032.
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Db 49 ggtgctacgggacatcgtgatgccagctctccagactccctgctgctctctggc 108
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Qy 46 GGTGTCCACTCCGATATCGTGATGACCCAGTCTCCAGACTCGCTAGCTGTCTCTGGGC 105
Db 109 gagaggccaccactcaactgcaagtccagccagagtctttttatcacagctccaacaataag 168
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Qy 106 GAGAGGCCACCATCAATCGAAGCCCTCCCAAGCTGTGATTAT-GATGTCG--ATAGT 162
Db 169 aactactagcttggtaccagcagaaccaggacagcctcctcaagtgtctcatttactgg 228
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Qy 163 TA-TGAAC T-GTATCAGCAGAAACCCGGCAGCCTCTAAGTTGCTCATTTACGCT 219
Db 229 gcattaccgggaatccgggtccctgaccgattcagtcgagcggtctgggacagat 288
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Qy 220 GCATCCATCTAGAATCTGGGTACTCTGACCGATTCACTGGCAGCGGCTCTGGGACAGAT 279
Db 289 ttctctctcaccatcagcagcctgcagctgaagatgtggcagtttatttattctgtcagcaa 348
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Qy 280 TTCACTCTCACCATCAGCAGCCTCGAGGCTGAAGATGGCAGTATATCTACTGTGACGAA 339
Db 349 tattatagctctccgattgttcggccaaggaggaagtggaatcaaacg 401
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Qy 340 ACTAATGAGGATCTCCGAGGTTCCGGCGAGGCCAACGAGGTGCAGATCAAAACG 392

RESULT 10
LOCUS S50732 460 bp mRNA PRI 10-FEB-1993
DEFINITION immunoglobulin M light chain V region-anti-lipid A antibody [human,
hybridoma cell line HR78, mRNA Partial, 460 nt].
ACCESSION S50732
NID g261239
KEYWORDS human hybridoma cell line HR78.
ORGANISM Homo sapiens
Unclassified.
REFERENCE 1 (bases 1 to 460)
AUTHORS Dorai,H., Bubbers,J.E. and Gillies,S.D.
TITLE Cloning and reexpression of a functional human IgM anti-lipid A
antibody
JOURNAL Hybridoma 11 (5), 667-675 (1992)
MEDLINE 93093632
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 120606] from the original journal article.
This sequence comes from Fig. 3A.
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Matches 90; Conservative 11; Mismatches 9; Indels 1; Gaps 1;

Db 1 divltqspaslavslgqratisckasqsl dydgd symnw yqqkpgppkllyaa snles 60
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Ov      80  GYPRFGSGSGTDTLTSSLOAEVAVYCOONEDPPFGGGTVEIK 130

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RESULT 8
ID KV4C HUMAN
STANDARD: PRT: 134 AA.

DT	01-JAN-1988 (REL. 06, CREATED)
DT	01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN PRECURSOR V-IV REGION (B17).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUETHERIA; PRIMATES.

RP SEQUENCE FROM N.A.
RY MEDLINE: 86041854

RA MARSH P., MILLS F., GOULD H.;
RL NUCLEIC ACIDS RES. 13:6531-6544(1985).

RP REVISION TO 76.

RL SUBMITTED (OCT-1986) TO EMBL/GENBANK/DBJ DATA BANKS.

DR LAMB, A02550, G31510.
DR PIR: A01905: K4HU17.

DR H33F, FOI807, ZIFEN.
KW IMMUNOGLOBULIN V REGION: SIGNAL.

FT	SIGNAL	I	ZO	IG KAPPA CHAIN V-III REGION (B17).
FT	CHAIN	21	134	

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FT	DOMAIN	44	COMPLEMENTARITY-DETERMINING 1.
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		60	

ET	DOMAIN	61	75	FRAMEWORK 2.
ET	DOMAIN	76	82	COMPLEMENTARITY-DETERMINING 2.

FI	DOMAIN	63	114	FRAMEWORK 3,
ET	DOMAIN	115	121	COMPLEMENTARITY-DETERMINING 3

FT	DOMAIN	122	133	FRAMEWORK 4.
FT	DISSEID	43	114	BY SIMILIADITY

ET	NON TER	I34	I34
CO	STANTINE	I24	1886 MJ.
			DRC2F0CA CDC22.

Содержание	Стр.	Содержание	Стр.
1. Общие сведения	1	2. Описание	2
3. Технические характеристики	3	4. Требования к эксплуатации	4
5. Заключение	5	6. Приложение	6

Best Local Similarity 75.0%; Pred. No. 7.99e-117;

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

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Qy	64	QPPKLLIYAASNLESGVDFRSGSGTDFLTLISSLAQEDVAVYTCQGSNEDPPREG	123
Db	127	gtkveikr	134
Qy	124	GTKVEIKR	131

RESULT	9	STANDARD;	PRT;	111 AA.
ID	KV34 MOUSE			
AC	P01660;			
DT	21-JUL-1986	(REL. 01, CREATED)		
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)		
DT	01-OCT-1993	(REL. 21, LAST ANNOTATION UPDATE)		
DE	IG KAPPA CHAIN V-III REGION	(PC 3741 AND TEPC 111).		

	OC	EUKARYOTA; METAZOA;	CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
	OC	EUTHERIA; RODENTIA.	
	[1]	RN	SEQUENCE (PC 3741).
	RN	RP	MEDLINE; 79073152.
	RX	RD	WEIGERT M., GATMAIAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 276: 785-790(1978).
	RI	RA	

RN	[2]
RP	SEQUENCE (TEPC 111).
RX	MEDLINE; 79012520.
RA	MCKEAN D.J., BELL M., POTTER M.;
RL	PROC. INTL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
CC	-!- THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.

DR FIR; R01334; KVM337;
DR HSSP; P01679; 1GGB.
KW IMMUNOGLOBULIN V REGION.

FT	DOMAIN	1	23	FRAMEWORK 1.	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN	24	38	FRAMEWORK 2.	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	39	53	FRAMEWORK 3.	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN	54	60	FRAMEWORK 4.	COMPLEMENTARITY-DETERMINING 4.
FT	DOMAIN	61	92	BY SIMILARITY.	
FT	DOMAIN	93	101		
FT	DOMAIN	102	111		
FT	DISULFID	23	92		
FT	NON TER	111	111		
111	AA:	12099	MW:	76502E89	CRC32;
SO	SEQUENCE	111	AA:		

Query Match	67.0%;	Score 622;	DB 5;	Length 111;
Best Local Similarity	78.4%;	Pred. No. 6.99e-116;		
Matches	87;	Conservative 15;	Mismatches 9;	Indels 0; Gaps 0;

[illegible]

Db 61 giparfgsggrt dftltinpv eadrvatyvqqgsnedpyrfgggtkleik 111
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Q: 80 cyndpsccsmfcttisiiaenivaivvycoonsnrbfcgscckfk 130

RESULT	10	
ID	KV3C MOUSE	STANDARD.
		PRT. 112 AA

AC	P01659;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN V-III REGION (TEPC 124).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC	EUTHERIA; RODENTIA.	
RR	[1]	
RP	SEQUENCE.	
RR	MEDLINE; 73140225.	
RR	MCKEAN D.J., POTTER M., HOOD L.E.;	
RRL	BIOCHEMISTRY 12:760-771(1973).	
DR	PIR; A01933; KVMG32.	
DR	HSP; P01679; 1GGB.	
KW	IMMUNOGLOBULIN V REGION.	
FT	DOMAIN 1	23
FT	DOMAIN 24	38
FT	DOMAIN 39	53
FT	DOMAIN 54	60
FT	DOMAIN 61	92
FT	DOMAIN 93	101
FT	DOMAIN 102	111
FT	DISULFID 23	92
FT	NON TER 112	112
SO	SEQUENCE 112 AA;	12339 MW; 4504DD0E CRC32;

Query Match	66.9%;	Score 621;	DB 5;	Length 112;
Best Local Similarity	67.0%;	Pred. No. 1.20e-115;		
Matches	75;	Conservative	27;	Mismatches 10;
			Indels	0;
			Gaps	0;

1 divltqpslavslgratiscraezsvmygnfzmzywzkkpzppklliyaaenlzs 60
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 20 dlvmtospdslaivsigerattncaksovdvdygdsymnytookpgopklliyaaenlzs 79

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61 g1parfsgsgstrbftlt1bpwzabduatycfzcszozapwtfgsqtkslelkr 112
      1:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
80 cvpbrfscsgcsmftt1ssloafvavvycoosnedprgggkwyelkr 131

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[illegible]

RA MCKEAN D.J., POTTER M., HOOD L.E.;
RL BIOCHEMISTRY 12:749-759(1973).
CC -!- THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN
CC WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE
CC MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.

CC	MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.
DR	PIR; A01933; KVM532.
DR	HSSP; P01679; 1GGB.
KW	IMMUNOGLOBULIN V REGION; BENICE-JONES PROTEIN; SIGNAL.
FT	SIGNAL
	1 20
FT	CHAIN
	21 132
FT	DOMAIN
	21 43
FT	DOMAIN
	44 58
FT	DOMAIN
	59 73
	IG KAPPA CHAIN V-III REGION (MOPC 321).
	FRAMEWORK 1.
	COMPLEMENTARITY-DETERMINING 1.
	FRAMEWORK 2.

FT	DOMAIN	74	80	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	81	112	FRAMEWORK 3
FT	DOMAIN	113	121	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN	122	131	FRAMEWORK 4.
FT	DISULFID	43	112	BY SIMILARITY.
FT	NON TER	132	132	
SO	SEQUENCE	132 AA;	14523 MW;	E572F824 CRC32;

Query Match 66.7%; Score 619; DB 5; Length 132;
Best Local Similarity 65.5%; Pred. No. 3.55e-115;
Matches 76; Conservative 28; Mismatches 12; Indels 0; Gaps 0;

Db	17	gsgtdvltgspaelavalgratiscraekavmtynofmewyzztgpgppklllyras	76
Qy	16	GVSHDIVMTQSPDLSAVSLGERATITCKGASQSDYDGSVMNYVQOKPGPKLLIYAS	75
Db	77	nlsqglparfegsgsrftltibpvyzabdvatfczszbzbpwtfggckkleikr	132
Qy	76	niesgvnpsfscsgcmpttltissioadvaivvycoosnfprefgggkckleikr	131

RESULT 12
ID KV4A HUMAN STANDARD: PRT: 114 AA.

AC	21-JUL-1986 (REL. 01, CREATED)	
DC	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)	
DT	01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)	
DT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)	
DE	IG KAPPA CHAIN V-IV REGION (LEN).	
OS	HOMO SAPIENS (HUMAN).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; PRIMATES.	
RP	[1]	
RN	SEQUENCE.	
RX	MEDLINE: 76004342.	
RA	SCHNEIDER M., HILLSCHMANN N.;	
RL	HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:507-557(1975).	
CC	-1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.	
CC	-1- THIS IS A BENCE-JONES PROTEIN.	
CC	PIR; A01903; K4HULN.	
DR	HSPB; P01607; IMCP.	
DR	IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.	

KW	IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.	1	23	FRAMEWORK 1.
FT	DOMAIN	24	40	COMPLEMENTARITY-FRAMEWORK 2.
FT	DOMAIN	41	55	COMPLEMENTARITY-FRAMEWORK 3.
FT	DOMAIN	56	62	COMPLEMENTARITY-FRAMEWORK 4.
FT	DOMAIN	63	94	BY SIMILARITY.
FT	DOMAIN	95	101	
FT	DOMAIN	102	113	
FT	DISULFID	123	94	
FT	NON TER	114	114	
SO	SEQUENCE	114	114	
		17639 MW:	36347616A CRC32	

Query Match 66.2%; Score 614; DB 5; Length 114;
Best Local Similarity 81.6%; Pred. No. 5.33e-114;
Matches 93; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

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Db      1 divmtqspnslavslgeratlnckssgsvlyssnsknylawyqqtpgqpkllywast 60
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C:"     20 divmrcpsnsiavglceratinckaqsqvmyndgs---ymkwyoorpgospklllyaaSNL 77
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Db 61 esgvpdfsfsgsgtfdltlsislaqaedvavyvcqyystpsfsggkkleir 114
|||||
Cn 78 tscvndfscfscmeflftssiafnvaivycoosennpprfgggtkvlekr 131
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RESULT 13
ID: KV31 MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 63).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE; 78235887.
RA BURSTEIN Y., SCHECHTER I.;
RL BIOCHEMISTRY 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE; 73140225.
RA MCKEAN D.J., POTTER M., HOOD L.E.;
RL BIOCHEMISTRY 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KYMSM6.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION (MOPC 63).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; 9055A06B CRC32;

Query Match 65.9%; Score 612; DB 5; Length 131;
Best Local Similarity 74.8%; Pred. No. 1.58e-113;
Matches 86; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

Db 17 getgnivltspaelavslgratiscraesvdygnsmfhwgkpgqpklllylas 76
| :||:||||| |||||:|||||:||||| :||:||||| |||||:|||||
Qy 16 GVHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGDSDYNNWYQKPGQPPLLYAAS 75

Db 77 nlesyparfsgsgartftltidpveaddaatyccqnnedpwtfggktleik 131
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Qy 76 NLESYVDRFSGSGGTFTLTITSSLAQEDVAVYYCQSNEDPPRFGGGTRVEIK 130

RESULT 14
ID: KV31 MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (ABPC 22 AND PC 9245).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

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OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
RX MEDLINE; 79073152.
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
CC -|- THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KYMSM6.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; 711C554A CRC32;

Query Match 65.7%; Score 610; DB 5; Length 111;
Best Local Similarity 76.6%; Pred. No. 4.65e-113;
Matches 85; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

Db 1 nivltqspaslavlsgqratiscrasvdygnsmfhwgkpgqpklllylasnles 60
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Qy 20 DIVMTQSPDSLAVSLGERATINCKASQSDYDGDSDYNNWYQKPGQPPLLYAASNLES 79

Db 61 gparfsgsgartftltidpveaddaatyccqnnedpwtfggktleik 111
||| ||||| ||||| :||:||||| |||||:|||||
Qy 80 GVPDRFSGSGGTFTLTITSSLAQEDVAVYYCQSNEDPPRFGGGTRVEIK 130

RESULT 15
ID: KV31 MOUSE STANDARD; PRT; 111 AA.
AC P01663;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 4050).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; A01935; KYMSM6.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 FRAMEWORK 4.
FT DOMAIN 102 111

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FT	DISULFID	23	92	BY SIMILARITY.
FT	NON TER	111	111	
SEQ	SEQUENCE	111 AA;	12005 MW; 5EEF3264 CRC32;	
	Query Match		65.0%;	Score 603; DB 5; Length 111;
	Best Local Similarity		74.8%;	Pred. No. 2.05e-111;
	Matches	83; Conservative	17; Mismatches	11; Indels 0; Gaps 0;
Db	1	nivltqtgsaaslawsgqratiscrasesvdsygnsmhvyqqkqppkllilylaasnes	60	
Qy	20	DIWVTQSPDSLAVSGERATINCKASQSDVGDSTYNNVYIQKPGQPPKLLIYAASNLES	79	
Db	61	gyprafsgsgrtdftltdipveaddaatyvcgqmedpltfagtkleik	111	
Qy	80	GVYDFRSGSGSGTDFTLTSSIAQEDAVVYVCOOSNEDPREGGKTVEIK	130	

Search completed: Tue Mar 18 10:07:47 1997
Job time : 17 secs.

Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	676	72.8	112	5	S19971	Ig kappa chain V reg	1.40e-61
2	674	72.6	131	5	PH1226	Ig kappa chain precu	2.39e-61
3	664	71.6	111	2	KWMS43	Ig kappa chain V reg	3.43e-60
4	662	71.3	111	2	KWMS83	Ig kappa chain V reg	5.84e-60
5	660	71.1	111	2	KWMS08	Ig kappa chain V reg	9.95e-60
6	650	70.1	111	2	KWMS69	Ig kappa chain V reg	1.42e-58
7	648	69.8	111	2	KWMS01	Ig kappa chain V reg	2.42e-58
8	646	69.6	112	5	S19976	Ig kappa chain V reg	4.13e-58
9	643	69.3	133	2	K4HUJ1	Ig kappa chain precu	9.16e-58
10	640	69.0	112	5	S19972	Ig kappa chain V reg	2.03e-57
11	637	68.6	112	2	KWMS10	Ig kappa chain V reg	4.51e-57
12	635	68.4	127	14	S21680	Ig heavy chain precu	7.67e-57

Query Match 72.8%; Score 676; DB 5; Length 112;
Best Local Similarity 82.1%; Pred. No. 1.40e-61;

Query Match 72.8%; Score 676; DB 5; Length 112;
Best Local Similarity 82.1%; Pred. No. 1.40e-61;


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30-Sep-1993
ACCESSIONS C01937; A01937
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce immunoglobulin diversity.
#cross-references MUID:79073152
#accession C01937
#molecule_type protein
##residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
23-92
SUMMARY
#disulfide bonds #status predicted
#length 111 #molecular-weight 12071 #checksum 2195
Query Match 71.1%; Score 660; DB 2; Length 111;
Best Local Similarity 82.9%; Pred. No. 9.95e-60;
Matches 92; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
Db 1 divltcpsalavslqgratiscasqsvdydgsymnyqqkpgppklllytaenles 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 20 DIVMTQSPDSLAVSLGERATINCKASQSDYDGSYMNWYQQKPGQPPKLLIYAASNLES 79
Db 61 giparfsgsgtdftlnihpveedaatyycqgsnedpwtfgsgtkleik 111
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Qy 80 GVPDRFSGSGGTDFTLTISSLQAEDVAVYCCQSNEDPFRFGGKVEIK 130
RESULT 6
ENTRY KWS69 #type complete
TITLE Ig kappa chain V region (PC7769) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
30-Sep-1993
ACCESSIONS E01937; A01937
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce immunoglobulin diversity.
#cross-references MUID:79073152
#accession E01937
#molecule_type protein
##residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
23-92
SUMMARY
#disulfide bonds #status predicted
#length 111 #molecular-weight 12011 #checksum 662
Query Match 70.0%; Score 650; DB 2; Length 111;
Best Local Similarity 82.0%; Pred. No. 1.42e-58;
Matches 91; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
Db 1 divltcpsalavslqgratiscasqsvdydgsymnyqqkpgppklllyfaenles 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 20 DIVMTQSPDSLAVSLGERATINCKASQSDYDGSYMNWYQQKPGQPPKLLIYAASNLES 79
Db 61 giparfsgsgtdftlnihpveedaatyycqgsnedpwtfgsgtkleik 111
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 80 GVPDRFSGSGGTDFTLTISSLQAEDVAVYCCQSNEDPFRFGGKVEIK 130
```

```
7
RESULT
ENTRY KWS61 #type complete
TITLE Ig kappa chain V region (CBPC 101) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change
05-Apr-1995
ACCESSIONS A01936
REFERENCE A93822
#authors McKean, D.J.; Bell, M.; Potter, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1978) 75:3913-3917
#title Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.
#cross-references MUID:79012520
#accession A01936
#molecule_type protein
##residues 1-111 ##label MCK
COMMENT This chain was isolated from a myeloma protein.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
23-92
SUMMARY
#disulfide bonds #status predicted
#length 111 #molecular-weight 11964 #checksum 1507
Query Match 69.8%; Score 648; DB 2; Length 111;
Best Local Similarity 81.1%; Pred. No. 2.42e-58;
Matches 90; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
Db 1 divltcpsalavslqgratiscasqsvdydgsymnyqqkpgppklllyaaenles 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 20 DIVMTQSPDSLAVSLGERATINCKASQSDYDGSYMNWYQQKPGQPPKLLIYAASNLES 79
Db 61 giparfsgsgtdftlnihpveedaatyycqgsnedpwtfgsgtkleik 111
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 80 GVPDRFSGSGGTDFTLTISSLQAEDVAVYCCQSNEDPFRFGGKVEIK 130
RESULT 8
ENTRY S19976 #type fragment
TITLE Ig kappa chain V region (M-7413) - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
12-Apr-1995
ACCESSIONS S19976
REFERENCE S19963
#authors Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
#submission submitted to the EMBL Data Library, March 1992
#description Structural characterization of CD4 mAb.
#accession S19976
#status preliminary
#molecule_type mRNA
##residues 1-112 ##label WEI
#cross-references EMBL:X65093
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY
#length 112 #checksum 4816
Query Match 69.6%; Score 646; DB 5; Length 112;
Best Local Similarity 79.5%; Pred. No. 4.13e-58;
Matches 89; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
Db 1 divltcpsalavslqgratiscasqsvdydgsymnyqqkpgppklllyaaenles 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 20 DIVMTQSPDSLAVSLGERATINCKASQSDYDGSYMNWYQQKPGQPPKLLIYAASNLES 79
Db 61 giparfsgsgtdftlnihpveedaatyycqgsiqdpytfgsgtkleikr 112
```


#journal Eur. J. Immunol. (1993) 23:846-851
#title Nucleotide sequence analysis of the variable domains of four
human monoclonal IgM with an antibody activity to
myelin-associated glycoprotein.

#accession S34003
#status preliminary

#molecule_type mRNA

#residues 1-113 #label MAR

SUMMARY #length 113 #molecular-weight 12312 #checksum 3087

Query Match 67.3%; Score 625; DB 11; Length 113;
Best Local Similarity 83.2%; Pred. No. 1.09e-55;
Matches 94; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Db 1 divmtqspdelavclgeratincsksgvlysenknkylawycqkagppklliywastr 60

Qy 20 DIVMTQSPDSELAVALGERATINCKASQSDYDGDGDS--YMMWYQQRPGQPPKLLIYAASNL 77

Db 61 esgvpdrfsgsgsgtdftltislaqaedvavvyccqylttptfgggtkveik 113

Qy 78 ESGVPDRFSGSGGTDFTLTISLAQEDVAVVYCCQSNEDPPRFGGGTKEIK 130

Search completed: Tue Mar 18 10:08:28 1997
Job time : 24 secs.

WPPREH

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:08:45 1997; MasPar time 4.11 Seconds
Tabular output not generated. 328.441 Million cell updates/sec

Title: >US-08-612-929-14
Description: (1-131) from US08612929.pep
Perfect Score: 928
Sequence: 1 MGVSCILFLVATGTVHSD.....QQSNEDPRFGGKTVEIKR 131

Scoring table: PAM 150
Gap 11

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 29.954; Variance 160.271; scale 0.187

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description	Pred. No.
1	928	100.0	131 13	R75355	Humanized antibody 3B	1.38e-62		
2	917	98.8	131 13	R70202	Humanized antibody 3B	1.02e-61		
3	701	75.5	132 13	R70189	Mouse MAb 389 light c	1.02e-44		
4	679	73.2	233 6	R30777	pH52-9.0 humanised m	5.39e-43		
5	674	72.6	131 6	R32123	Anti-CD4 antibody MT	1.33e-42		
6	671	72.3	131 1	R04132	Anti-Leu 3a light cha	2.28e-42		
7	669	72.1	127 1	P90918	Light chain antibody	3.27e-42		
8	669	72.1	233 4	R22754	Reshaped CAMPATH-1 an	3.27e-42		
9	666	71.8	124 11	R59943	Anti-VLA4 rAb humanis	5.61e-42		
10	665	71.7	111 11	R60302	Anti HIV antibody lig	6.71e-42		
11	665	71.7	111 10	R55123	Mouse anti-HIV mu5.5	6.71e-42		
12	664	71.6	112 5	R24575	Human x mouse modifie	8.04e-42		

13	661	71.2	127 8	R40180	Humanised antibody CM	1.38e-41
14	661	71.2	127 8	R40176	Humanised antibody CM	1.38e-41
15	660	71.1	127 8	R40184	Humanised antibody CM	1.65e-41
16	659	71.0	131 1	P90543	Amino acids sequence	1.98e-41
17	657	70.8	126 6	R29013	pUC-RVH-PM1a.	2.83e-41
18	657	70.8	126 6	R29015	pUC-RV1-PM1a.	2.83e-41
19	653	70.4	111 10	R55127	Mouse-human chimeric	5.82e-41
20	653	70.4	111 11	R60306	Chimeric anti HIV ant	5.82e-41
21	652	70.3	111 1	P90541	Immunoglobulin L chai	6.97e-41
22	651	70.2	127 8	R40178	Humanised antibody CM	8.34e-41
23	650	70.0	126 8	R41468	MAB 25D2 humanised li	9.98e-41
24	650	70.0	233 4	R22755	Reshaped CD4 antibody	9.98e-41
25	649	69.9	128 11	R58752	Anti-VLA4 SYMDY V-kap	1.19e-40
26	649	69.9	129 13	R70256	Anti-VLA-4 humanized	1.19e-40
27	647	69.7	120 9	R48618	Sequence of the monoc	1.71e-40
28	647	69.7	126 15	R89479	Anti-human IL-4 human	1.71e-40
29	647	69.7	128 10	R55211	Humanised HP1/2 light	1.71e-40
30	647	69.7	232 15	R80616	Anti-human IL-4 human	1.71e-40
31	646	69.6	125 13	R67656	Anti-human IL-6 chima	2.05e-40
32	646	69.6	126 18	R92758	Human/murine chimaeri	2.05e-40
33	644	69.4	128 11	R59935	VK3 (DQMDY) VL.	2.94e-40
34	642	69.2	125 13	R67657	Anti-human IL-6 chima	4.21e-40
35	641	69.1	599 16	R90837	3B1 single chain anti	5.04e-40
36	639	68.9	127 1	P90938	Humanised light chain	7.22e-40
37	639	68.9	128 11	R59933	VK1 (DQL) VL.	7.22e-40
38	639	68.9	128 10	R55209	Humanised HP1/2 kappa	7.22e-40
39	639	68.9	128 13	R70254	Transplanted V-kappa	7.22e-40
40	637	68.6	218 6	R33312	Humanised MaE11 Verel	1.03e-39
41	636	68.5	126 18	R92759	Human/murine chimaeri	1.24e-39
42	634	68.3	111 18	R52059	Light chain variable	1.77e-39
43	629	67.8	111 9	R47494	Murine anti-CD18 Ab 6	4.35e-39
44	629	67.8	125 8	R41467	Humanised MAB 25D2 li	4.35e-39
45	629	67.8	126 14	R76678	Human/murine chimeric	4.35e-39

ALIGNMENTS

RESULT 1
ID R75355 standard; Protein; 131 AA.
AC R75355;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 389 light chain.
KW MAb; interleukin-4; IL-4; allergy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Sig_peptide
FT Region 43..57
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 73..79
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 112..120
FT /label= CDR
FT /note= "complementarity determining region"
FT /note= "complementarity determining region"
FN M09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR N-PSDB; Q73986.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Fig.5; 97pp; English.
 CC A humanized antibody light chain variable region and signal
 CC sequence is given in R75355. The signal sequence is also
 CC provided in R70194. The sequences of the first 2 CDRs
 CC are identical to mouse anti-human IL-4 Mab 3B9 light chain
 CC CDRs (given in R70195-96), but the third (R70201) differs
 CC by a single amino acid from the native mouse CDR (R70197).
 SQ Sequence 131 AA;

Query Match 100.0%; Score 928; DB 13; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.38e-62;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mqwscilflvatatgvhsdivmtqpsdslavslgeratincasqsvdygdymwyq 60
 QY 1 MWMSCILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGSYMNWYQ 60
 Db 61 qkpggppklliyaanlesgvpdrfsgsgtdftltiselaedvavyyccqsgnedprr 120
 QY 61 QKPGQPPLLIYAASNLESGVDPDRFSGSGTDFTLTISLSQAEDVAVYYCQSQSNEDPPR 120
 Db 121 fgggtkveikr 131
 QY 121 FGGGTRVEIKR 131

RESULT 2

ID R70202 standard; Protein; 131 AA.
 AC R70202;
 DT 20-SEP-1995 (first entry)
 DE Humanized antibody 3B9 light chain.
 KW Humanized antibody; antibody engineering; monoclonal antibody;
 KW Mab; interleukin-4; IL-4; allergy.
 OS Homo sapiens.
 PN WO9507301-A.
 PD 16-MAR-1995.
 PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR N-PSDB; Q83520.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Page 71-72; 97pp; English.
 CC A humanized antibody light chain variable region and signal
 CC sequence is given in R75355. The signal sequence is also
 CC provided in R70194. The sequences of the 3 CDRs
 CC are identical to mouse anti-human IL-4 Mab 3B9 light chain
 CC CDRs (given in R70195-97).
 SQ Sequence 131 AA;

Query Match 98.8%; Score 917; DB 13; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.02e-61;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 mqwscilflvatatgvhsdivmtqpsdslavslgeratincasqsvdygdymwyq 60
 QY 1 MWMSCILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGSYMNWYQ 60
 Db 61 qkpggppklliyaanlesgvpdrfsgsgtdftltiselaedvavyyccqsgnedprr 120
 QY 61 QKPGQPPLLIYAASNLESGVDPDRFSGSGTDFTLTISLSQAEDVAVYYCQSQSNEDPPR 120
 Db 121 fgggtkveikr 131
 QY 121 FGGGTRVEIKR 131

RESULT 3

ID R70189 standard; Protein; 132 AA.
 AC R70189;
 DT 20-SEP-1995 (first entry)
 DE Mouse Mab 3B9 light chain.
 KW Chimeric antibody; humanized antibody; antibody engineering;
 KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= Sig_peptide
 FT Region 44..58
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT Region 74..80
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT Region 113..121
 FT /label= CDR
 FT /note= "complementarity determining region"
 PN WO9507301-A.
 PD 16-MAR-1995.
 PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR N-PSDB; Q83490.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Fig.1; 97pp; English.
 CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 CC chains were cloned into pGEM7f+ and transformed into E. coli
 CC DH5-alpha. The clones were sequenced (Q83490-91), and used for
 CC antibody engineering.
 SQ Sequence 132 AA;

Query Match 75.5%; Score 701; DB 13; Length 132;
 Best Local Similarity 78.7%; Pred. No. 1.02e-44;
 Matches 100; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

Db 6 illwvllwvpgstgdivltqpsaslavslgratincasqsvdygdymwyqktpg 65
 QY 6 IILV-LVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGSYMNWYQKPG 64


```
FT /label= CDR1 39..53
FT Region
FT /label= FR2 54..60
FT Region
FT /label= CDR2 61..92
FT Region
FT /label= FR3 93..101
FT Region
FT /label= CDR3 102..111
FT Region
FT /label= FR4
FT J06125783-A.
PN 10-MAY-1994.
PF 28-DEC-1991; 359808.
PR 28-DEC-1991; JP-359808.
PA (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
DR WPI; 94-187942/23.
DR N-PSDB; Q6554.
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
PT and recombinant antibody consisting of the H- and L-chains,
PT useful in AIDS therapy
PS Example 3; Fig 4; 22pp; Japanese.
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (R55120-R55123). The murine anti-HIV CDRs were
CC introduced into human framework regions to construct chimeric
CC antibodies (R55124-R55127).
SQ Sequence 111 AA;
```

Query Match 71.7%; Score 665; DB 10; Length 111;
Best Local Similarity 84.7%; Pred. No. 6.71e-42;
Matches 94; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

```
Db 1 divltqpsaslaqlgratiscasqsdvdgdsymwvqqkpgkplliyaasnles 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 20 DIVMTQSPDLSAVSLGERATINCKASQSDVDGDSYNNWYQKPGKPLLIYAASNLES 79

Db 61 giparfsgsgtdftlnlhvveedatyyccqnedpwtfgggtkleik 111
   !: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 80 GVPDRFSGSGTDFLTITISLQAEDVAVYYCQSNEDPPRFGGGTKEIK 130
```

```
RESULT 12
ID R24575 standard; Protein; 112 AA.
AC R24575;
DT 08-DEC-1992 (first entry)
DE Human x mouse modified anti-HIV antibody Light chain R10.5beta.
KW Heavy; light; CDR; HIV; AIDS; REI; 0.5beta.
OS Synthetic.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT Region 24..38
FT /label= CDR1
FT Region 39..53
FT /label= FR2
FT Region 54..60
FT /label= CDR2
FT Region 61..92
FT /label= FR3
FT Region 93..101
FT /label= CDR3
FT Region 102..112
FT /label= FR4
```

```
PN J04141095-A.
PD 14-MAY-1992.
PF 02-OCT-1990; 266091.
PR 02-OCT-1990; JP-266091.
PA (KAGA ) KAGAKU OYOBI KESSEI RYOHO.
DR WPI; 92-212765/26.
PT New recombinant modified anti-HIV antibodies - comprise human x
PT mouse modified antibody H and L chains
PS Disclosure; Fig 2; 15pp; Japanese.
CC The framework regions (FR) are derived from the human antibody
CC REI. The CDRs are mouse monoclonal antibody 0.5beta derived
CC sequences. The anti-HIV modified antibody can be used for the
CC prophylaxis and treatment of AIDS.
CC Specific examples of the H chain are given in R24556-58 and
CC R24560-62. A specific example of the L chain is given in R24575.
SQ Sequence 112 AA;
```

Query Match 71.6%; Score 664; DB 5; Length 112;
Best Local Similarity 83.9%; Pred. No. 8.04e-42;
Matches 94; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

```
Db 1 divltqpsaslaasvgrvtitckasqsdvdgdsymwvqqkpgkplliyaasnles 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 20 DIVMTQSPDLSAVSLGERATINCKASQSDVDGDSYNNWYQKPGKPLLIYAASNLES 79

Db 61 gyparfsgsgtdftlslqlpediatyyccqnedpftfgggtkveikr 112
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 80 GVPDRFSGSGTDFLTITISLQAEDVAVYYCQSNEDPPRFGGGTKEIKR 131
```

RESULT 13
ID R40180 standard; Protein; 127 AA.

```
AC R40180;
DT 14-FEB-1994 (first entry)
DE Humanised antibody CMX5-3 light chain variable region.
KW Primer; polymerase chain reaction; amplify; PCR; human; kappa; L;
KW constant region; heavy; H; chain; pUC19; humanised; antibody;
KW light; REI; VL3 fragment; CMX5-1; CMX5-3.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Secretory leader peptide"
FT Protein 20..127
FT /note= "CMX5-3 light chain variable region"
PN W09316184-A.
PD 19-AUG-1993.
PF 04-FEB-1993; U00759.
PR 06-FEB-1992; US-832842.
PA (SCHE ) SCHERING CORP.
PI Abrams JS, Chou C, Jenh C, Murgolo NJ, Petro ME;
PI Silver JE, Tindall S, Windsor WT, Zavodny RJ;
DR WPI; 93-272888/34.
PT Humanised monoclonal antibody - comprises variable animal region
PT and constant human region, binds to human interleukin-5
PS Example; Page 92-93; 118pp; English.
CC The sequences given in R40179-80 represent the variable regions of
CC the heavy and light chains of the humanised antibody CMX5-3
CC respectively. These sequences were based on the humanised antibody
CC CMX5-1. These sequences were generated using the primer sequences
CC given in Q48068-71. These primers were based on sequences derived
CC from antibody JES1-39D10 and human LAY VH framework sequences. The
CC amplification products were used to replace the VH1 and VH3 fragments
CC of CMX5-1 H chain cDNA in pSV.Sport (see also R40175).
SQ Sequence 127 AA;
```

WATERMAN

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:14:15 1997; MasPar time 67.08 Seconds
295.872 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-15
Description: (1-45) from US08612929.seq
Perfect Score: 45
N.A. Sequence: 1 AAGCGCAGCAAGCTGTGATTATGATGCTGATAGTTATATGAC 45
Comp: TTCCGGTCGGTTTCACACTATATACCATCACTATATCTTG

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 04
Listing first 45 summaries

Database: EST-STS
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98
99:EST99
EST-STS-TWO
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124
125:EST125 126:EST126 127:EST127 128:EST128 129:EST129

Database:

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7
136:STS8 137:STS9 138:STS10 139:STS11 140:STS12
141:STS13 142:STS14 143:STS15 144:STS16 145:STS17
146:STS18 147:STS19 148:STS20 149:STS21 150:STS22
151:STS23 152:STS24 153:STS25 154:STS26 155:STS27
156:STS28 157:STS29 158:STS30 159:STS31 160:STS32
161:STS33 162:STS34 163:STS35 164:STS36 165:STS37
166:STS38 167:STS39 168:STS40 169:STS41 170:STS42
171:STS43 172:STS44 173:STS45

Statistics: Mean 7.676; Variance 1.785; scale 4.299

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
c 1	21	46.7	380	128	T97605	ye5d07.s1	Homo sapie	1.73e-06
c 2	21	46.7	387	128	T98507	ye6d02.s1	Homo sapie	1.73e-06
c 3	21	46.7	413	74	R09757	ye27f09.s1	Homo sapie	1.73e-06
c 4	20	44.4	246	33	H87767	ye75b05.s1	Homo sapie	2.74e-05
c 5	19	42.2	315	138	HUMUT8000	Human STS UT8000		4.03e-04
c 6	19	42.2	330	6	CELK121G3F	C.elegans cDNA clone		4.03e-04
c 7	19	42.2	339	2	CELK002DYF	C.elegans cDNA clone		4.03e-04
c 8	19	42.2	362	174	HS690296	human STS SHGC-6155 c		4.03e-04
c 9	19	42.2	362	134	G17690	human STS SHGC-6155 c		4.03e-04
c 10	19	42.2	427	66	N63295	yz88h06.s1	Homo sapie	4.03e-04
c 11	19	42.2	427	160	HS295292	yz88h06.s1	Homo sapie	4.03e-04
c 12	19	42.2	442	88	R59112	yh03h11.r1	Homo sapie	4.03e-04
c 13	19	42.2	497	86	R51415	y972d03.r1	Homo sapie	4.03e-04
c 14	19	42.2	520	118	T63218	yci5b07.r1	Homo sapie	4.03e-04
c 15	19	42.2	600	122	T77507	yc94h02.r1	Homo sapie	4.03e-04
c 16	18	40.0	182	108	T25334	EST060	Homo sapiens c	5.44e-03
c 17	18	40.0	227	125	T88534	12230	Arabidopsis tha	5.44e-03
c 18	18	40.0	297	87	R54253	y974f04.r1	Homo sapie	5.44e-03
c 19	18	40.0	299	22	H52906	SW31CA458SK	Brugia ma	5.44e-03
c 20	18	40.0	305	136	HSB344YE5	H.sapiens (D20S893)	D	5.44e-03
c 21	18	40.0	305	174	HSB344YE5	H.sapiens (D20S893)	D	5.44e-03
c 22	18	40.0	309	112	T41640	10221	Arabidopsis tha	5.44e-03
c 23	18	40.0	313	1	ATT22998	A. thaliana transcrib		5.44e-03
c 24	18	40.0	334	48	HUM224A03B	Human aorta cDNA 5'-e		5.44e-03
c 25	18	40.0	344	135	HS299YF1	H. sapiens (D185476)		5.44e-03
c 26	18	40.0	354	129	G00573	fruit fly STS Dm0285		5.44e-03
c 27	18	40.0	385	107	T19193	d08013t	Homo sapiens	5.44e-03
c 28	18	40.0	391	132	G09820	human STS CHLC.GC11H		5.44e-03
c 29	17	37.8	158	137	HUMSWS2017	human STS aWSS2017,		6.69e-02
c 30	17	37.8	188	158	HS098360	za79f12.r1	Soares fet	6.69e-02
c 31	17	37.8	188	147	W05098	za79f12.r1	Soares fet	6.69e-02
c 32	17	37.8	240	102	R1CS1121A	Rice cDNA, partial sc		6.69e-02
c 33	17	37.8	270	107	T20181	D193F	Homo sapiens cd	6.69e-02
c 34	17	37.8	292	131	G06364	human STS WI-7035.		6.69e-02
c 35	17	37.8	303	98	R90210	16565	Arabidopsis tha	6.69e-02
c 36	17	37.8	326	138	HUMUT8005B	Human STS UT8005, 3'		6.69e-02
c 37	17	37.8	329	113	T44985	8248	Arabidopsis thal	6.69e-02
c 38	17	37.8	339	37	HS455H012	H. sapiens partial cd		6.69e-02
c 39	17	37.8	344	73	R05096	pk41a04.s1	Caenorhabd	6.69e-02
c 40	17	37.8	353	174	HS4046YB1	H.sapiens (D17S1873)		6.69e-02
c 41	17	37.8	400	135	G19182	human STS SHGC-18387		6.69e-02
c 42	17	37.8	416	51	M78296	EST00444	Homo sapiens	6.69e-02

FEATURES	Email:ykohara@dbj.nig.ac.jp.
source	Location/Qualifiers
	1..330
	/organism="Caenorhabditis elegans"
	/strain="CB1489 him-8(e1489)"
	/dev_stage="varied"
	/sequenced_mol="cDNA to mRNA"
	/sex="Hermaphrodite, male"
	/tissue_type="whole animal"
	/clone_lib="Fuji kohara unpublished cDNA"
BASE COUNT	76 a 90 c 74 g 83 t 7 others
ORIGIN	
Query Match	42.2%; Score 19; DB 6; Length 330;
Best Local Similarity	77.1%; Pred. No. 4,03e-04;
Matches	27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db	105	cttccaacatcccaatcatcactttgttgagctt 139
Cp	35	CTATCACCATCATAAACAACACTTTGCCTGGCGCTT 1
RESULT	7	
LOCUS	CELK002DYF	339 bp mRNA EST 18-NOV-1995
DEFINITION	C.elegans cDNA clone yk2d11 : 5' end, single read.	
ACCESSION	D27216	
NID	9521324	
KEYWORDS	EST (expressed sequence tag).	
SOURCE	Caenorhabditis elegans (strain CB1489 him-8(e1489),) (library: Yuji Kohara unpublished cDNA) Hermaphrodite, male varied whole animal cDNA to mRNA.	
ORGANISM	Caenorhabditis elegans	

REFERENCE	Secernentea; Rhabditia; Rhabditidae; Rhabditina; Rhabditoidea; Rhabditidae; Caenorhabditis.
AUTHORS	Kohara, Y., Mitsuiki, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and Tabara, H.
TITLE	Toward an expression map of the C.elegans genome
JOURNAL	Unpublished (1994)
COMMENT	Submitted (22-Dec-1993) to DBJ by: Yuji Kohara National Institute of Genetics Gene Library Lab Yata 1111, Mishima Shizuoka 411 Japan Phone: 0559-75-0771 Fax: 0559-75-6240 Email: ykohara@dbj.nig.ac.jp. Location/Qualifiers
FEATURES	

```

1..339
source
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/dev_stage="varied"
/sequenced_mol="cDNA to mRNA"
/sex="Hermaphrodite, male"
/tissue_type="whole animal"
/clone_lib="Yuji Kohara unpublished cDNA"
81 a      84 c      76 g      93 t      5 others
BASE COUNT
ORIGIN
Query Match      42.2%; Score 19; DB 2; Length 339;
Best Local Similarity 77.1%; Pred. No. 4.03e-04;

```


Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 135 ctttcaacatcccaatcatcattgttggtgacatt 169
 || ||| |||| ||||| ||||| || |||

Cp 35 CTATCACCATCATATCAACACTTTTGGCTGGCGCTT 1

RESULT 8

ID HS690296 standard; DNA; STS; 362 BP.
 AC G17690;
 DT 07-MAR-1996 (Rel. 47, Created)
 DT 07-MAR-1996 (Rel. 47, Last updated, Version 1)
 DE human STS SHGC-6155 clone pg-2635.
 KW primer; sequence tagged site; STS sequence.
 OS Homo sapiens (human)
 OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 RN [1]
 RP 1-362
 RA Myers R.M.;
 RT ;
 RL Unpublished.

CC Contact: Richard M. Myers Stanford Human Genome Center (SHGC)
 CC Stanford University School of Medicine Department of Genetics,
 CC M-344, Stanford, CA 94305, USA Tel: 4157259687 Fax: 4157259689
 CC Email: myers@shgc.stanford.edu Primer A: TTGTGCTATTTCACAGGAA
 CC Primer B: GCTCAATGGCTTATCATCTG STS size: 268 PCR Profile: Initial
 CC incubation: 94 degrees C for 90 seconds Denaturation: 94 degrees C
 CC for 15 seconds Annealing: 62 degrees C for 23 seconds
 CC Polymerization: 72 degrees C for 30 seconds PCR Cycles: 30 Thermal
 CC Cycler: Perkin Elmer 9600 Protocol: Template: 25 ng Primer: each 1
 CC uM dNTPs: each 200 uM Taq Polymerase: 0.05 units/ul Total Vol: 10
 CC ul Buffer: MgCl2: 2.5 mM KCl: 50 mM Tris-HCl: 20 mM pH: 8.3
 CC Chromosome 13. NCBI gi: 1215116
 FH Key Location/Qualifiers

FT source 1..362
 FT /organism="Homo sapiens"
 FT /note="human"
 FT STS 52..319
 FT /map="13"
 FT primer_bind 52..71
 FT /map="13"
 FT primer_bind complement(300..319)
 FT /map="13"

SQ Sequence 362 BP; 104 A; 75 C; 54 G; 113 T; 16 other;

Query Match 42.2%; Score 19; DB 174; Length 362;
 Best Local Similarity 76.5%; Pred. No. 4.03e-04;
 Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 21 tcanatcatcatcatcatcatcatcacttg 54
 ||| || | |||| ||||| |||| |||

Cp 43 TCATATACTATCACCATCATATCAACTTTG 10

RESULT 9

LOCUS G17690 362 bp DNA STS 05-MAR-1996
 DEFINITION human STS SHGC-6155 clone pg-2635.
 ACCESSION G17690
 NID g1215116
 KEYWORDS STS sequence; primer; sequence tagged site.
 SOURCE human Plasmid clones, generated from a lymphoblastoid cell line
 from a human male. Localized to human chromosome 13 by analysis on

the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell
 Institute for Medical Research, Camden, NJ 08103.

ORGANISM Homo sapiens
 Eukaryota; Eukaryotes; Metazoa; Chordata;
 Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
 Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 362)
 AUTHORS Myers, R.M.
 JOURNAL Unpublished (1996)
 COMMENT

Contact: Richard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine
 Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 4157259687
 Fax: 4157259689
 Email: myers@shgc.stanford.edu

Primer A: TTGTGCTATTTCACAGGAA
 Primer B: GCTCAATGGCTTATCATCTG
 STS size: 268
 PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
 Annealing: 62 degrees C for 23 seconds
 Polymerization: 72 degrees C for 30 seconds
 PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:
 Template: 25 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Taq Polymerase: 0.05 units/ul
 Total Vol: 10 ul

Buffer:
 MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.3

Chromosome 13.
 Location/Qualifiers
 1..362
 /organism="Homo sapiens"
 /note="human"
 STS 52..319
 /map="13"
 primer_bind 52..71
 /map="13"
 primer_bind complement(300..319)
 /map="13"

BASE COUNT 104 a 75 c 54 g 113 t 16 others
 ORIGIN

Query Match 42.2%; Score 19; DB 134; Length 362;
 Best Local Similarity 76.5%; Pred. No. 4.03e-04;
 Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 21 tcanatcatcatcatcatcatcacttg 54
 ||| || | |||| ||||| |||| |||

Cp 43 TCATATACTATCACCATCATATCAACTTTG 10

Mar 19 08:13

US-08-612-929-15.rst

13

REFERENCE

1 (bases 1 to 442)
 AUTHORS
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 TITLE
 The WashU-Merck EST Project
 JOURNAL
 Unpublished (1995)
 COMMENT

GDB: G00-414-804
 Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 344
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source
 1..442
 /organism="Homo sapiens"
 /clone="42263"
 /note="human"

BASE COUNT 93 a 89 c 119 g 136 t 5 others
 ORIGIN

Query Match 42.2%; Score 19; DB 88; Length 442;
 Best Local Similarity 85.2%; Pred. No. 4.03e-04;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 123 accatctttatctacacttgggtggc 149
 ||||| | ||| ||||| |||||

Cp 30 ACCATCATATCAACACTTTGGCTGGC 4

RESULT 13

LOCUS R51415 497 bp mRNA EST 18-MAY-1995
 DEFINITION Yg72d03-r1 Homo sapiens cDNA clone 38881 5'.
 ACCESSION R51415
 NID g813317
 KEYWORDS EST.
 SOURCE human clone=38881 library=Soares infant brain INTB vector=Iafmid BA host=BH10B (ampicillin resistant) primer=M13RPI Rsite1=Not I Rsite2=Hind III Whole brain from a 73 days post natal female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGCAAGATTTCGGCGCCAGCAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Iafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 497)
 AUTHORS
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

Mar 19 08:13

US-08-612-929-15.rst

14

Wilson, R.

The WashU-Merck EST Project
 Unpublished (1995)
 COMMENT

GDB: G00-411-422

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 413

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

Location/Qualifiers
 source
 1..497
 /organism="Homo sapiens"
 /clone="38881"
 /note="human"

BASE COUNT 103 a 102 c 135 g 154 t 3 others
 ORIGIN

Query Match 42.2%; Score 19; DB 86; Length 497;
 Best Local Similarity 85.2%; Pred. No. 4.03e-04;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 154 accatctttatctacacttgggtggc 180
 ||||| | ||| ||||| |||||

Cp 30 ACCATCATATCAACACTTTGGCTGGC 4

RESULT 14

LOCUS T63218 520 bp mRNA EST 17-FEB-1995
 DEFINITION ycl5b07.r1 Homo sapiens cDNA clone 80725 5'.
 ACCESSION T63218
 NID g667083
 KEYWORDS EST.
 SOURCE human clone=80725 library=Stratagene lung (#937210)

vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
 primer=M13RPI Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72 year old male. Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence: 5'-GAATTCGGCAGG-3'; 3' adaptor sequence: 5'-CTCGAGTTTTTTTTTTTTTTT-3'.

ORGANISM

Homo sapiens
 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 520)
 AUTHORS
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 WashU-Merck EST Project
 Unpublished (1995)

TITLE

WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

Mar 19 08:13

US-08-612-929-15.fst

15

High quality sequence stops: 360
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source
1..520
/organism="Homo sapiens"
/clone="80725"
/note="human"

BASE COUNT 113 a 104 c 133 g 161 t 9 others
ORIGIN

Query Match 42.2%; Score 19; DB 118; Length 520;
Best Local Similarity 85.2%; Pred. No. 4.03e-04;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 221 accatctttatctacacttggctggc 247
||||| | ||| ||||| |||||
Cp 30 ACCATCATAATCAACACTTTGGCTGGC 4

RESULT 15

LOCUS T77507 600 bp mRNA EST 06-MAR-1995
DEFINITION yc94h02.r1 Homo sapiens cDNA clone 23907 5'.
ACCESSION T77507
NID g694710
KEYWORDS EST.
SOURCE human clone=23907 library=Soares infant brain LNIB vector=Lafmid BA
host=DHI0B (ampicillin resistant) primer=M13RP1 Rsite1=Not I
Rsite2=Hind III Whole brain from a 73 days post natal female. 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AATCGAGAAATTCGGCGCCGAGCAATTTTTTTTTTTTTTTT 3']; double-stranded
cDNA was ligated to Hind III adaptors (Pharmacia), digested with
Not I and directionally cloned into the Not I and Hind III sites of
the Lafmid BA vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.Fatima
Bonaldo.

ORGANISM

Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 600)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawking,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlffing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

GDB: G00-396-254
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence stops: 454
Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source
1..600
/organism="Homo sapiens"

Mar 19 08:13

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16

/clone="23907"
/note="human"

BASE COUNT 142 a 123 c 148 g 181 t 6 others
ORIGIN

Query Match 42.2%; Score 19; DB 122; Length 600;
Best Local Similarity 85.2%; Pred. No. 4.03e-04;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 319 accatctttatctacacttggctggc 345
||||| | ||| ||||| |||||
Cp 30 ACCATCATAATCAACACTTTGGCTGGC 4

Search completed: Wed Mar 19 08:15:31 1997
Job time : 76 secs.

M A P S E R F

(TM)

Release 2.1D John F. Collins, Blocomputing Research Unit.
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MPPerch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:13:33 1997; MasPar time 11.66 Seconds
Tabular output not generated. 336.606 Million cell updates/sec

Title: >US-08-612-929-15
Description: (1-45) from US08612929.seq
Perfect Score: 45
N.A. Sequence: 1 AAGCGAGCGCAAGCTGATTATGATGGTGATGATATATGAAAC 45
Comp: TTCCGTCGGTTCACACTTACTTACCACTATCATATATCTTC

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 6.151; Variance 4.302; scale 1.430

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.
1	45	100.0	333 12	Q70376	Chimeric anti HIV ant 1.41e-13
2	45	100.0	333 12	Q70372	Anti HIV antibody lig 1.41e-13
3	45	100.0	333 11	Q65554	Mouse anti-HIV mu5.5 1.41e-13
4	45	100.0	333 11	Q65558	Mouse-human chimeric 1.41e-13
5	45	100.0	334 1	N90492	Gene fragment of immu 1.41e-13
6	45	100.0	393 14	Q73986	Humanized antibody 3B 1.41e-13
7	45	100.0	396 14	Q83490	Mouse MAb 3B9 light c 1.41e-13
8	45	100.0	733 4	Q25658	Mouse 0.3beta anti-HI 1.41e-13

9	45	100.0	780 1	N90495	A V chi region gene. 1.41e-13
10	45	100.0	900 1	Q04039	Anti-Leu 3a light cha 1.41e-13
11	43	95.6	393 6	Q36609	Anti-CD4 antibody MT 1.73e-12
12	43	95.6	717 18	T04019	Anti-EGFR single chai 1.73e-12
13	41	91.1	393 14	Q83520	Humanized antibody 3B 2.10e-11
14	41	91.1	397 1	Q04041	Anti-Leu 3a light cha 2.10e-11
15	40	88.9	63 14	Q83508	IL-4 CDRI gene fragme 7.27e-11
16	40	88.9	67 14	Q83507	IL-4 CDRI gene fragme 7.27e-11
17	28	62.2	312 3	Q20309	B cell hybridoma 4:3. 1.36e-04
18	28	62.2	451 1	Q04694	Light chain variable 1.36e-04
19	28	62.2	7305 18	T15933	Anti-IgE VL expressio 1.36e-04
20	26	57.8	91 9	Q51746	Oligonucleotide probe 1.36e-03
21	26	57.8	333 18	T15726	3B1 light chain varia 1.36e-03
22	26	57.8	339 18	T04015	Anti-EGFR antibody li 1.36e-03
23	26	57.8	339 18	T04013	Anti-EGFR antibody li 1.36e-03
24	26	57.8	1797 18	T15733	3B1 single chain anti 1.36e-03
25	24	53.3	333 14	Q82818	Murine NM-01 variable 1.30e-02
26	24	53.3	334 9	Q55002	Murine anti-CD18 Ab 6 1.30e-02
27	24	53.3	334 9	Q55000	Humanised anti-CD18 A 1.30e-02
28	24	53.3	336 2	Q10379	Chimeric MAb 9.2.27 1 1.30e-02
29	24	53.3	336 16	Q96285	Human IgE receptor-bi 1.30e-02
30	24	53.3	363 10	Q56686	Sequence of the monoc 1.30e-02
31	24	53.3	393 5	Q30757	p64-k4. 1.30e-02
32	23	51.1	91 9	Q51746	Oligonucleotide probe 3.94e-02
33	22	48.9	122 4	Q26782	Oligomer ma6 used to 1.18e-01
34	22	48.9	261 17	T04628	Mouse derived light c 1.18e-01
35	22	48.9	336 16	Q96283	Human IgE receptor-bi 1.18e-01
36	22	48.9	363 6	Q37472	Sequence encoding the 1.18e-01
37	22	48.9	396 7	Q42987	Mouse 4C10 anti-idiot 1.18e-01
38	22	48.9	632 10	Q56690	Genomic sequence of t 1.18e-01
39	22	48.9	632 10	Q56691	Genomic sequence of t 1.18e-01
40	22	48.9	783 17	T08490	Anti-c5 MAb N19/8 scF 1.18e-01
41	21	46.7	333 11	Q63908	Light chain variable 3.48e-01
42	21	46.7	334 11	Q73749	Light chain variable 3.48e-01
43	21	46.7	363 10	Q56688	Sequence of the monoc 3.48e-01
44	20	44.4	336 2	Q12684	Murine 1B4 light chai 1.01e+00
45	19	42.2	336 16	Q74148	Human thyroid stimula 2.88e+00

ALIGNMENTS

RESULT 1
ID Q70376 standard; cDNA to mRNA; 333 BP.
AC Q70376;
DT 13-MAR-1995 (first entry)
DE Chimeric anti HIV antibody light chain variable region.
KW Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS; treatment;
KW prophylaxis; Mus musculus; Homo sapiens; ss.
OS Chimeric Homo sapiens
FH Key location/Qualifiers
FT CDS 1..333
FT /*tag= a
FT /product= Antibody light chain variable region.
PN W09415969-A.
PD 21-JUL-1994.
PF 14-JAN-1993; J00039.
PR 14-JAN-1993; AU-032671.
PR 14-JAN-1993; WO-100039.
PA (KAGA) CEMO SERO THERAPEUTIC RES INST.
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
PI Tokiyoshi S;
DR WPI; 94-249145/30.

DR P-PSDB; R60306.
PT Recombinant chimeric anti HIV antibody - useful for the treatment
PT and prevention of HIV
PS Claim 14; Figure 12; 51pp; Japanese.
CC The recombinant antibody light chain has neutralising activity
CC against HIV. Chimeric antibodies comprising both mouse and human
CC sequences are useful in the treatment/prevention of AIDS caused by
CC HIV. This sequence is derived from the mu5.5 anti HIV monoclonal
CC antibody producing cell.
SQ Sequence 333 BP; 95 A; 90 C; 88 G; 60 T;

Query Match 100.0%; Score 45; DB 12; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.41e-13;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aagccagccaaaagttgattatgatggtgatgattatgaac 114
|||||
Qy 1 AAGGCCAGCCAAAAGTGTGATTATGATGCGTAGTATTATGAAC 45

RESULT 2

ID Q70372 standard; cDNA to mRNA; 333 BP.
AC Q70372;
DT 09-MAR-1995 (first entry)
DE Anti HIV antibody light chain variable region.
KW Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS; treatment;
KW prophylaxis; Mus musculus; Homo sapiens; ss.
OS Mus musculus.
EF Key Location/Qualifiers
FH CDS 1..333
FT /*tag= a
FT /product= Antibody light chain variable region.
PN W09415969-A.
PD 21-JUL-1994.
PF 14-JAN-1993; J00039.
PP 14-JAN-1993; AU-032671.
PR 14-JAN-1993; WO-J00039.
PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shioesaki K;
PI Tokiyoshi S;
DR WPI; 94-249145/30.
DR P-PSDB; R60302.
PT Recombinant chimeric anti HIV antibody - useful for the treatment
PT and prevention of HIV
PS Claim 15; Figure 4; 51pp; Japanese.
CC The recombinant antibody light chain has neutralising activity
CC against HIV. Chimeric antibodies comprising both mouse and human
CC sequences are useful in the treatment/prevention of AIDS caused by
CC HIV. This sequence is obtained from the mu5.5 anti HIV monoclonal
CC antibody producing cell.
SQ Sequence 333 BP; 88 A; 83 C; 86 G; 76 T;

Query Match 100.0%; Score 45; DB 12; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.41e-13;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aagccagccaaaagttgattatgatggtgatgattatgaac 114
|||||
Qy 1 AAGGCCAGCCAAAAGTGTGATTATGATGCGTAGTATTATGAAC 45

RESULT 3

ID Q65554 standard; cDNA; 333 BP.

AC	Q65554;	
DE	27-JAN-1995 (first entry)	
DT	Mouse anti-HIV mu5.5 light chain variable region cDNA.	
DE	Immunoglobulin; light chain; anti-HIV antibody; neutralisation;	
KW	human immunodeficiency virus; variable region; VL chain; murine; ds.	
OS	Mus musculus.	
FT	Key	Location/Qualifiers
FT	misc_feature	70..114
FT	/*tag= a	
FT	/note= "encodes CDR1"	
FT	misc_feature	160..180
FT	/*tag= b	
FT	/note= "encodes CDR2"	
FT	misc_feature	277..303
FT	/*tag= c	
FT	/note= "encodes CDR3"	
PN	J06125783-A.	
PD	10-MAY-1994.	
PF	28-DEC-1991; 359808.	
PR	28-DEC-1991; JP-359808.	
PA	(KAGA-) ZH KAGAKO KESSEI-RYOHO KENKYUSHO.	
DR	WPI; 94-187942/23.	
DR	P-PSDB; R55123.	
PT	Mouse-human chimeric anti-HIV antibody heavy and light chains -	
PT	and recombinant antibody consisting of the H- and L-chains,	
PT	useful in AIDS therapy	
PS	Example 3; Fig 4; 22pp; Japanese.	
CC	Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.	
CC	The heavy and light chain variable regions from these antibodies	
CC	were sequenced (Q65551-Q65554). The murine anti-HIV CDRs were	
CC	introduced into human framework regions to construct chimeric	
CC	antibodies (Q65555-Q65558).	
SQ	Sequence 333 BP; 88 A; 83 C; 86 G; 76 T;	
Query Match 100.0%; Score 45; DB 11; Length 333;		
Best Local Similarity 100.0%; Pred. No. 1.41e-13;		
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	70 aagccagcagaagtgtgattatgattatgattgattgattatgaac 114	
QY	1 AAGGCCGCCAAAGTGTTCATTATGATGCGTGATGTTATATGAAC 45	
RESULT	4	
ID	Q65558 standard; cDNA; 333 BP.	
AC	Q65558;	
DT	30-JAN-1995 (first entry)	
DE	Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.	
KW	Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;	
KW	human immunodeficiency virus; variable region; VL chain; murine;	
KW	chimeric; humanised; ds.	
OS	Chimeric Mus musculus.	
OS	Chimeric Homo sapiens.	
FT	Key	Location/Qualifiers
FT	misc_feature	70..114
FT	/*tag= a	
FT	/note= "encodes murine CDR1"	
FT	misc_feature	160..180
FT	/*tag= b	
FT	/note= "encodes murine CDR2"	
FT	misc_feature	277..303
FT	/*tag= c	
FT	/note= "encodes murine CDR3"	
PN	J06125783-A.	

PD 10-MAY-1994.
PF 28-DEC-1991; 359808.
PR 28-DEC-1991; JP-359808.
PA (KAGA-) ZH KAGAKU KESSEL-RYOHO KENKYUSHO.
DR WPI; 94-187942/23.
DR P-PSDB; R55127.
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
PT and recombinant antibody consisting of the H- and L-chains,
PT useful in AIDS therapy
PS Claim 5; Fig 12; 22pp; Japanese.
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (Q65551-Q65554). The murine anti-HIV CDRs were
CC introduced into human framework regions to construct chimeric
CC antibodies (Q65555-Q65558).
SQ Sequence 333 BP; 95 A; 90 C; 88 G; 60 T;
Query Match 100.0%; Score 45; DB 11; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.41e-13;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 70 aagccagcagcaagtgttgattatgatgtgatgtatgtatgaac 114
|||||
QY 1 AAGGCCAGCCAAAGTGTGATTATGATGCTGATGTTATATGAAC 45
RESULT 5
ID N90492 standard; DNA; 334 BP.
AC N90492;
DT 20-OCT-1989 (first entry)
DE Gene fragment of immunoglobulin L chain variable region.
KW Gene fragment; immunoglobulin; L chain variable region; HIV.
OS Mus musculus
FH Key Location/Qualifiers
FT CDS 1..333
FT /*tag= a
FT EP-327000-A.
PD 09-AUG-1989.
PF 30-JAN-1989; 101583.
PR 30-JAN-1988; JP-20255.
PR 08-JUL-1988; JP-171385.
PA (KAGA) The Chemo-Sero-Therapeutic Research Institute.
PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,
PI Takatsuki K;
DR WPI; 89-229050/32.
PT Chimeric anti-human immune virus antibodies - contg. mouse variable
PT regions and human constant regions for diagnosis, treatment and
PT prevention of AIDS
PS Claim 6; page 15; 33pp; English.
CC The gene fragment encodes an L chain variable region from an
CC immunoglobulin with anti-HIV neutralising activity. It is used, with an
CC H chain variable region gene fragment (see N90491), to produce a chimeric
CC anti-HIV antibody with mouse variable regions and human constant regions.
CC The antibody retains its original specificity, but have much lower
CC antigenicity to humans. See also P90541, N90493 and N90495.
SQ Sequence 334 BP; 91 A; 83 C; 81 G; 79 T;
Query Match 100.0%; Score 45; DB 1; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.41e-13;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 70 aagccagcagcaagtgttgattatgatgtgatgtatgtatgaac 114
|||||
QY 1 AAGGCCAGCCAAAGTGTGATTATGATGCTGATGTTATATGAAC 45

RESULT 6
ID Q73986 standard; cDNA; 393 BP.
AC Q73986;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW Mab; interleukin-4; IL-4; allergy; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..393
FT /*tag= a
FT sig_peptide 1..60
FT /*tag= b
FT mat_peptide 61..393
FT /*tag= c
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 14-OCT-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR P-PSDB; R75355.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.5; 97pp; English.
CC A humanized antibody light chain variable region and signal
CC sequence is given in R75355. The signal sequence is also
CC provided in R70194. The sequences of the first 2 CDRs
CC are identical to mouse anti-human IL-4 Mab 3B9 light chain
CC CDRs (given in R70195-96), but the third (R70201) differs
CC by a single amino acid from the native mouse CDR (R70197).
SQ Sequence 393 BP; 97 A; 96 C; 108 G; 92 T;
Query Match 100.0%; Score 45; DB 14; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.41e-13;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 127 aagccagcagcaagtgttgattatgatgtgatgtatgtatgaac 171
|||||
QY 1 AAGGCCAGCCAAAGTGTGATTATGATGCTGATGTTATATGAAC 45
RESULT 7
ID Q83490 standard; cDNA; 396 BP.
AC Q83490;
DT 20-SEP-1995 (first entry)
DE Mouse Mab 3B9 light chain.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; ds.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 1..396
FT /*tag= a
FT sig_peptide 1..60
FT /*tag= b
FT mat_peptide 61..396
FT /*tag= c
PN W09507301-A.

PD 16-MAR-1995.
 PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Groas MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR P-PSDB; R70189.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Fig.1; 97pp; English.
 CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 MAb secretion. *Only
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 CC chains were cloned into pCEM7f+ and transformed into E. coli
 CC DH5-alpha. The clones were sequenced (Q83490-91), and used for
 CC antibody engineering.
 SQ Sequence 396 BP; 99 A; 103 C; 103 G; 91 T;
 Query Match 100.0%; Score 45; DB 14; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1.41e-13;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 130 aaggccagccaaagtgtgattatgatggtgatgtatgatgaac 174
 ||||||||||||||||||||||||||||||||||||||||||||
 QY 1 AAGCCAGCCAAAGTGTGATTATGATGCTGCTAGTATATGAAC 45

RESULT 8
 ID Q25658 standard; DNA; 733 BP.
 AC Q25658;
 DT 08-DEC-1992 (first entry)
 DE Mouse 0.5beta anti-HIV antibody Light chain.
 KW Heavy; light; CDR; HIV; AIDS; FR; framework region; ds.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT primer_bind complement (77..106)
 FT /*tag= a
 FT /note= "binding site for the primer
 FT represented Q30550"
 FT primer_bind 709..730
 FT /*tag= b
 FT /note= "binding site for the primer
 FT represented Q30551"
 PN J04141095-A.
 PD 14-MAY-1992.
 PF 02-OCT-1990; 266091.
 PR 02-OCT-1990; JP-266091.
 PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.
 DR WPI; 92-212765/26.
 PT New recombinant modified anti-HIV antibodies - comprise human x
 PT mouse modified antibody H and L chains
 PS Disclosure; Fig 4; 15pp; Japanese.
 CC Recombinant modified anti-HIV antibodies comprise framework regions
 CC derived from human antibody and CDRs derived from mouse monoclonal
 CC antibody 0.3beta. The anti-HIV modified antibody can be used for
 CC the prophylaxis and treatment of AIDS.
 SQ Sequence 733 BP; 194 A; 162 C; 161 G; 216 T;
 Query Match 100.0%; Score 45; DB 4; Length 733;
 Best Local Similarity 100.0%; Pred. No. 1.41e-13;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 451 aaggccagccaaagtgtgattatgatggtgatgtatgatgaac 495
 ||||||||||||||||||||||||||||||||||||||||||||
 QY 1 AAGCCAGCCAAAGTGTGATTATGATGCTGCTAGTATATGAAC 45

RESULT 9
 ID N90495 standard; DNA; 780 BP.
 AC N90495;
 DT 24-OCT-1989 (first entry)
 DE A V chi region gene.
 KW V chi region gene; immunoglobulin; L chain variable region; HIV.
 OS Mus musculus
 FH Key Location/Qualifiers
 FT exon 119..167
 FT /*tag= a
 FT exon 398..742
 FT /*tag= b
 PN EP-327000-A.
 PD 09-AUG-1989.
 PF 30-JAN-1989; 101583.
 PR 30-JAN-1988; JP-20255.
 PR 08-JUL-1988; JP-171385.
 PA (KAGA) The Chemo-Sero-Therapeutic Research Institute.
 PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,
 PI Takatsuki K;
 DR WPI; 89-229050/32.
 DR P-PSDB; P90543.
 PT Chimeric anti-human immune virus antibodies - contg. mouse variable
 PT regions and human constant regions for diagnosis, treatment and
 PT prevention of AIDS
 PS Disclosure; Fig 7; 33pp; English.
 CC The sequence is a V chi region gene, encoding an L chain variable region
 CC (see P90543). See also N90491-3.
 SQ Sequence 780 BP; 205 A; 172 G; 171 G; 232 T;
 Query Match 100.0%; Score 45; DB 1; Length 780;
 Best Local Similarity 100.0%; Pred. No. 1.41e-13;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 478 aaggccagccaaagtgtgattatgatggtgatgtatgatgaac 522
 ||||||||||||||||||||||||||||||||||||||||||||
 QY 1 AAGCCAGCCAAAGTGTGATTATGATGCTGCTAGTATATGAAC 45

RESULT 10
 ID Q04039 standard; DNA; 900 BP.
 AC Q04039;
 DT 06-SEP-1990 (first entry)
 DE Anti-Leu 3a light chain variable region gene, 206 Vx.
 KW HIV; AIDS; anti-Leu3A; vaccine; ds.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT exon 259..307
 FT /*tag= a
 FT intron 308..537
 FT /*tag= b
 FT exon 538..882
 FT /*tag= c
 PN EP-365209-A.
 PD 25-APR-1990.
 PF 11-OCT-1989; 010415.
 PR 17-OCT-1988; US-260558.
 PA (BECT) Becton Dickinson Co.

PI Hinton R, Oi VT;
DR WPI; 90-126329/17.
DR P-PSDB; R04132.
PT New chimeric variants of murine antibody anti-leucine -
PT contg. human antibody regions, and DNA encoding sequences.
PS Claim 1; Fig 2; 12pp; English.
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
CC used to form chimeric mouse-variable, human-constant region Abs
CC suggested as being useful as a vaccine to HIV.
SQ Sequence 900 BP; 261 A; 206 C; 187 G; 246 T;

Query Match 100.0%; Score 45; DB 1; Length 900;
Best Local Similarity 100.0%; Pred. No. 1.41e-13;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 618 aagccagcacaagtgttgattatgatgtgatgttatgatgaac 662
|||||
QY 1 AAGCCAGCCAAAGTGTGATTATGATGCTGATGATTATATGAAC 45

RESULT 11

ID Q36609 standard; DNA; 393 BP.
AC Q36609;
DT 02-JUN-1993 (first entry)
DE Anti-CD4 antibody MT 3.10 light chain variable region.
KW immunosuppression; tissue transplantation; graft; L chain; V region;
KW T-helper cell inhibition; transplant rejection; MAb;
KW interleukin-2 receptor; ss.
FH Key Location/Qualifiers
FT sig_peptide 1..60
FT /*tag= a
FT mat_peptide 61..393
FT /*tag= b
FT /*note= "J1 region begins at position 361"
PN D04143214-A.
PD 28-JAN-1993.
PF 30-DEC-1991; 143214.
PR 25-JUL-1991; DE-124759.
PR 30-DEC-1991; DE-143214.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
PI Kaluza B, Riethmuller G, Scheuer W, Weidle U;
DR WPI; 93-037582/05.
DR P-PSDB; R32123.
PT Synergistic antibody compen. for use as immunosuppressant -
PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
PT alpha- or anti-IL2R beta antibodies
PS Claim 5; Page 11; 18pp; German.
CC This sequence encodes the light chain variable region of a preferred
CC anti-CD4 monoclonal antibody for use in the claimed synergistic
CC composition. MAb MT 3.10 is deposited as clone 3.101/SB10 (ECACC
CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R
CC alpha or beta antibody. Individually the antibodies are strongly
CC inhibiting and when used together their immunosuppressive properties
CC are improved; they synergistically inhibit T-helper cell
CC proliferation to effectively inhibit transplant rejection at low
CC doses without significantly reducing the general immune response.
CC See Q36607-Q36616.
SQ Sequence 393 BP; 100 A; 105 C; 98 G; 90 T;

Query Match 95.6%; Score 43; DB 6; Length 393;
Best Local Similarity 97.8%; Pred. No. 1.73e-12;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 130 aagccagcacaagtgttgattatgatgtgatgttatgatgaac 174

QY 1 AAGCCAGCCAAAGTGTGATTATGATGCTGATGATTATATGAAC 45
|||||

RESULT 12

ID T04019 standard; cDNA; 717 BP.
AC T04019;
DT 02-JUL-1996 (first entry)
DE Anti-EGFR single chain antibody (Clone 4 B 2).
KW Single chain antibody; antibody; epidermal growth factor receptor;
KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
KW assessment; phage antibody library; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 1..717

FT /*tag= a
FT /product= Single chain antibody.
PN W09525167-A1.
PD 21-SEP-1995.
PF 16-MAR-1995; E00978.
PR 17-MAR-1994; EP-104160.
PR 02-DEC-1994; EP-118970.
PA (MERE) MERCK PATENT GMBH.

PI Adan J, Ansell KH, Bendig MM, Blasco F, Guesow D;
PI Kettleborough AC, Mitjans F, Piulats J, Rosell E;
DR WPI; 95-336972/43.
DR P-PSDB; R79866.
PT Anti-EGFR antibodies and single chain Fv antibody fragments -
PT obtained from phage-antibody libraries, useful for diagnosis and
PT therapy of tumours
PS Claim 4; Page 57; 93pp; English.
CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies
CC and antibodies constructed from anti-EGFR antibody fragments can be
CC used for diagnosis of tumours and assessment of tumour growth in
CC vitro and in vivo. They may also be used in a pharmaceutical
CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
CC The antibodies and fragments are derived from mice but are humanised
CC so as to cause minimum reaction against them. They are produced
CC using the phage antibody library. (See T04011-T04026 and
CC R79858-R79873)

SQ Sequence 717 BP; 165 A; 169 C; 213 G; 170 T;

Query Match 95.6%; Score 43; DB 18; Length 717;
Best Local Similarity 97.8%; Pred. No. 1.73e-12;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 472 aagccagcacaagtgttgattatgatgtgatgttatgatgaac 516
|||||
QY 1 AAGCCAGCCAAAGTGTGATTATGATGCTGATGATTATATGAAC 45

RESULT 13

ID Q83520 standard; cDNA; 393 BP.
AC Q83520;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW MAb; interleukin-4; IL-4; allergy; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..393

FT /*tag= a

PN W09507301-A.

PD 16-MAR-1995.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SCLEROGLIANT, RYONOLAPINE, SURGEON, BURLING, AND
1 (bases 1 to 262)
Mo, J. A., Bona, C. A. and Holmdahl, R.
TITLE
Variable region gene selection of immunoglobulin G expressing B
cells with specificity for a defined epitope on type II collagen

JOURNAL Eur. J. Immunol. (1993) In press
REFERENCE 2 (bases 1 to 262)
AUTHORS Mo, J.A.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE 3 (bases 1 to 262)
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE 94009207
FEATURES Location/Qualifiers
source
1..262
/organism="Mus musculus"
/strain="DBA/1"
/dev_stage="adult"
/tissue_type="lymph node"
/cell_type="B cell hybridoma"
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BASE COUNT 71 a 66 c 66 g 59 t
ORIGIN
Query Match 100.0%; Score 45; DB 64; Length 262;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 35 aagggcagccaaagtgtgattgatggtgatgattatgaac 79
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Qy 1 AAGGCCACCAAGTTGATTATGATGCTGATGCTATATGAAC 45
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RESULT 4
LOCUS MWIGKCVRI 264 bp RNA ROD 13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION 225458
NID 9407844
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
1 (bases 1 to 264)
Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. (1993) In press
REFERENCE 2 (bases 1 to 264)
AUTHORS Mo, J.A.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE 3 (bases 1 to 264)
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE 94009207
FEATURES Location/Qualifiers
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/gene="Igk"
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BASE COUNT 71 a 67 c 67 g 59 t
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Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 37 aagggcagccaaagtgtgattgatggtgatgattatgaac 81
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Qy 1 AAGGCCACCAAGTTGATTATGATGCTGATGCTATATGAAC 45
|||||
RESULT 5
LOCUS MWIGKCVRC 266 bp RNA ROD 13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION 225446
NID 9407834
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
1 (bases 1 to 266)
Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. (1993) In press
REFERENCE 2 (bases 1 to 266)
AUTHORS Mo, J.A.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE 3 (bases 1 to 266)

AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE 94009207
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/db_xref="PID:g407835"
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BASE COUNT 71 a 67 c 68 g 60 t
ORIGIN

Query Match 100.0%; Score 45; DB 64; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 39 aagggcagcaagtggtgattatgatgtgatgtatgatgaac 83
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Qy 1 AAGGCCAGCCAAAGTGTGATTATGATGTCGATGATGATGATGAAC 45

RESULT 6
LOCUS MMIGKCVRF 270 bp RNA ROD 13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION Z25452
NID 9407840
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 270)
AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. (1993) In press
REFERENCE 2 (bases 1 to 270)
AUTHORS Mo,J.A.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE 3 (bases 1 to 270)
AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)

MEDLINE 94009207
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/chromosome="6"
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BASE COUNT 71 a 68 c 68 g 63 t
ORIGIN

Query Match 100.0%; Score 45; DB 64; Length 270;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagggcagcaagtggtgattatgatgtgatgtatgatgaac 87
|||||
Qy 1 AAGGCCAGCCAAAGTGTGATTATGATGTCGATGATGATGATGAAC 45

RESULT 7
LOCUS MMIGKCVRB 270 bp RNA ROD 13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION Z25444
NID 9407832
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 270)
AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. (1993) In press
REFERENCE 2 (bases 1 to 270)
AUTHORS Mo,J.A.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE 3 (bases 1 to 270)
AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE 94009207
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/db_xref="PID:g407833"
/translation="SLAVSLGQRATISCKASQSDYDGSYNNWYQQRPGQPPKLLIY
AASNLESGIPARFSGSGGTDFTLNHPVEEEDAATYYCQSNEDP"

BASE COUNT      71 a      68 c      68 g      63 t
ORIGIN
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Query Match 100.0%; Score 45; DB 64; Length 270;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagccagcacaagtgtgattgatgtgatgtatgaac 87
|||||
Qy 1 AAGCCAGCCCAAGTGTGATTATGATGGTGATGATTATGAAC 45

RESULT 8
LOCUS MM1GKCVRG 270 bp RNA ROD 13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION Z25454
NID g407842
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 270)
AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen Eur. J. Immunol. (1993) In press
JOURNAL 2 (bases 1 to 270)
AUTHORS Mo,J.A.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE 3 (bases 1 to 270)
AUTHORS Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen Eur. J. Immunol. 23 (10), 2503-2510 (1993)
JOURNAL 94009207
MEDLINE
FEATURES
source Location/Qualifiers
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BASE COUNT      71 a      68 c      68 g      63 t
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Query Match 100.0%; Score 45; DB 64; Length 270;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 aagccagcacaagtgtgattgatgtgatgtatgaac 87
|||||
Qy 1 AAGCCAGCCCAAGTGTGATTATGATGGTGATGATTATGAAC 45

RESULT 9
LOCUS MUSICKAANA 279 bp mRNA ROD 07-MAR-1995
DEFINITION Mouse Igk chain mRNA, VJ5 region.
ACCESSION M57978
NID g196402
KEYWORDS J-region; V-region; anti-cytochrome c antibody; immunoglobulin kappa-chain; immunoglobulin light chain.
SOURCE (BALB/c) secondary B cell hybridoma 1G3 mRNA, clone 1G3.E3.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 279)
AUTHORS Goshorn,S.C., Retzel,E. and Jemmerson,R.
TITLE Common structural features among monoclonal antibodies binding the same antigenic region of cytochrome c
JOURNAL 91115823
MEDLINE
FEATURES Location/Qualifiers
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/clone="1G3.E3"
/strain="BALB/c"
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/sequenced_mol="cDNA to mRNA"
/tissue_type="hybridoma"
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/gene="Igk"
1..279
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/gene="Igk"
/map="chromosome 6"
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/db_xref="PID:g196403"
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103..123
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/ note="CDR2"
220..246
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/ map="chromosome 6"
/ note="CDR3"
241..279
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misc_feature
75 a 73 c 69 g 62 t
ORIGIN Chromosome 6.

Query Match 100.0%; Score 45; DB 66; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 aagccagcaagtgttattatgatgtgtagttatatgaac 57
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Qy 1 AAGGCCAGCCAAAGTGTGATTATGATGCTGATGTTATATGAAC 45

RESULT 10
LOCUS MMU29628 286 bp mRNA ROD 08-DEC-1995
DEFINITION Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region,
hybridoma 52.60, partial cds.
ACCESSION U29628
NID 9896124
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 286)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Light chain contribution to specificity in anti-DNA antibodies
JOURNAL J. Immunol. 155 (6), 3223-3233 (1995)
MEDLINE 95403997
REFERENCE 2 (bases 1 to 286)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology,
Princeton University, Princeton, NJ 08544, USA
FEATURES
source
location/Qualifiers
1..286
/organism="Mus musculus"
/strain="BALB/c"
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/ note="V-J region"
/codon_start=1
/product="Ig kappa chain"
/db_xref="PID:g896125"
/translation="DIVLTQSPASIVSLQQRATISKASQSVYDGDSYMMYQQKP
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CDS
74 a 75 c 69 g 68 t
ORIGIN

BASE COUNT 74 a 75 c 69 g 68 t
ORIGIN
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Query Match 100.0%; Score 45; DB 65; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aagccagcaagtgttattatgatgtgtagttatatgaac 114
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Qy 1 AAGGCCAGCCAAAGTGTGATTATGATGCTGATGTTATATGAAC 45

RESULT 11
LOCUS MMU29629 297 bp mRNA ROD 08-DEC-1995
DEFINITION Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region,
hybridoma 52.468, partial cds.
ACCESSION U29629
NID 9896126
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 297)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Light chain contribution to specificity in anti-DNA antibodies
JOURNAL J. Immunol. 155 (6), 3223-3233 (1995)
MEDLINE 95403997
REFERENCE 2 (bases 1 to 297)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology,
Princeton University, Princeton, NJ 08544, USA
FEATURES
source
location/Qualifiers
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<1..>297
/ note="V-J region"
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/product="Ig kappa chain"
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/translation="DIVLTQSPASIVSLQQRATISKASQSVYDGDSYMMYQQKP
GQPKLLIYAASNLSCVPARFSGSGTDFTLIHVPEEDAAITYCQOSNEDP"

BASE COUNT 78 a 77 c 72 g 70 t
ORIGIN

Query Match 100.0%; Score 45; DB 65; Length 297;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aagccagcaagtgttattatgatgtgtagttatatgaac 114
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Qy 1 AAGGCCAGCCAAAGTGTGATTATGATGCTGATGTTATATGAAC 45

RESULT 12
LOCUS MMU07207 333 bp mRNA ROD 08-OCT-1994
DEFINITION Mus musculus clone 31 anti-C5a Ig light chain V region mRNA,
partial cds.
ACCESSION U07207
NID 9459212
KEYWORDS .
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SOURCE
ORGANISM      mouse.
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Rodentia; Myomorpha; Muridae; Mus.
REFERENCE
1 (bases 1 to 333)
AUTHORS      Ames,R.S., Tornetta,M.A., Jones,C.S. and Tsui,P.
TITLE        Isolation of neutralizing anti-C5a monoclonal antibodies from a
              filamentous phage monovalent Fab display library [published erratum
              appears in J Immunol 1994 Jul 15;153(2):910]
JOURNAL      J. Immunol. 152 (9), 4572-4581 (1994)
MEDLINE      94209678
REFERENCE
2 (bases 1 to 333)
AUTHORS      Ames,R.S.
TITLE        Direct Submission
JOURNAL      Submitted (28-FEB-1994) Robert S. Ames, Molecular Genetics,
              SmithKline Beecham Pharmaceuticals, 709 Swedeland Road, PO Box
              1539, King of Prussia, PA 19406-0939, USA
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            GGGTKLEIK"
            89 a      86 c      81 g      77 t
BASE COUNT
ORIGIN
Query Match      100.0%; Score 45; DB 64; Length 333;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 70 aagccagccaaagtgtgattgatgtatgtatgtatgtatgaac 114
|||||
QY 1 AAGGCCAGCCAAAGCTTGATTGATTGATGCTAGTATTATATGAAC 45
|||||

RESULT 13
LOCUS      MUSIGL5B      333 bp      DNA      ROD      01-NOV-1991
DEFINITION      Mouse IgL chain H2L2 V-region, partial cds.
ACCESSION      M80406
NID           g197577
KEYWORDS      V-region; immunoglobulin light chain.
SOURCE        Mus musculus (strain BALB/c, sub_species domesticus) (library:
              lambda-gt11) DNA.
ORGANISM      Mus musculus
              Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
              Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE
1 (bases 1 to 333)
AUTHORS      Matsushita,S., Maeda,H., Kimachi,K., Eda,Y., Maeda,Y., Hattori,T.,
              Tokiyoshi,S. and Takatsuki,K.
TITLE        Characterization of a mouse/human chimeric monoclonal antibody
              (C-beta-1) to a principal neutralizing domain of the human
              immunodeficiency virus type 1 envelope protein
JOURNAL      Unpublished (1991)
FEATURES
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/db_xref="PID:g197578"
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70..114
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/gene="0.5 beta-VL"
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304..333
/gene="0.5 beta-VL"
/note="FR4"
BASE COUNT      91 a      82 c      81 g      79 t
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Query Match      100.0%; Score 45; DB 67; Length 333;
Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 70 aagccagccaaagtgtgattgatgtatgtatgtatgaac 114
|||||
QY 1 AAGGCCAGCCAAAGCTTGATTGATTGATGCTAGTATTATATGAAC 45
|||||

RESULT 14
LOCUS      S42888      333 bp      DNA      ROD      09-NOV-1992
DEFINITION      Ig V kappa =immunoglobulin V kappa region [mice, hybridoma 54' CB1,
              Genomic, nt].
ACCESSION      S42888
NID           q254222
KEYWORDS      .
SOURCE        mice hybridoma 54' CB1.
ORGANISM      Mus sp.
              Unclassified.
REFERENCE      1 (bases 1 to 333)
AUTHORS      Matsushita,S., Maeda,H., Kimachi,K., Eda,Y., Maeda,Y., Murakami,T.,
              Tokiyoshi,S. and Takatsuki,K.
TITLE        Characterization of a mouse/human chimeric monoclonal antibody (C
              beta 1) to a principal neutralizing domain of the human
              immunodeficiency virus type 1 envelope protein
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LOCUS MUSIGKABC 350 bp mRNA ROD 29-OCT-1994
DEFINITION Mouse Ig kappa chain mRNA, V-J region from hybridoma MOR8.2.1,
partial cds.
ACCESSION M92401
NID g196481
KEYWORDS J-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa; morphine specific antibody; processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) B-lymphocyte
cDNA to mRNA.

ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 350)
AUTHORS Sawada, J., Yamazaki, T. and Terao, T.
TITLE Molecular and biochemical analyses of combining sites of monoclonal
anti-morphine antibodies
JOURNAL Mol. Immunol. 30 (1), 77-86 (1993)
MEDLINE 93109376
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LOCUS MUSIGKAF 360 bp mRNA ROD 30-AUG-1991
DEFINITION Mouse Ig active kappa chain mRNA V-region (V-D-J).
ACCESSION M61046
NID g196679
KEYWORDS anti-CD4; immunoglobulin light chain; monoclonal antibody.
SOURCE Mouse, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 360)
AUTHORS Attanasio, R., Dilley, D., Buck, D.W., Maino, V.C., Lohman, K.L.,
Kanda, P. and Kennedy, R.C.
TITLE Structural characterization of a cross-reactive idiotype shared by
monoclonal antibodies specific for the human CD4 molecule
JOURNAL J. Biol. Chem. 266, 14611-14619 (1991)
MEDLINE 91317827
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ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 354)
AUTHORS Lohman, K.L., Buck, D.W., Carrillo, M.A. and Kennedy, R.C.
TITLE Characterization of murine monoclonal anti-CD4; epitope
recognition, idiotope expression, and variable gene sequence
JOURNAL Unpublished (1992)
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Qy 1 AAGGCCAGCCAAAGTGTGATTATGATGCTGATGTTATATGAAC 45

LOCUS MUSIGKAF 360 bp mRNA ROD 30-AUG-1991
DEFINITION Mouse Ig active kappa chain mRNA V-region (V-D-J).
ACCESSION M61046
NID g196679
KEYWORDS anti-CD4; immunoglobulin light chain; monoclonal antibody.
SOURCE Mouse, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 360)
AUTHORS Attanasio, R., Dilley, D., Buck, D.W., Maino, V.C., Lohman, K.L.,
Kanda, P. and Kennedy, R.C.
TITLE Structural characterization of a cross-reactive idiotype shared by
monoclonal antibodies specific for the human CD4 molecule
JOURNAL J. Biol. Chem. 266, 14611-14619 (1991)
MEDLINE 91317827
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RESULT 20
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DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial
          cds.
ACCESSION M97871
NID g198669
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
          processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c
          fusion hybridoma cDNA to mRNA.
ORGANISM Mus musculus
          Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
          Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 363)
AUTHORS Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.
TITLE Characterization of murine monoclonal anti-CD4; epitope
        recognition, idiotope expression, and variable gene sequence
JOURNAL Unpublished (1992)
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DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial
          cds.
ACCESSION M97879
NID g198681
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
          processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c
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fusion hybridoma cDNA to mRNA.
Mus musculus
          Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
          Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 363)
AUTHORS Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.
TITLE Characterization of murine monoclonal anti-CD4; epitope
        recognition, idiotope expression, and variable gene sequence
JOURNAL Unpublished (1992)
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Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 aagccagccaaagtgttgattgatggtgatgatttatgaac 114
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Qy 1 AAGGCCAGCCAAAGTCTTGATTATGATGCTGATGTTATATGAAC 45

RESULT 22
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DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial
          cds.
ACCESSION M97869
NID g198667
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
          processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c
          fusion hybridoma cDNA to mRNA.
ORGANISM Mus musculus
          Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
          Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 363)
AUTHORS Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.
TITLE Characterization of murine monoclonal anti-CD4; epitope
        recognition, idiotope expression, and variable gene sequence
JOURNAL Unpublished (1992)
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US-08-612-929-15 rge

21

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Best Local Similarity 100.0%; Pred. No. 2.65e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 23
LOCUS I08223 900 bp PAT 14-NOV-1994

DEFINITION Sequence 1 from patent EP 0365209.

ACCESSION I08223

NID g589062

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 900)

AUTHORS Hinton,R. and Oi,V.T.

TITLE Anti-leu 3A amino acid sequence

JOURNAL Patent: EP 0365209-A2 1 25-APR-1990;

FEATURES Location/Qualifiers

source 1..900

BASE COUNT 261 a 206 c 187 g 246 t

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Search completed: Wed Mar 19 15:53:40 1997
Job time : 98 secs.

WUQREH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPerch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:17:42 1997; MasPar time 57.36 Seconds
161.474 Million cell updates/sec

Tabular output not generated.

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Perfect Score: 21
N.A. Sequence: 1 CGTCATCCCAATCTAGAATCT 21
Comp: CGAGTAGGTAGATCTTAGA

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

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171:STS43 172:STS44 173:STS45 174:STS46

Statistics: Mean 6.496; Variance 1.216; scale 5.342

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c 3	17	81.0	493	24	H59381	yl19b06.r1 Homo sapie	6.90e-06
c 4	15	71.4	265	154	W25331	zb70b03.r1 Soares fet	4.79e-03
c 5	15	71.4	265	160	H531330	zb70b03.r1 Soares fet	4.79e-03
c 6	15	71.4	391	174	H5692294	human STS SHGC-1306 c	4.79e-03
c 7	15	71.4	391	134	G16692	human STS SHGC-1306 c	4.79e-03
c 8	15	71.4	449	87	R55382	yj77b04.r1 Homo sapie	4.79e-03
c 9	15	71.4	563	17	H36087	14609 Arabidopsis tha	4.79e-03
c 10	15	71.4	598	58	N38958	yv21b03.s1 Homo sapie	4.79e-03
c 11	14	66.7	195	41	HSC10A042	H. sapiens partial cd	1.03e-01
c 12	14	66.7	248	173	DM123F11S	D. melanogaster STS d	1.03e-01
c 13	14	66.7	248	156	DM123F11S	D. melanogaster STS d	1.03e-01
c 14	14	66.7	248	129	DM123F11S	D. melanogaster STS d	1.03e-01
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c 16	14	66.7	262	170	MM4079	mb58b09.r1 Soares mou	1.03e-01
c 17	14	66.7	262	151	W17407	mb58b09.r1 Soares mou	1.03e-01
c 18	14	66.7	279	16	H31326	EST105261 Rattus sp.	1.03e-01
c 19	14	66.7	291	16	H33946	EST110402 Rattus sp.	1.03e-01
c 20	14	66.7	360	40	HSC19D091	H. sapiens partial cd	1.03e-01
c 21	14	66.7	360	3	CEIK016H7F	C.elegans cDNA clone	1.03e-01
c 22	14	66.7	365	91	R68496	yl14h11.r1 Homo sapie	1.03e-01
c 23	14	66.7	383	8	H08973	yl18g12.r1 Homo sapie	1.03e-01
c 24	14	66.7	384	24	H60570	yr41c04.s1 Homo sapie	1.03e-01
c 25	14	66.7	391	122	T78239	yr79a08.r1 Homo sapie	1.03e-01
c 26	14	66.7	396	105	T08896	EST06788 Homo sapiens	1.03e-01
c 27	14	66.7	400	174	HS883301	human STS SHGC-10649	1.03e-01
c 28	14	66.7	400	134	G16583	human STS SHGC-10649	1.03e-01
c 29	14	66.7	415	75	R14485	yf83d06.r1 Homo sapie	1.03e-01
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c 31	14	66.7	422	169	MM1305	ma42f07.r1 Soares mou	1.03e-01
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c 33	14	66.7	437	169	MM2226	ma76e06.r1 Soares mou	1.03e-01
c 34	14	66.7	462	27	H67785	yu54h10.s1 Homo sapie	1.03e-01
c 35	14	66.7	496	165	H5726325	zb36f03.r1 Soares par	1.03e-01
c 36	14	66.7	496	152	W19726	zb36f03.r1 Soares par	1.03e-01
c 37	14	66.7	504	113	T45032	8295 Arabidopsis thal	1.03e-01
c 38	14	66.7	573	153	W22023	60C10 Human retina cd	1.03e-01
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c 40	13	61.9	400	173	HS147297	human STS SHGC-9426 c	1.88e+00
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44 13 61.9 470 31 H82823 yq48q01.s1 Homo sapie 1.89e+00
45 13 61.9 487 94 R77454 yi76e04.s1 Homo sapie 1.88e+00

ALIGNMENTS

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LOCUS R91891 442 bp mRNA EST 25-AUG-1995
DEFINITION yq04d10.r1 Homo sapiens cDNA clone 195955 5'.
ACCESSION R91891
NID q959431
KEYWORDS EST.
SOURCE human clone=195955 library=Soares fetal liver spleen INFLS
vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=M13Rpl Reitel=Pac I Reitel=Eco RI
Liver and spleen from a 20 week-post conception male fetus. 1st
strand cDNA was primed with a Pac I - oligo(dT) primer [5'
AACTGAGAGATTAAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 442)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence stops: 311
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source
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mRNA
BASE COUNT 131 a 84 c 102 g 122 t 3 others
ORIGIN

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Best Local Similarity 90.5%; Pred. No. 6.90e-06;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Cp 21 AGATTCTAGATTGGATGCAGC 1

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4

RESULT 2
LOCUS R99960 468 bp mRNA EST 14-SEP-1995
DEFINITION yq77d10.r1 Homo sapiens cDNA clone 201811 5'.
ACCESSION R99960
NID g986561
KEYWORDS EST.

SOURCE human clone=201811 primer=M13Rpl library=Soares fetal liver spleen
INFLS vector=pT7T3D (Pharmacia) with a modified polylinker
host=DH10B (ampicillin resistant) Reitel=Pac I Reitel=Eco RI Liver
and spleen from a 20 week-post conception male fetus. 1st strand
cDNA was primed with a Pac I - oligo(dT) primer [5'
AACTGAGAGATTAAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 468)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence stops: 356
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source
1..468
/organism="Homo sapiens"
/clone="201811"
/note="human"
<1..>468

mRNA
BASE COUNT 132 a 95 c 111 g 128 t 2 others
ORIGIN

Query Match 81.0%; Score 17; DB 101; Length 468;
Best Local Similarity 90.5%; Pred. No. 6.90e-06;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 156 agactctacattggtgacgc 176
||||| ||||| ||||| |||||

Cp 21 AGATTCTAGATTGGATGCAGC 1

RESULT 3
LOCUS H59381 493 bp mRNA EST 06-OCT-1995
DEFINITION yr19b06.r1 Homo sapiens cDNA clone 205715 5'.

ACCESSION H59381
 NID g1012213
 KEYWORDS EST.
 SOURCE human clone=205715 primer=M13R1 library=Soares fetal liver spleen
 INFLS vector=pT7T3D (Pharmacia) with a modified polylinker
 host=DH10B (ampicillin resistant) Reitel=Pac I Reite2=Eco RI Liver
 and spleen from a 20 week-post conception male fetus. 1st strand
 cDNA was primed with a Pac I - oligo(dT) primer [5'
 AACTGCAGATTAATTAAGATCTTTTTTTTTTTTTTT 3'], double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
 I and cloned into the Pac I and Eco RI sites of the modified pT7T3
 vector. Library went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 493)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.

TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 383
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
 source
 Location/Qualifiers
 1..493
 /organism="Homo sapiens"
 /clone="205715"
 /note="human"
 mRNA <1..>493
 BASE COUNT 142 a 100 c 113 g 132 t 6 others
 ORIGIN

Query Match 81.0%; Score 17; DB 24; Length 493;
 Best Local Similarity 90.5%; Pred. No. 6.90e-06;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 157 agactctacattggtgcagc 177
 ||| ||||| ||||| ||||| |||||
 Cp 21 AGATTCTAGATTGGATGCAGC 1

RESULT 4
 LOCUS W25331 265 bp mRNA EST 07-MAY-1996
 DEFINITION zb70b03.r1 Soares fetal lung NBHL19W Homo sapiens cDNA clone 308909
 5'.
 ACCESSION W25331
 NID g1303223
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 265)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.

TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: mob.REGA+ET.

NCBI gi: 1303223
 Location/Qualifiers
 1..265
 /organism="Homo sapiens"
 /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer
 [5'-TCTTACCAATCTGAAGTGGGAGCGGCCCAATTTTTTTTTTTT-3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. This library was constructed
 from the same fetus as the fetal heart library, Soares
 fetal heart NBHL19W."
 /clone="308909"
 /clone_lib="Soares fetal lung NBHL19W"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 mRNA <1..>265
 BASE COUNT 72 a 46 c 57 g 88 t 2 others
 ORIGIN

Query Match 71.4%; Score 15; DB 154; Length 265;
 Best Local Similarity 89.5%; Pred. No. 4.79e-03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 141 gattctagttttgatgcag 159
 ||||| ||| ||||| |||
 Cp 20 GATTCTAGATTGATGCAG 2

RESULT 5
 ID H5331330 standard; RNA; EST; 265 BP.
 AC W25331;
 DT 09-MAY-1996 (Rel. 47, Created)
 DT 09-MAY-1996 (Rel. 47, Last updated, Version 1)
 DE zb70b03.r1 Soares fetal lung NBHL19W Homo sapiens cDNA clone 308909
 DE 5'.
 KW EST.


```
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea;
RN [1]
RP 1-265
RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
RA Trevaskis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;
RT "The WashU-Merck EST Project";
RL Unpublished.
CC Contact: Wilton RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu This clone is available royalty-free through
CC LNL; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: mob.REGA+ET. NCBI gi: 1303223
FH Key Location/Qualifiers
FH source 1..265
FH /organism="Homo sapiens"
FH /note="Organ: lung; Vector: pT7n3D (Pharmacia) with a
FH modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
FH strand cDNA was primed with a Not I - oligo(dT) primer
FH [5'-TGTTACCAATCTGATGGGAGCGGCCCAATTTTTTTTTTTT-3']
FH double-stranded cDNA was size selected, ligated to Eco RI
FH adapters (Pharmacia), digested with Not I and cloned into
FH the Not I and Eco RI sites of a modified pT7n3 vector
FH (Pharmacia). Library went through one round of
FH normalization to a Cot = 5. Library constructed by Bento
FH Soares and M.Fatima Bonaldo. This library was constructed
FH from the same fetus as the fetal heart library, Soares
FH fetal heart NbH19W."
FH /clone="308909"
FH /clone_lib="Soares fetal lung NbH19W"
FH /dev stage="19 weeks"
FH /lab host="DH10B (ampicillin resistant)"
FH mRNA <1...>265
SQ Sequence 265 BP; 72 A; 46 C; 57 G; 88 T; 2 other;

Query Match 71.4%; Score 15; DB 160; Length 265;
Best Local Similarity 89.5%; Pred. No. 4.79e-03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 141 gattctagtttgatgcag 159
||||||| |||||
CP 20 GATTCTAGATGGATGCAG 2

RESULT 6
ID HS692294 standard; DNA; STS; 391 BP.
AC G16692;
DT 07-MAR-1996 (Rel. 47, Created)
DT 07-MAR-1996 (Rel. 47, Last updated, Version 1)
DE human STS SHGC-1306 clone pg-299.
KW primer; sequence tagged site; STS sequence.
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea;
RN [1]
RP 1-391
RA Myers R.M.;
RT ;
RL Unpublished.
```

```
CC Contact: Richard M. Myers Stanford Human Genome Center (SHGC)
CC Stanford University School of Medicine Department of Genetics,
CC M-344, Stanford, CA 94305, USA Tel: 4157259687 Fax: 4157259689
CC Email: myers@shgc.stanford.edu Primer A: GATGCTGTGTGATGGTACAGTTC
CC Primer B: TCAGCTGCCACCTAACTTCTC STS size: 140 PCR Profile:
CC Initial incubation: 94 degrees C for 90 seconds Denaturation: 94
CC degrees C for 15 seconds Annealing: 62 degrees C for 23 seconds
CC Polymerization: 72 degrees C for 30 seconds PCR Cycles: 30 Thermal
CC Cycler: Perkin Elmer 9600 Protocol: Template: 25 ng Primer: each 1
CC uM dNTPs: each 200 uM Taq Polymerase: 0.05 units/ul Total Vol: 10
CC ul Buffer: MgCl2: 2.5 mM KCl: 50 mM Tris-HCl: 20 mM pH: 8.3
CC Chromosome 4. NCBI gi: 1214118
FH Key Location/Qualifiers
FH source 1..391
FH /organism="Homo sapiens"
FH /note="human"
FH STS 132..271
FH /map="4"
FH primer_bind 132..154
FH /map="4"
FH primer_bind complement(249..271)
FH /map="4"
SQ Sequence 391 BP; 108 A; 78 C; 88 G; 94 T; 23 other;

Query Match 71.4%; Score 15; DB 174; Length 391;
Best Local Similarity 100.0%; Pred. No. 4.79e-03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 199 tagattgattgcagc 213
||||||| |||||
CP 15 TAGATTGATGCAGC 1

RESULT 7
LOCUS G16692 391 bp DNA STS 05-MAR-1996
DEFINITION human STS SHGC-1306 clone pg-299.
ACCESSION G16692
NID g1214118
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human Plasmid clones, generated from a lymphoblastoid cell line
from a human male. Localized to human chromosome 4 by analysis on
the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell
Institute for Medical Research, Camden, NJ 08103.
ORGANISM Homo sapiens
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 391)
AUTHORS Myers, R.M.
JOURNAL Unpublished (1996)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: GATGCTGTGTGATGGTACAGTTC
Primer B: TCAGCTGCCACCTAACTTCTC
STS size: 140
```


PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl₂: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.3

Chromosome 4.

Location/Qualifiers

1..391

/organism="Homo sapiens"

/note="human"

/map="4"

/map="4"

132..154

/map="4"

complement(249..271)

/map="4"

BASE COUNT 108 a 78 c 88 g 94 t 23 others

ORIGIN

Query Match

Best Local Similarity 71.4%; Score 15; DB 134; Length 391;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 199 tagattgacgac 213

Cp 15 TAGATTGGATGCAGC 1

RESULT

LOCUS R55382 449 bp mRNA EST 22-MAY-1995

DEFINITION yj77b04.r1 Homo sapiens cDNA clone 154735 5'.

ACCESSION R55382

NID 9824677

KEYWORDS EST.

SOURCE human clone=154735 library=Soares breast 2NHBst vector=pf7T3D

(Pharmacia) with a modified polylinker host=DHI08 (ampicillin

resistant) primer=M13Rpi Rsite1=Not I Rsite2=Eco RI Adult female.

1st strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAATGGAGCGCGCCCTTTTTTTTTTT 3',

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),

digested with Not I and cloned into the Not I and Eco RI sites of a

modified pT73 vector (Pharmacia). Library went through one round

of normalization to a Cot = 230. Library constructed by Bento

Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 449)

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfs,T., Soares,M., Tan,F.,

Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 155

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LINL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

1..449

/organism="Homo sapiens"

/clone="154735"

/note="human"

BASE COUNT 124 a 87 c 108 g 124 t 6 others

ORIGIN

Query Match 71.4%; Score 15; DB 87; Length 449;

Best Local Similarity 85.7%; Pred. No. 4.79e-03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 169 agactctacattgggtgcacg 189

Cp 21 AGATTCTAGATTGGATGCAGC 1

RESULT

LOCUS H36087 563 bp mRNA EST 25-JUL-1995

DEFINITION 14609 Arabidopsis thaliana cDNA clone 17339T7.

ACCESSION H36087

NID 9905586

KEYWORDS EST.

SOURCE

thale cress clone=17339T7 library=Lambda-PRL2 strain=var columbia

vector=Lambda Zip-Lox primer=T7 dye primer Rsite1=Sal Rsite2=Not

Lambda PRL2 is a cDNA library derived from equal quantities of 4

pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated

seedlings; 2) tissue culture grown roots; 3) staged plants half

with 24 hour light cycle, half on 16 hr light, 8 hour dark-

rosettes; 4) same plants as 3 but aerial tissue (stems, flowers

and siliques). The vector is BRL's Lambda Zip-Lox. The cDNA

inserts were directionally cloned with Sal-Not arms using oligo dT

primed cDNA.

ORGANISM Arabidopsis thaliana

Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;

Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 563)

AUTHORS

Newman,T., de Bruijn,F.J., Green,P., Keegstra,K., Kende,H.,

McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M.,

Retzel,E. and Somerville,C.

Genes galore: a summary of methods for accessing results from

large-scale partial sequencing of anonymous Arabidopsis cDNA clones

Plant Physiol. 106, 1241-1255 (1994)

Mar 19 08:16

US-08-612-929-17.rst

11

COMMENT

Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.ci.msu.edu.

FEATURES

source
1..563
/organism="Arabidopsis thaliana"
/clone="173097"
/strain="var columbia"
/note="thale cress"

BASE COUNT 126 a 95 c 145 g 175 t 22 others
ORIGIN

Query Match 71.4%; Score 15; DB 17; Length 563;
Best Local Similarity 89.5%; Pred. No. 4.79e-03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 353 agaattcatattggatgca 371
||||| ||||| ||||| ||||| |||||
Cp 21 AGATTCTAGATTGGATGCA 3

RESULT 10

LOCUS N38958 598 bp mRNA EST 19-JAN-1996
DEFINITION Yv21b03.e1 Homo sapiens cDNA clone 243341 3'.
ACCESSION N38958
NID g1162165
KEYWORDS EST.
SOURCE human clone=243341 primer=m13 -40 forward library=Soares fetal liver spleen 1NPLS vector=p7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Reitel=Pac I

Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAGATCTTTTITTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 598)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Mar 19 08:16

US-08-612-929-17.rst

12

Email: est@watson.wustl.edu

High quality sequence stops: 465
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

Location/Qualifiers
source
1..598
/organism="Homo sapiens"
/clone="243341"
/note="human"

BASE COUNT 174 a 113 c 122 g 184 t 5 others
ORIGIN

Query Match 71.4%; Score 15; DB 58; Length 598;
Best Local Similarity 89.5%; Pred. No. 4.79e-03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 545 agactctaggttgatgca 563
||||| ||||| ||||| ||||| |||||
Cp 21 AGATTCTAGATTGGATGCA 3

RESULT 11

LOCUS HSC10A042 195 bp RNA EST 21-SEP-1995
DEFINITION H. sapiens partial cDNA sequence; clone c-10a04.
ACCESSION Z41644

NID g566018

KEYWORDS partial cDNA sequence; transcribed sequence fragment.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Genexpress.
Direct Submission

TITLE Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry Cedex France
JOURNAL and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr

REFERENCE 2 (bases 1 to 195)

Genexpress.

The Genexpress cDNA program

Unpublished

REFERENCE 3 (bases 1 to 195)

Aufay, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pletu, G., Poulliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.

TITLE IMAGE: molecular integration of the analysis of the human genome and its expression

C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

JOURNAL 95277534

MEDLINE
COMMENT Clone library from B.Soaes, Psychiatry Dept. Columbia University USA;

Cloning method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector;

Sequencing method: single read, full automatic;

Primer: (-21)M13 universal;

cDNA sequence complementary to mRNA (3' end)

Stretch removed: 20 T removed at sequence 5' end

Normalization method: Bento Soares, P.N.A.S in press;

Genexpress_library_idt: C;

Genexpresse_sequence_id: a2c-10a04;

No significant homology found with :
genbank release 81 swissprot release 28.

FEATURES

source
1..195
/organism="Homo sapiens"
/isolate="muscular atrophy patient"
/dev stage="3 months old"
/tissue type="total brain"
/clone lib="normalized infant brain cDNA"
/sex="female"

BASE COUNT 57 a 32 c 48 g 56 t 2 others
ORIGIN

Query Match 66.7%; Score 14; DB 41; Length 195;
Best Local Similarity 93.8%; Pred. No. 1.03e-01;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 50 ctgcattcaatctaga 65
||||| |||||||
Qy 2 CTGCATCAATCTAGA 17

RESULT 12

ID DM123F11S standard; DNA; STS; 248 BP.

AC 232433;

DT 11-APR-1994 (Rel. 39, Created)

DT 17-APR-1996 (Rel. 47, Last updated, Version 4)

DE D. melanogaster STS determined from European Mapping Project
DE cosmid.

KW sequence tagged site.

OS Drosophila melanogaster (fruit fly)

OC Eukaryota; Animalia; Metazoa; Arthropoda; Insecta;

OC Pterygota; Neoptera; Holometabola; Diptera; Brachycera;

OC Cyclorhapha; Schizophora; Drosophiloidea; Drosophilidae.

RN [1]

RP 1-248

RA European Drosophila Mapping Consortium;

RT Submitted (08-APR-1994) to the EMBL/GenBank/DBJ databases.

RL Michael Ashburner, Department of Genetics, Downing St., Cambridge

RL CB2 3EH, England

RN [2]

RC Updated comments

RA European Drosophila Mapping Consortium;

RT Submitted (15-APR-1996) to the EMBL/GenBank/DBJ databases.

RL Michael Ashburner, Department of Genetics, Downing St., Cambridge

RL CB2 3EH, England

RN [3]

RP 1-248

RX MEDLINE; 95309678.

RA Madueno E., Papagiannakis G., Rimmington G.A., Saunders R.D.C.,

RA Savakis C., Siden-Kiamos I., Skavdis G., Spanos L., Trenear J.,

RA Adam P., Ashburner M., Benos P., Bolshakov V.N., Coulson D.,

RA Glover D.M., Herrmann S., Kafatos F.C., Louis C., Majerus T.,

RA Modolell J.;

RT "A physical map of the X chromosome of Drosophila melanogaster:

RT Cosmid contigs and sequence tagged sites.*;

RL Genetics 139:1631-1647(1995).

CC STS name = Dm123F11S

CC clone name = 123F11

CC STS from promoter = SP6

CC vector class = cosmid, Lorient 6
CC origin_of_clone = Oregon-R
CC in situ site primary = 2B1-10
CC STS dbSTS AC = 4219
CC BLAST_program = BLASTN
CC database_searched = EMBL
CC database_version = 45.0 and updates till date_of_search
CC date_of_search = 08-01-1996
CC BLAST_program = BLASTX
CC database_searched = SWISSPROT
CC database_version = 32.0
CC date_of_search = 15-12-1995
FH Key Location/Qualifiers
FT source 1..248
FT /organism="Drosophila melanogaster"
FT /strain="Oregon-R"
FT /clone="123F11"
SQ Sequence 248 BP; 59 A; 52 C; 51 G; 81 T; 5 other;

Query Match 66.7%; Score 14; DB 173; Length 248;
Best Local Similarity 93.8%; Pred. No. 1.03e-01;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 126 agattctagattgat 141
||||| |||||||
Cp 21 AGATTCTAGATTGAT 6

RESULT 13

LOCUS DM123F11S 248 bp DNA STS 17-APR-1996
DEFINITION D. melanogaster STS determined from European Mapping Project

cosmid.

ACCESSION Z32433

NID 9471188

KEYWORDS sequence tagged site.

SOURCE fruit fly.

ORGANISM

Drosophila melanogaster
Eukaryota; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 248)

AUTHORS European Drosophila Mapping Consortium.

TITLE Direct Submission

JOURNAL Submitted (08-APR-1994) Michael Ashburner, Department of Genetics,

Downing St., Cambridge CB2 3EH, England

REFERENCE 2 (bases 1 to 248)

AUTHORS European Drosophila Mapping Consortium.

TITLE Direct Submission

JOURNAL Submitted (15-APR-1996) Michael Ashburner, Department of Genetics,

Downing St., Cambridge CB2 3EH, England

REMARK Updated comments

REFERENCE 3 (bases 1 to 248)

AUTHORS Madueno E., Papagiannakis G., Rimmington G.A., Saunders R.D.C.,
Savakis C., Siden-Kiamos I., Skavdis G., Spanos L., Trenear J.,
Adam P., Ashburner M., Benos P., Bolshakov V.N., Coulson D.,
Glover D.M., Herrmann S., Kafatos F.C., Louis C., Majerus T. and
Modolell J.

TITLE A physical map of the X chromosome of Drosophila melanogaster:

cosmid contigs and sequence tagged sites

JOURNAL Genetics 139 (4), 1631-1647 (1995)

MEDLINE 95309678

CC STS name = Dm123F11S

CC clone name = 123F11

STS from promoter = SP6
vector_class = cosmid, Loris 6
origin_of_clone = Oregon-R
in_situ_site_primary = 2B1-10
STS dbSTS AC = 4219
BLAST_program = BLASTN
database_searched = EMBL
database_version = 45.0 and updates till date_of_search
date_of_search = 08-01-1996
BLAST_program = BLASTX
database_searched = SWISSPROT
database_version = 32.0
date_of_search = 15-12-1995.

NCBI gi: 471188
FEATURES
source
1..248
/organism="Drosophila melanogaster"
/strain="Oregon-R"
/clone="123F11"

BASE COUNT 59 a 52 c 51 g 81 t 5 others
ORIGIN

Query Match 66.7%; Score 14; DB 156; Length 248;
Best Local Similarity 93.8%; Pred. No. 1.03e-01;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 126 agattctagattgat 141
|||||
Cp 21 AGATTCTAGATTGGAT 6

RESULT 14
LOCUS DM123F11S 248 bp DNA STS 24-OCT-1995
DEFINITION D. melanogaster STS determined from European Mapping Project
cosmid.
ACCESSION 232433
NID 9471188
KEYWORDS sequence tagged site.
SOURCE fruit fly.

ORGANISM
Drosophila melanogaster
Eukaryota; Eukaryota; Metazoa; Arthropoda;
Tracheata; Insecta; Pterygota; Diptera; Brachycera; Cyclorhapha;
Drosophilidae; Drosophila; Sophophora; melanogaster group;
melanogaster subgroup.

REFERENCE 1 (bases 1 to 248)
AUTHORS European Drosophila Mapping Consortium.
DIRECT SUBMISSION
TITLE Submitted (08-APR-1994) to the EMBL/GenBank/DBJ databases. Michael
JOURNAL Ashburner, Department of Genetics, Downing St., Cambridge CB2 3EH,
England

REFERENCE 2 (bases 1 to 248)
AUTHORS Madueno, E., Papanikolaou, G., Rimmington, G.A., Saunders, R.D.C.,
Savakis, C., Siden-Kiamos, I., Skavdis, G., Spanos, L., Treneer, J.,
Adam, P., Ashburner, M., Benos, P., Bolshakov, V.N., Coulson, D.,
Glover, D.M., Herrmann, S., Kafatos, F.C., Louis, C., Majerus, T. and
Mordell, J.

TITLE A physical map of the X chromosome of *Drosophila melanogaster*:
cosmid contigs and sequence tagged sites

JOURNAL Genetics 139 (4), 1631-1647 (1995)

MEDLINE 95309678

COMMENT STS name = Dm123F11S

clone_name = 123F11

STS_from_promoter = SP6

vector_class = cosmid, Loris 6
origin_of_clone = Oregon-R
in_situ_site_primary = 2B1-10
in_situ_site_secondary = 0
in_situ_site_repetitive_number = 0
in_situ_site_heterochromatin = 0
BLAST_program = BLASTN
database_searched = EMBL
database_version = 37.0
parameters_of_search = default; only HSP scores >200 are reported
date_of_update = 02 April 1994
AC number of hit =
probability_of_hit =
HSP_score_of_hit =.

FEATURES
source
1..248
/organism="Drosophila melanogaster"
BASE COUNT 59 a 52 c 51 g 81 t 5 others
ORIGIN

Query Match 66.7%; Score 14; DB 129; Length 248;
Best Local Similarity 93.8%; Pred. No. 1.03e-01;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 126 agattctagattgat 141
|||||
Cp 21 AGATTCTAGATTGGAT 6

RESULT 15
LOCUS H64221 260 bp mRNA EST 16-OCT-1995
DEFINITION RRAMCA026SK Brugia malayi cDNA clone RRAMCA026 5' similar to
ZKS46.14 gene product.

ACCESSION H64221
NID g1019982
KEYWORDS EST.
SOURCE clone=RRAMCA026 primer=pBluescript SK library=Brugia malayi adult
male cDNA (SAM94NL-BmM) strain=FRS Labs vector=lambda UniZap XR

host=XLI-Blue MRF. Reite=EcoR I Rsite2=Xho I lymphatic filarial
nematode parasite of humans. mRNA was prepared from adult males of
Brugia malayi isolated from jirds and converted to double stranded
cDNA using reverse transcriptase and oligo(dT) followed by RNase H
and DNase I. The library had 4.6 x 10E6 independent
recombinants and average insert size was 800 base pairs. The
library was constructed by Noelle Ling. The library is available
from Dr. S.A. Williams, email swilliams@smith.smith.edu.

ORGANISM
Brugia malayi
Eukaryota; Eukaryota; Metazoa; Eumycota group;
Metazoa; Eumycota; Bilateria; Pseudocoelomata; Nematoda;
Secernentea; Spiruria; Spirurida; Spirurina; Filarioidea;
Onchocercidae; Onchocercinae; Brugia.

REFERENCE 1 (bases 1 to 260)
AUTHORS Williams, S.A.
TITLE Genes expressed in adult males of *Brugia malayi*
JOURNAL Unpublished (1995)
COMMENT

Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: swilliams@smith.smith.edu.

Mar 19 08:16

US-08-612-929-17.rst

17

FEATURES Location/Qualifiers

source 1..260
/organism="Brugia malayi"
/clone="RRAMCA026"
/strain="TRS Labs"

mRNA
BASE COUNT 103 a 35 c 62 g 60 t
ORIGIN

Query Match 66.7%; Score 14; DB 26; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.03e-01;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 244 ttctagattggatg 257
|||||
Cp 18 TTCTAGATTGGATG 5

Search completed: Wed Mar 19 08:18:47 1997
Job time : 65 secs.

Result	No.	Score	Query		DB	ID	Description	Pred. No.
			Match	Length				
c	1	21	100.0	51	14	Q83510	IL-4 CDR2 gene fragment	4.15e-03
	2	21	100.0	55	14	Q83509	IL-4 CDR2 gene fragment	4.15e-03
	3	21	100.0	333	11	Q65554	Mouse anti-HIV mu5.5	4.15e-03
	4	21	100.0	333	12	Q70376	Chimeric anti HIV ant	4.15e-03
	5	21	100.0	333	11	Q65558	Mouse-human chimeric	4.15e-03
	6	21	100.0	333	12	Q70372	Anti HIV antibody lig	4.15e-03
	7	21	100.0	334	1	N90492	Gene fragment of Immu	4.15e-03
	8	21	100.0	333	6	Q36609	Anti-CD4 antibody MT	4.15e-03

ID	Q83510 standard; DNA; 51 BP.
AC	Q83510;
DT	20-SEP-1995 (first entry)
DE	IL-4 CDR2 gene fragment.
DE	Humanized antibody; antibody engineering; monoclonal antibody;
KW	Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;
KW	complementarity determining region; <i>ss</i> .
OS	Synthetic.
PN	WO9507301-A.
PD	16-MAR-1995.
PP	07-SEP-1994; U10308.
PP	07-SEP-1993; US-117366.
PP	14-OCT-1993; US-136783.
PP	(SMIK) SMITHKLINE BEECHAM CORP.
PPA	(SMIK) SMITHKLINE BEECHAM P.C.
PPI	Gross MS, Holmes SD, Sylvester DR;
DR	WP1; 95-123387/16.
PPT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PPT	from high affinity mAbs - useful in treatment of IL-4-mediated
PPT	and IgE-mediated allergic conditions
PPT	Example 3; Page 28; 97pp; English.
PSS	A humanized antibody was designed to contain mouse CDRs (from
CCC	

CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A
CC synthetic heavy chain was made using the oligonucleotides given
CC in Q83498-502 and amplified by PCR using the primers given in
CC Q83503-04. The construct was ligated into vector pCD, along
CC with a signal sequence (Q83494) and an IgG1 human constant
CC region. The CDR gene regions of a pre-existing light chain
CC framework were replaced with synthetic IL-4 CDR genes constructed
CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),
CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into
CC the vector. The anti-IL4 engineered antibody was expressed in
CC COS and CHO cells.
SQ Sequence 51 BP; 14 A; 12 C; 14 G; 11 T;

Query Match 100.0%; Score 21; DB 14; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.15e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 agattctagattggtgcagc 24
|||||
Cp 21 AGATTCTAGATTGCGTGCAGC 1

RESULT 2

ID Q83509 standard; DNA; 55 BP.
AC Q83509;
DT 20-SEP-1995 (first entry)
DE IL-4 CDR2 gene fragment.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;
KW complementarity determining region; ss.
OS Synthetic.
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Example 3; Page 28; 9/pp; English.
CC A humanized antibody was designed to contain mouse CDRs (from
CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A
CC synthetic heavy chain was made using the oligonucleotides given
CC in Q83498-502 and amplified by PCR using the primers given in
CC Q83503-04. The construct was ligated into vector pCD, along
CC with a signal sequence (Q83494) and an IgG1 human constant
CC region. The CDR gene regions of a pre-existing light chain
CC framework were replaced with synthetic IL-4 CDR genes constructed
CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),
CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into
CC the vector. The anti-IL4 engineered antibody was expressed in
CC COS and CHO cells.
SQ Sequence 55 BP; 12 A; 15 C; 13 G; 15 T;

Query Match 100.0%; Score 21; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 4.15e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 28 gctgcattcattcagaatct 48
|||||

Qy 1 GCTGCATCCAATCTAGAAATCT 21

RESULT 3

ID Q65554 standard; cDNA; 333 BP.
AC Q65554;
DT 27-JAN-1995 (first entry)
DE Mouse anti-HIV mu5.5 light chain variable region cDNA.
KW Immunoglobulin; light chain; anti-HIV antibody; neutralisation;
KW human immunodeficiency virus; variable region; VL chain; murine; ds.
OS Mus musculus.
FH Key Location/Qualifiers
FT misc_feature 70..114
FT /tag= a
FT /note= "encodes CDR1"
FT misc_feature 160..180
FT /tag= b
FT /note= "encodes CDR2"
FT misc_feature 277..303
FT /tag= c
FT /note= "encodes CDR3"
PN J06125783-A.
PD 10-MAY-1994.
PF 28-DEC-1991; 359808.
PR 28-DEC-1991; JP-359808.
PA (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.
DR WPI; 94-187942/23.
DR P-PSDB; R55123.
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
PT and recombinant antibody consisting of the H- and L-chains,
PT useful in AIDS therapy
PS Example 3; Fig 4; 22pp; Japanese.
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (Q65551-Q65554). The murine anti-HIV CDRs were
CC introduced into human framework regions to construct chimeric
CC antibodies (Q65555-Q65558).
SQ Sequence 333 BP; 88 A; 83 C; 86 G; 76 T;

Query Match 100.0%; Score 21; DB 11; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.15e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcattcattcagaatct 180
|||||

Qy 1 GCTGCATCCAATCTAGAAATCT 21

RESULT 4

ID Q70376 standard; cDNA to mRNA; 333 BP.
AC Q70376;
DT 13-MAR-1995 (first entry)
DE Chimeric anti HIV antibody light chain variable region.
KW Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS; treatment;
KW prophylaxis; Mus musculus; Homo sapiens; ss.
OS Chimeric Homo sapiens
OS Chimeric Mus musculus.
FH Key Location/Qualifiers
FT CDS 1..333
FT /tag= a
FT /product= Antibody light chain variable region.
PN W09415969-A.
PD 21-JUL-1994.

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US-08-612-929-17.rng

5

PF 14-JAN-1993; J00039.
PR 14-JAN-1993; AU-032671.
PR 14-JAN-1993; WO-J00039.
PA (KAGA) CHERO SERO THERAPEUTIC RES INST.
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
PI Tokiyoshi S;
DR WPI; 94-249145/30.
DR P-PSDB; R60306.
PT Recombinant chimeric anti HIV antibody - useful for the treatment
PT and prevention of HIV
PS Claim 14; Figure 12; 51pp; Japanese.
CC The recombinant antibody light chain has neutralising activity
CC against HIV. Chimeric antibodies comprising both mouse and human
CC sequences are useful in the treatment/prevention of AIDS caused by
CC HIV. This sequence is derived from the mu5.5 anti HIV monoclonal
CC antibody producing cell.
SQ Sequence 333 BP; 95 A; 90 C; 88 G; 60 T;

Query Match 100.0%; Score 21; DB 12; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.15e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcacccaatcagaatct 180
|||||
QY 1 GCTGCATCCAATCTAGAATCT 21

RESULT 5

ID Q65558 standard; cDNA; 333 BP.
AC Q65558;
DT 30-JAN-1995 (first entry)
DE Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.
KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
KW human immunodeficiency virus; variable region; VL chain; murine;
KW chimeric; humanised; db.
OS Chimeric Mus musculus.
OS Chimeric Homo sapiens.
FH Key Location/Qualifiers
FT misc feature 70..114
FT /*tag= a
FT /note= "encodes murine CDR1"
FT misc feature 160..180
FT /*tag= b
FT /note= "encodes murine CDR2"
FT misc feature 277..303
FT /*tag= c
FT /note= "encodes murine CDR3"
PN J06125783-A.
PD 10-MAY-1994.
PF 28-DEC-1991; 359808.
PR 28-DEC-1991; JP-359808.
PA (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.
DR WPI; 94-187942/23.
DR P-PSDB; R55127.
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
PT and recombinant antibody consisting of the H- and L-chains,
PT useful in AIDS therapy
PS Claim 5; Fig 12; 22pp; Japanese.
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (Q65551-Q65554). The murine anti-HIV CDRs were
CC introduced into human framework regions to construct chimeric
CC antibodies (Q65555-Q65558).
SQ Sequence 333 BP; 95 A; 90 C; 88 G; 60 T;

Mar 19 08:15

US-08-612-929-17.rng

6

Query Match 100.0%; Score 21; DB 11; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.15e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcacccaatcagaatct 180
|||||
QY 1 GCTGCATCCAATCTAGAATCT 21

RESULT 6

ID Q70372 standard; cDNA to mRNA; 333 BP.
AC Q70372;
DT 09-MAR-1995 (first entry)
DE Anti HIV antibody light chain variable region.
KW Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS; treatment;
KW prophylaxis; Mus musculus; Homo sapiens; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 1..333
FT /*tag= a
FT /product= Antibody light chain variable region.
PN W09415969-A.
PD 21-JUL-1994.
PF 14-JAN-1993; J00039.
PR 14-JAN-1993; AU-032671.
PR 14-JAN-1993; WO-J00039.
PA (KAGA) CHERO SERO THERAPEUTIC RES INST.
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
PI Tokiyoshi S;
DR WPI; 94-249145/30.
DR P-PSDB; R60302.
PT Recombinant chimeric anti HIV antibody - useful for the treatment
PT and prevention of HIV
PS Claim 15; Figure 4; 51pp; Japanese.
CC The recombinant antibody light chain has neutralising activity
CC against HIV. Chimeric antibodies comprising both mouse and human
CC sequences are useful in the treatment/prevention of AIDS caused by
CC HIV. This sequence is obtained from the mu5.5 anti HIV monoclonal
CC antibody producing cell.
SQ Sequence 333 BP; 88 A; 83 C; 86 G; 76 T;

Query Match 100.0%; Score 21; DB 12; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.15e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcacccaatcagaatct 180
|||||
QY 1 GCTGCATCCAATCTAGAATCT 21

RESULT 7

ID N90492 standard; DNA; 334 BP.
AC N90492;
DT 20-OCT-1989 (first entry)
DE Gene fragment of immunoglobulin L chain variable region.
KW Gene fragment; immunoglobulin; L chain variable region; HIV.
OS Mus musculus
FH Key Location/Qualifiers
FT CDS 1..333
FT /*tag= a
PN EP-327000-A.
PD 09-AUG-1989.

PF 30-JAN-1989; 101583.
 PR 30-JAN-1988; JP-20255.
 PR 08-JUL-1988; JP-171385.
 PA (KAGA) The Chemo-Sero-Therapeutic Research Institute.
 PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Mateushita S, Hattori T,
 PI Takatsuki K;
 DR WPI; 89-229050/32.
 PT Chimeric anti-human immune virus antibodies - contg. mouse variable
 PT regions and human constant regions for diagnosis, treatment and
 PT prevention of AIDS
 PS Claim 6; page 15; 33pp; English.
 CC The gene fragment encodes an L chain variable region from an
 CC immunoglobulin with anti-HIV neutralising activity. It is used, with an
 CC H chain variable region gene fragment (see N90491), to produce a chimeric
 CC anti-HIV antibody with mouse variable regions and human constant regions.
 CC The antibody retains its original specificity, but have much lower
 CC antigenicity to humans. See also P90541, N90493 and N90495.
 SQ Sequence 334 BP; 91 A; 83 C; 81 G; 79 T;

Query Match 100.0%; Score 21; DB 1; Length 334;
 Best Local Similarity 100.0%; Pred. No. 4.15e-03;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcattcaatctagaatct 180
 |||||
 QY 1 GCTGCATCCAATCTAGAAATCT 21

RESULT 8
 ID Q36609 standard; DNA; 393 BP.
 AC Q36609;
 DT 02-JUN-1993 (first entry)
 DE Anti-CD4 antibody MT 3.10 light chain variable region.
 KW immunosuppression; tissue transplantation; graft; L chain; V region;
 KW T-helper cell inhibition; transplant rejection; MAb;
 KW interleukin-2 receptor; ss.
 FH Key Location/Qualifiers
 FT sig_peptide 1..60
 FT /*tag= a
 FT mat_peptide 61..393
 FT /*tag= b
 FT /note= "J1 region begins at position 361"
 PN DE4143214-A.
 PD 28-JAN-1993.
 PF 30-DEC-1991; 143214.
 PR 25-JUL-1991; DE-124759.
 PR 30-DEC-1991; DE-143214.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 PI Kaluza B, Rietheumeller G, Scheuer W, Weidle U;
 DR WPI; 93-037582/05.
 DR P-PSDB; R32123.
 PT Synergistic antibody compen. for use as immunosuppressant -
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
 PT alpha- or anti-IL2R beta antibodies
 PS Claim 5; Page 11; 18pp; German.
 CC This sequence encodes the light chain variable region of a preferred
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic
 CC composition. MAB MT 3.10 is deposited as clone 3.101/sB10 (ECACC
 CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R
 CC alpha or beta antibody. Individually the antibodies are strongly
 CC inhibiting and when used together their immunosuppressive properties
 CC are improved; they synergistically inhibit T-helper cell
 CC proliferation to effectively inhibit transplant rejection at low
 CC doses without significantly reducing the general immune response.

CC See Q36607-Q36616.
 SQ Sequence 393 BP; 100 A; 105 C; 98 G; 90 T;

Query Match 100.0%; Score 21; DB 6; Length 393;
 Best Local Similarity 100.0%; Pred. No. 4.15e-03;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 220 gctgcattcaatctagaatct 240
 |||||
 QY 1 GCTGCATCCAATCTAGAAATCT 21

RESULT 9
 ID Q73986 standard; cDNA; 393 BP.
 AC Q73986;
 DT 20-SEP-1995 (first entry)
 DE Humanized antibody 3B9 light chain.
 KW Humanized antibody; antibody engineering; monoclonal antibody;
 KW MAb; interleukin-4; IL-4; allergy; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..393
 FT /*tag= a
 FT sig_peptide 1..60
 FT /*tag= b
 FT mat_peptide 61..393
 FT /*tag= c
 PN W09507301-A.
 PD 16-MAR-1995.
 PE 07-SEP-1994; US-117366.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR P-PSDB; R75355.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Fig. 5; 97pp; English.
 CC A humanized antibody light chain variable region and signal
 CC sequence is given in R75355. The signal sequence is also
 CC provided in R70194. The sequences of the first 2 CDRs
 CC are identical to mouse anti-human IL-4 MAb 3B9 light chain
 CC CDRs (given in R70195-96), but the third (R70201) differs
 CC by a single amino acid from the native mouse CDR (R70197).
 SQ Sequence 393 BP; 97 A; 96 C; 108 G; 92 T;

Query Match 100.0%; Score 21; DB 14; Length 393;
 Best Local Similarity 100.0%; Pred. No. 4.15e-03;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 217 gctgcattcaatctagaatct 237
 |||||
 QY 1 GCTGCATCCAATCTAGAAATCT 21

RESULT 10
 ID Q83520 standard; cDNA; 393 BP.
 AC Q83520;
 DT 20-SEP-1995 (first entry)
 DE Humanized antibody 3B9 light chain.
 KW Humanized antibody; antibody engineering; monoclonal antibody;

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KW MAb; interleukin-4; IL-4; allergy; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..393
FT /tag= a
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR P-PSDB; R70202.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions
PS Disclosure; Page 71-72; 97pp; English.
CC A humanized antibody light chain variable region and signal sequence is given in R75355. The signal sequence is also provided in R70194. The sequences of the 3 CDRs are identical to mouse anti-human IL-4 MAb 3B9 light chain CC CDRs (given in R70195-97).
SQ Sequence 393 BP; 97 A; 98 C; 105 G; 93 T;

Query Match 100.0%; Score 21; DB 14; Length 393;
Best Local Similarity 100.0%; Pred. No. 4.15e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 217 gctgcacccaatctagaatct 237
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QY 1 GCTGCATCCAACTAGAACTCT 21

RESULT 11
ID Q83490 standard; cDNA; 396 BP.
AC Q83490;
DT 20-SEP-1995 (first entry)
DE Mouse MAb 3B9 light chain.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 1..396
FT /tag= a
FT sig_peptide 1..60
FT /tag= b
FT mat_peptide 61..396
FT /tag= c
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR P-PSDB; R70189.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions
PS Disclosure; Fig.1; 97pp; English.

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CC Spleen cells from mice immunised with human IL-4 were used to prepare CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy CC chains were cloned into pGEM7f+ and transformed into E. coli CC DH5-alpha. The clones were sequenced (Q83490-91), and used for CC antibody engineering.
SQ Sequence 396 BP; 99 A; 103 C; 103 G; 91 T;

Query Match 100.0%; Score 21; DB 14; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.15e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 220 gctgcacccaatctagaatct 240
|||||
QY 1 GCTGCATCCAACTAGAACTCT 21

RESULT 12
ID Q25658 standard; DNA; 733 BP.
AC Q25658;
DT 08-DEC-1992 (first entry)
DE Mouse 0.5beta anti-HIV antibody Light chain.
KW Heavy; light; CDR; HIV; AIDS; FR; framework region; ds.
OS Synthetic.
FH Key Location/Qualifiers
FT primer_bind complement (77..106)
FT /tag= a
FT /note= "binding site for the primer
FT represented Q30550"
FT primer_bind 709..730
FT /tag= b
FT /note= "binding site for the primer
FT represented Q30551"
PN J04141095-A.
PD 14-MAY-1992.
PF 02-OCT-1990; 266091.
PR 02-OCT-1990; JP-266091.
PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.
DR WPI; 92-212765/26.
PT New recombinant modified anti-HIV antibodies - comprise human x PT mouse modified antibody H and L chains
PS Disclosure; Fig 4; 15pp; Japanese.
CC Recombinant modified anti-HIV antibodies comprise framework regions CC derived from human antibody and CDRs derived from mouse monoclonal CC antibody 0.5beta. The anti-HIV modified antibody can be used for CC the prophylaxis and treatment of AIDS.
SQ Sequence 733 BP; 194 A; 162 C; 161 G; 216 T;

Query Match 100.0%; Score 21; DB 4; Length 733;
Best Local Similarity 100.0%; Pred. No. 4.15e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 541 gctgcacccaatctagaatct 561
|||||
QY 1 GCTGCATCCAACTAGAACTCT 21

RESULT 13
ID N90495 standard; DNA; 780 BP.
AC N90495;
DT 24-OCT-1989 (first entry)
DE A V chi region gene.
KW V chi region gene; immunoglobulin; L chain variable region; HIV.
OS Mus musculus

FH Key Location/Qualifiers
 FT exon 119..167
 FT /*tag= a 398..742
 FT exon /*tag= b
 PN EP-327000-A.
 PD 09-AUG-1989. 101583.
 PR 30-JAN-1988; JP-20255.
 PR 08-JUL-1988; JP-171385.
 PA (KAGA) The Chemo-Sero-Therapeutic Research Institute.
 PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,
 PI Takatsuki K;
 DR WPI; 89-229050/32.
 DR P-PSDB; P90543.
 PT Chimeric anti-human immune virus antibodies - contg. mouse variable
 PT regions and human constant regions for diagnosis, treatment and
 PT prevention of AIDS
 PS Disclosure; Fig 7; 33pp; English.
 CC The sequence is a v chi region gene, encoding an L chain variable region
 CC (see P90543). See also N90491-3.
 SQ Sequence 780 BP; 205 A; 172 C; 171 G; 232 T;

Query Match 100.0%; Score 21; DB 1; Length 780;
 Best Local Similarity 100.0%; Pred. No. 4.15e-03;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 568 gctgcattcccaatctagaatct 588
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 QY 1 GCTGCATCCAATCTAGAATCT 21

RESULT 14

ID Q04039 standard; DNA; 900 BP.
 AC Q04039;
 DT 06-SEP-1990 (first entry)
 DE Anti-leu 3a light chain variable region gene, 206 Vx.
 KW HIV; AIDS; anti-leu3A; vaccine; ds.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT exon 259..307
 FT /*tag= a
 FT intron 308..537
 FT /*tag= b
 FT exon 538..882
 FT /*tag= c
 PN EP-365209-A.
 PD 25-APR-1990.
 PE 11-OCT-1989; 010415.
 PR 17-OCT-1988; US-260558.
 PA (BECT) Becton Dickinson Co.
 PI Hinton R, Oi VT;
 DR WPI; 90-126329/17.
 DR P-PSDB; R04132.
 PT New chimeric variants of murine antibody anti-leucine -
 PT contg. human antibody regions, and DNA encoding sequences.
 PS Claim 1; Fig 2; 12pp; English.
 CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
 CC used to form chimeric mouse-variable, human-constant region Abs
 CC suggested as being useful as a vaccine to HIV.
 SQ Sequence 900 BP; 261 A; 206 C; 187 G; 246 T;

Query Match 100.0%; Score 21; DB 1; Length 900;
 Best Local Similarity 100.0%; Pred. No. 4.15e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 708 gctgcattcccaatctagaatct 728
 |||||
 QY 1 GCTGCATCCAATCTAGAATCT 21

RESULT 15

ID Q04041 standard; DNA; 397 BP.
 AC Q04041;
 DT 06-SEP-1990 (first entry)
 DE Anti-leu 3a light chain variable region gene, KOL/206 V1.
 KW HIV; AIDS; anti-leu3A; vaccine; ds.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT exon 43..387
 FT /*tag= a
 PN EP-365209-A.
 PD 25-APR-1990.
 PE 11-OCT-1989; 010415.
 PR 17-OCT-1988; US-260558.
 PA (BECT) Becton Dickinson Co.
 PI Hinton R, Oi VT;
 DR WPI; 90-126329/17.
 DR P-PSDB; R04134.
 PT New chimeric variants of murine antibody anti-leucine -
 PT contg. human antibody regions, and DNA encoding sequences.
 PS Claim 4; Fig 4; 12pp; English.
 CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
 CC used to form chimeric mouse-variable, human-constant region Abs
 CC suggested as being useful as a vaccine to HIV.
 SQ Sequence 397 BP; 105 A; 99 C; 84 G; 109 T;

Query Match 90.5%; Score 19; DB 1; Length 397;
 Best Local Similarity 95.2%; Pred. No. 6.13e-02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 210 gctgcattcccaatctagaatct 230
 |||||
 QY 1 GCTGCATCCAATCTAGAATCT 21

Search completed: Wed Mar 19 08:17:22 1997
 Job time : 15 secs.

WVPPREH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 15:54:13 1997; MacPar time 51.42 Seconds
336.386 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-17
Description: (1-21) from US08612929.seq
Perfect Score: 21
N.A. Sequence: 1 GCTGCATCCAACTAGAACTCT 21
Comp: CGACGTAGTTCAGTCTTGA

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-new5
1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI
10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

Database: genbank94
16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7
23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5
30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2
37:VRT3 38:VRT4 39:VRT5 40:VRT6 41:VRT7 42:VRT8 43:VRT9
44:PLN1 45:PLN2 46:PLN3 47:PLN4 48:PLN5 49:PLN6 50:PLN7
51:PRI1 52:PRI2 53:PRI3 54:PRI4 55:PRI5 56:PRI6 57:PRI7
58:PRI8 59:PRI9 60:PRI10 61:PRI11 62:PRI12 63:PRI13
64:ROD1 65:ROD2 66:ROD3 67:ROD4 68:ROD5 69:ROD6 70:ROD7
71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4
78:VRL5 79:VRL6 80:VRL7 81:VRL8

Database: genbank-new5
82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG
89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL

Database: u-embl46_94
96:part1

Statistics: Mean 6.819; Variance 2.532; scale 2.693

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description	Pred. No.
1	21	100.0	195 66	MUSIGKAAAC	Mouse Igk chain mRNA,	5.82e-04
2	21	100.0	195 66	MUSIGKAAAB	Mouse Igk chain mRNA,	5.82e-04
3	21	100.0	228 65	MMU18577	Mus musculus immunogl	5.82e-04
4	21	100.0	238 65	MMU18563	Mus musculus immunogl	5.82e-04
5	21	100.0	255 64	MMIGKVRD	M.musculus immunoglob	5.82e-04
6	21	100.0	262 64	MMIGKVRP	M.musculus immunoglob	5.82e-04
7	21	100.0	264 64	MMIGKVRP	M.musculus immunoglob	5.82e-04
8	21	100.0	266 64	MMIGKVRP	M.musculus immunoglob	5.82e-04
9	21	100.0	270 64	MMIGKVRG	M.musculus immunoglob	5.82e-04
10	21	100.0	270 64	MMIGKVRP	M.musculus immunoglob	5.82e-04
11	21	100.0	270 64	MMIGKVRB	M.musculus immunoglob	5.82e-04
12	21	100.0	279 66	MUSIGKAAA	Mouse Igk chain mRNA,	5.82e-04
13	21	100.0	286 65	MMU29628	Mus musculus anti-DNA	5.82e-04
14	21	100.0	292 65	MMU18599	Mus musculus immunogl	5.82e-04
15	21	100.0	297 65	MMU29629	Mus musculus anti-DNA	5.82e-04
16	21	100.0	313 70	S74550	Ig V kappa -rheumatoi	5.82e-04
17	21	100.0	317 67	MUSIGVACR	Mus musculus Ig rearr	5.82e-04
18	21	100.0	318 66	MUSIGVKRB	Mus musculus immunoglob	5.82e-04
19	21	100.0	333 70	S42888	Ig V kappa -immunoglob	5.82e-04
20	21	100.0	333 67	MUSIGLSB	Mouse Igl chain H2L2	5.82e-04
21	21	100.0	336 64	MMIGLC404	M.musculus mRNA for I	5.82e-04
22	21	100.0	336 67	MUSIGVACP	Mus musculus Ig rearr	5.82e-04
23	21	100.0	336 64	MMIGLC413	M.musculus mRNA for I	5.82e-04
24	21	100.0	336 64	MMIGLC310	M.musculus mRNA for I	5.82e-04
25	21	100.0	350 66	MUSIGKABC	Mouse Ig kappa chain	5.82e-04
26	21	100.0	353 66	MUSIGKABBE	Mouse Ig kappa chain	5.82e-04
27	21	100.0	354 67	MUSL71IGKV	Mouse hybridoma Ig re	5.82e-04
28	21	100.0	360 67	MUSIGKAF	Mouse Ig active kappa	5.82e-04
29	21	100.0	363 67	MUSL93IGKV	Mouse hybridoma Ig re	5.82e-04
30	21	100.0	363 67	MUSL2021GK	Mouse hybridoma Ig re	5.82e-04
31	21	100.0	393 70	S50265	Ig VL=anti-CD4 mAb M-	5.82e-04
32	21	100.0	900 40	I08223	Sequence 1 from paten	5.82e-04
33	19	90.5	245 64	MMIGKVRH	Mus musculus immunoglob	2.34e-02
34	19	90.5	333 64	MMU07207	Mus musculus clone 31	2.34e-02
35	19	90.5	333 70	S54207	V kappa 21=immunoglob	2.34e-02
36	19	90.5	333 65	MMVLIE10	Mouse mRNA for kappa-	2.34e-02
37	19	90.5	351 66	MUSIGKABBH	Mouse Ig kappa chain	2.34e-02
38	19	90.5	353 66	MUSIGKABBG	Mouse Ig kappa chain	2.34e-02
39	19	90.5	353 66	MUSIGKABBD	Mouse Ig kappa chain	2.34e-02
40	19	90.5	363 67	MUSL34IGKV	Mouse hybridoma Ig re	2.34e-02
41	19	90.5	397 40	I08225	Sequence 5 from paten	2.34e-02
42	19	90.5	671 67	MUSIGKVS	Mouse Ig germline kap	2.34e-02
43	17	81.0	276 91	MMU26472	Mus musculus nucleoso	7.83e-01
44	17	81.0	333 63	MMALDICH	M.musculus mRNA for a	7.83e-01
45	17	81.0	2707 89	SCINR053C	S.cerevisiae chromoso	7.83e-01

ALIGNMENTS

RESULT 1
LOCUS MUSIGKAAAC 195 bp mRNA
DEFINITION Mouse Igk chain mRNA, VJ1 region.
ACCESSION M57980
NID gi196406
KEYWORDS J-region; V-region; anti-cytochrome c antibody;
immunoglobulin kappa-chain; immunoglobulin light chain.
SOURCE Mouse (BALB/c) secondary B cell hybridoma 2B5 mRNA, clone 2B5.F8.
ORGANISM Mus musculus

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3

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 195)
AUTHORS Goshorn,S.C., Retzel,E. and Jemmerson,R.
TITLE Common structural features among monoclonal antibodies binding the same antigenic region of cytochrome c
JOURNAL J. Biol. Chem. 266 (4), 2134-2142 (1991)
MEDLINE 91115823

FEATURES
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/organism="Mus musculus"
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/cell_type="secondary B cell"
/sequenced_mol="cDNA to mRNA"
/tissue_type="hybridoma"
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/partial
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/codon_start=1
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/db_xref="PID:g196407"
/translation="PKLLIYAASNLESGIPARFGSGSGTDFTLNHPVEEDGATYY
CQSNEDPRTEGCGTKLEIKR"
19..39
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136..162
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156..195
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V_region

CDS

misc_feature

misc_feature

J_segment

BASE COUNT 52 a 50 c 51 g 42 t
ORIGIN Chromosome 6.

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Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 gctgcaccaatctagaatct 39
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Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 2
LOCUS MUSICKAAB 195 bp mRNA
DEFINITION Mouse Igk chain mRNA, VJ5 region.
ACCESSION M57979
NID g196404
KEYWORDS J-region; V-region; anti-cytochrome c antibody; immunoglobulin kappa-chain; immunoglobulin light chain.
SOURCE Mouse (BALB/c) secondary B cell hybridoma 7D4 mRNA, clone 7D4.H4.
ORGANISM Mus musculus

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US-08-612-929-17.rge

4

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 195)
AUTHORS Goshorn,S.C., Retzel,E. and Jemmerson,R.
TITLE Common structural features among monoclonal antibodies binding the same antigenic region of cytochrome c
JOURNAL J. Biol. Chem. 266 (4), 2134-2142 (1991)
MEDLINE 91115823

FEATURES
source
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/organism="Mus musculus"
/clone="7D4.H4"
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/cell_type="secondary B cell"
/sequenced_mol="cDNA to mRNA"
/tissue_type="hybridoma"
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/map="chromosome 6"
/note="CDR2"
136..162
/gene="IgM"
/map="chromosome 6"
/note="CDR3"
157..195
/gene="IgM"
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/note="J5"

V_region

CDS

misc_feature

misc_feature

J_segment

BASE COUNT 47 a 54 c 50 g 44 t
ORIGIN Chromosome 6.

Query Match 100.0%; Score 21; DB 66; Length 195;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 gctgcaccaatctagaatct 39
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Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 3
LOCUS MW018577 228 bp mRNA
DEFINITION Mus musculus immunoglobulin kappa light chain, variable region mRNA, clone BALB/c-51, partial cds.
ACCESSION U18577
NID g619707
KEYWORDS .
SOURCE mouse.
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; eukaryote crown group;
Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Mus.
1 (bases 1 to 228)
Roark, J.H., Kuntz, C.L., Nguyen, K.A., Caton, A.J. and Erikson, J.
Breakdown of B cell tolerance in a mouse model of systemic lupus
erythematosus
J. Exp. Med. 181 (3), 1157-1167 (1995)
95173583
REFERENCE 2 (bases 1 to 228)
AUTHORS Roark, J.H.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Jessica H. Roark, Wistar Institute, 3601
Spruce St., Philadelphia, PA 19104, USA
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/cell_type="splenic B cell hybridoma"
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/product="Immunoglobulin kappa light chain, variable
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/db_xref="PID:g619708"
/translation="YGDGSYNNWYQKQPCKLLIYAASNLGSGIPARFSGSGTD
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BASE COUNT 61 a 57 c 57 g 53 t
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Query Match 100.0%; Score 21; DB 65; Length 228;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 70 gctgcacccaatctagaatct 90
|||||
Qy 1 GCTGCATCCAATCTAGAATCT 21
RESULT 4
LOCUS MMU18563 238 bp mRNA ROD 21-JUN-1995
DEFINITION Mus musculus immunoglobulin kappa light chain, variable region
mRNA, clone BALB/c-11, partial cds.
ACCESSION U18563
NID g619679
KEYWORDS
SOURCE mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; eukaryote crown group;
Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Mus.
1 (bases 1 to 238)
Roark, J.H., Kuntz, C.L., Nguyen, K.A., Caton, A.J. and Erikson, J.
Breakdown of B cell tolerance in a mouse model of systemic lupus
erythematosus
J. Exp. Med. 181 (3), 1157-1167 (1995)
95173583
REFERENCE 2 (bases 1 to 238)
AUTHORS Roark, J.H.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Jessica H. Roark, Wistar Institute, 3601
Spruce St., Philadelphia, PA 19104, USA
FEATURES Location/Qualifiers
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/strain="BALB/c"
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/cell_type="splenic B cell hybridoma"
/tissue_type="spleen"
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FTLNHPVEEDAATYCCQSNEDPTFGSGT"
BASE COUNT 61 a 57 c 57 g 53 t
ORIGIN
Query Match 100.0%; Score 21; DB 65; Length 228;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 70 gctgcacccaatctagaatct 90
|||||
Qy 1 GCTGCATCCAATCTAGAATCT 21
RESULT 4
LOCUS MMU18563 238 bp mRNA ROD 21-JUN-1995
DEFINITION Mus musculus immunoglobulin kappa light chain, variable region
mRNA, clone BALB/c-11, partial cds.
ACCESSION U18563
NID g619679
KEYWORDS
SOURCE mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; eukaryote crown group;
Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Mus.
1 (bases 1 to 238)
Roark, J.H., Kuntz, C.L., Nguyen, K.A., Caton, A.J. and Erikson, J.
Breakdown of B cell tolerance in a mouse model of systemic lupus
erythematosus
J. Exp. Med. 181 (3), 1157-1167 (1995)
95173583
REFERENCE 2 (bases 1 to 238)
AUTHORS Roark, J.H.

TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Jessica H. Roark, Wistar Institute, 3601
Spruce St., Philadelphia, PA 19104, USA
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 79 gctgcacccaatctagaatct 99
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Qy 1 GCTGCATCCAATCTAGAATCT 21
RESULT 5
LOCUS MMICKVRD 255 bp RNA ROD 13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION Z25448
NID g407836
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
1 (bases 1 to 255)
Mo, J.A., Bona, C.A. and Holmdahl, R.
Variable region gene selection of immunoglobulin G expressing B
cells with specificity for a defined epitope on type II collagen
Eur. J. Immunol. (1993) In press
REFERENCE 2 (bases 1 to 255)
AUTHORS Mo, J.A.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A
Mo, Department of Medical and Physiological, Department of, Medical
and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
3 (bases 1 to 255)
Mo, J.A., Bona, C.A. and Holmdahl, R.
Variable region gene selection of immunoglobulin G-expressing B
cells with specificity for a defined epitope on type II collagen
Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE 94009207
FEATURES Location/Qualifiers
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BASE COUNT 71 a 65 c 64 g 55 t
ORIGIN

Query Match 100.0%; Score 21; DB 64; Length 255;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 118 gctgcatccaatctagaatct 138
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Qy 1 CCTGCATCCAATCTAGAACT 21

RESULT 6
LOCUS MMIGKCVRE 262 bp RNA ROD 13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION Z25450
NID g407838
KEYWORDS IgK gene; immunoglobulin; light chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 262)
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. (1993) In press
REFERENCE 2 (bases 1 to 262)

AUTHORS Mo, J.A.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE 3 (bases 1 to 262)

AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE 94009207

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CDS <1..>262
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/db_xref="PID:g407839"
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BASE COUNT 71 a 66 c 66 g 59 t
ORIGIN

Query Match 100.0%; Score 21; DB 64; Length 262;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 125 gctgcatccaatctagaatct 145
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Qy 1 CCTGCATCCAATCTAGAACT 21

RESULT 7
LOCUS MMIGKCVRI 264 bp RNA ROD 13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION Z25458
NID g407844
KEYWORDS IgK gene; immunoglobulin; light chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 264)
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. (1993) In press
REFERENCE 2 (bases 1 to 264)

AUTHORS Mo, J.A.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE 3 (bases 1 to 264)

AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE 94009207

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source Location/Qualifiers
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BASE COUNT      71 a      67 c      67 g      59 t
ORIGIN
Query Match      100.0%; Score 21; DB 64; Length 264;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 127 gctgcatccaatctagaatct 147
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Oy 1 GCTGCATCCAATCTAGAATCT 21

RESULT 8
LOCUS      MMICKVRC      266 bp      RNA      ROD      13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/I) gene, v region.
ACCESSION  Z25446
NID        g407834
KEYWORDS   Igk gene; immunoglobulin; light chain; variable region.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 266)
AUTHORS   Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE     Variable region gene selection of Immunoglobulin G expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL   Eur. J. Immunol. (1993) In press
REFERENCE  2 (bases 1 to 266)
AUTHORS   Mo, J.A.
TITLE     Direct Submission
JOURNAL   Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A
Mo, Department of Medical and Physiological, Department of, Medical
and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE  3 (bases 1 to 266)
AUTHORS   Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE     Variable region gene selection of Immunoglobulin G-expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL   Eur. J. Immunol. 23 (10), 2503-2510 (1993)
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Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 129 gctgcatccaatctagaatct 149
|||||
Oy 1 GCTGCATCCAATCTAGAATCT 21

RESULT 9
LOCUS      MMICKVRC      270 bp      RNA      ROD      13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/I) gene, v region.
ACCESSION  Z25454
NID        g407842
KEYWORDS   Igk gene; immunoglobulin; light chain; variable region.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 270)
AUTHORS   Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE     Variable region gene selection of immunoglobulin G expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL   Eur. J. Immunol. (1993) In press
REFERENCE  2 (bases 1 to 270)
AUTHORS   Mo, J.A.
TITLE     Direct Submission
JOURNAL   Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A
Mo, Department of Medical and Physiological, Department of, Medical
and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE  3 (bases 1 to 270)
AUTHORS   Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE     Variable region gene selection of immunoglobulin G-expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL   Eur. J. Immunol. 23 (10), 2503-2510 (1993)
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ORIGIN
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Mar 19 15:53

US-08-612-929-17.rge

11

Query Match 100.0%; Score 21; DB 64; Length 270;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 133 gctgcattcaatctagaatct 153
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Qy 1 GCTGCATCCATCTAGAACT 21

RESULT 10
LOCUS MMIGKCVRF 270 bp RNA ROD 13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION Z25452
NID g407840
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 270)
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. (1993) In press
REFERENCE 2 (bases 1 to 270)
AUTHORS Mo, J.A.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE 3 (bases 1 to 270)
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE 94009207
FEATURES Location/Qualifiers
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BASE COUNT 71 a 68 c 68 g 63 t
ORIGIN

Query Match 100.0%; Score 21; DB 64; Length 270;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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12

Db 133 gctgcattcaatctagaatct 153
|||||
Qy 1 GCTGCATCCATCTAGAACT 21

RESULT 11
LOCUS MMIGKCVRF 270 bp RNA ROD 13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION Z25444
NID g407832
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 270)
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. (1993) In press
REFERENCE 2 (bases 1 to 270)
AUTHORS Mo, J.A.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE 3 (bases 1 to 270)
AUTHORS Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE 94009207
FEATURES Location/Qualifiers
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BASE COUNT 71 a 68 c 68 g 63 t
ORIGIN

Query Match 100.0%; Score 21; DB 64; Length 270;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 133 gctgcattcaatctagaatct 153
|||||
Qy 1 GCTGCATCCATCTAGAACT 21

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US-08-612-929-17.rge

13

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RESULT 12
LOCUS MUSICKAAAA 279 bp mRNA ROD 07-MAR-1995
DEFINITION Mouse IgK chain mRNA, VJ5 region.
ACCESSION M57978
NID g196402
KEYWORDS J-region; V-region; anti-cytochrome c antibody;
immunoglobulin kappa-chain; immunoglobulin light chain.
SOURCE Mouse (BALB/c) secondary B cell hybridoma 1G3 mRNA, clone 1G3.E3.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 279)
AUTHORS Goshorn,S.C., Retzel,E. and Jemerson,R.
TITLE Common structural features among monoclonal antibodies binding the
same antigenic region of cytochrome c
JOURNAL J. Biol. Chem. 266 (4), 2134-2142 (1991)
MEDLINE 91115823
FEATURES
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        /map="chromosome 6"
        /note="CDR3"
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BASE COUNT 75 a 73 c 69 g 62 t
ORIGIN
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Query Match 100.0%; Score 21; DB 66; Length 279;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Mar 19 15:53

US-08-612-929-17.rge

14

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Db 103 gctgcattcaatctagaatct 123
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Qy 1 GCTGCATCCAATCTAGATCT 21

RESULT 13
LOCUS MMU29628 286 bp mRNA ROD 08-DEC-1995
DEFINITION Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region,
hybridoma 52.60, partial cds.
ACCESSION U29628
NID g896124
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 286)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Light chain contribution to specificity in anti-DNA antibodies
JOURNAL J. Immunol. 155 (6), 3223-3233 (1995)
MEDLINE 95403997
REFERENCE 2 (bases 1 to 286)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology,
Princeton University, Princeton, NJ 08544, USA
FEATURES
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            QPPKLLIYAASNLESGVPARFSGSGTDTFTLNIHPVEEDAATYTCQQS"
BASE COUNT 74 a 75 c 69 g 58 t
ORIGIN

Query Match 100.0%; Score 21; DB 65; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcattcaatctagaatct 180
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Qy 1 GCTGCATCCAATCTAGATCT 21

RESULT 14
LOCUS MMU18599 292 bp mRNA ROD 21-JUN-1995
DEFINITION Mus musculus immunoglobulin kappa light chain variable region mRNA,
clone BALB/c-9, partial cds.
ACCESSION U18599
NID g623397
KEYWORDS .
SOURCE mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; eukaryote crown group;
Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Mus. 1 (bases 1 to 292)

Roark, J.H., Kuntz, C.L., Nguyen, K.A., Caton, A.J. and Erikson, J. Breakdown of B cell tolerance in a mouse model of systemic lupus erythematosus

J. Exp. Med. 181 (3), 1157-1167 (1995)

Roark, J.H. Direct Submission Submitted (14-DEC-1994) Jessica H. Roark, Wistar Institute, 3601 Spruce St., Philadelphia, PA 19104, USA

Location/Qualifiers

1..292

/strain="BALB/c"

/organism="Mus musculus"

/clone="BALB/c-9"

/cell_type="splenic B cell hybridoma"

/tissue_type="spleen"

/dev_stage="adult"

<1..>292

/codon_start=1

/product="immunoglobulin kappa light chain variable region"

/db_xref="PID:g23398"

/translation="SLAVSLGQRATISCKASQSDYDGDSDYNNWYQKPGQPPKLLIY AASNLGSGIPARFSGSGGTDTFTNIHPVEEDAATYYCQSQSNEDPMTGGT"

BASE COUNT 75 a 72 c 78 g 67 t

ORIGIN

Query Match 100.0%; Score 21; DB 65; Length 292;

Best Local Similarity 100.0%; Pred. No. 5.82e-04;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 133 gctgcaccaatctagaatct 153
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Qy 1 GCTGCATCCAATCTAGAACT 21

RESULT 15

LOCUS MMU29629 297 bp mRNA ROD 08-DEC-1995

DEFINITION Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region, hybridoma 52.468, partial cds.

ACCESSION U29629

NID g896126

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

1 (bases 1 to 297)

Ibrahim, S.M., Weigert, M., Basu, C., Erikson, J. and Radic, M.Z. Light chain contribution to specificity in anti-DNA antibodies

J. Immunol. 155 (6), 3223-3233 (1995)

95403997

2 (bases 1 to 297)

Ibrahim, S.M., Weigert, M., Basu, C., Erikson, J. and Radic, M.Z. Direct Submission Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology, Princeton University, Princeton, NJ 08544, USA

Location/Qualifiers

1..297

source

/organism="Mus musculus"

/strain="BALB/c"

/isolate="hybridoma 52.468"

/chromosome="6"

<1..>297

/note="V-J region"

/codon_start=1

/product="Ig kappa chain"

/db_xref="PID:g896127"

/translation="DIVLTQSPASLAIVSLGQRATISCKASQSDYDGDSDYNNWYQKPGQPPKLLIY AASNLGSGIPARFSGSGGTDTFTNIHPVEEDAATYYCQSQSNEDP"

BASE COUNT 78 a 77 c 72 g 70 t

ORIGIN

Query Match 100.0%; Score 21; DB 65; Length 297;

Best Local Similarity 100.0%; Pred. No. 5.82e-04;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcaccaatctagaatct 180
|||||

Qy 1 GCTGCATCCAATCTAGAACT 21

RESULT 16

LOCUS S74550 313 bp mRNA ROD 12-MAY-1995

DEFINITION Ig V kappa r-rheumatoid factor RF3-SA (clone I) [mice, MRL/lpr, spleen, B cell hybridoma, mRNA Partial Mutant, 313 nt].

ACCESSION S74550

NID g806981

KEYWORDS mice spleen MRL/lpr B cell hybridoma.

SOURCE Mus sp

ORGANISM Mus sp

Unclassified.

REFERENCE 1 (bases 1 to 313)

AUTHORS Shan, H., Shlomchik, M.J., Marshak-Rothstein, A., Pisetsky, D.S., Litwin, S. and Weigert, M.G.

TITLE The mechanism of autoantibody production in an autoimmune MRL/lpr mouse

J. Immunol. 153 (11), 5104-5120 (1994)

95052677

GenBank staff at the National Library of Medicine created this entry [NCBI gibseq 158647] from the original journal article. This sequence comes from Fig. 2B.

FEATURES

source Location/Qualifiers

1..313

/organism="Mus sp."

/note="mice"

1..312

/partial

/genes="Ig V<kappa>"

/notes="IgA autoantibody kappa chain variable region; anti-IgG2a-specific. Method: conceptual translation supplied by author. This sequence comes from Fig. 2B."

/codon_start=1

/product="rheumatoid factor RF3-SA"

/db_xref="PID:g806982"

/translation="SLAVSLGQRATISCKASQSDYDGDSDYNNWYQKPGQPPKLLIY AASNLGSGIPARFSGSGGTDTFTNIHPVEEDAATYYCQSQSNEDPMTGGT"

BASE COUNT 82 a 75 c 79 g 77 t

ORIGIN

Query Match 100.0%; Score 21; DB 70; Length 313;

Best Local Similarity 100.0%; Pred. No. 5.82e-04;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 133 gctgcacccaatctagaatct 153
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Qy 1 GCTGCATCCCAATCTAGAATCT 21

RESULT 17
LOCUS MUSIGVACR 317 bp mRNA ROD 08-MAR-1993
DEFINITION Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
sequence.
ACCESSION L09042
NID g198040
KEYWORDS V-region; immunoglobulin V region; processed gene.
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 317)
AUTHORS Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
TITLE V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
mice

J. Immunol. 150, 1591-1610 (1993)

MEDLINE 93163585

FEATURES Location/Qualifiers

source
1..317
/organism="Mus musculus"
/strain="mrl/mp-lpr/lpr"
/cell_line="anti-Sm hybridoma 3G2K"
/cell_type="B-cell"
/dev_stage="adult"
/sequenced_mol="mRNA"
/tissue_type="spleen"

BASE COUNT 81 a 80 c 79 g 74 t 3 others
ORIGIN

Query Match 100.0%; Score 21; DB 67; Length 317;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 143 gctgcacccaatctagaatct 163
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Qy 1 GCTGCATCCCAATCTAGAATCT 21

RESULT 18
LOCUS MUSIGVKB 318 bp mRNA ROD 29-OCT-1994
DEFINITION Mouse immunoglobulin kappa light chain variable region anti-DNA
antibody (VK21E family) mRNA.
ACCESSION L14734
NID g793392
KEYWORDS V-region; anti-DNA antibody; immunoglobulin light chain;
immunoglobulin-kappa.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) female somatic
variant spleen cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 318)
AUTHORS Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.
TITLE Both IgM and IgG anti-DNA antibodies are the products of clonally
selective B cell stimulation in (NZB x NZW)F1 mice
J. Exp. Med. 176 (3), 761-779 (1992)

MEDLINE 92381444
REFERENCE 2 (bases 1 to 318)
AUTHORS Krishnan,M.R. and Marion,T.N.
TITLE Structural similarity of antibody variable regions from immune and
autoimmune anti-DNA antibodies
J. Immunol. (1993) In press
FEATURES Location/Qualifiers
1..318
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/cell_line="bfd05"
/cell_type="hybridoma"
/dev_stage="somatic variant"
/sequenced_mol="cDNA to mRNA"
/sex="female"
/tissue_type="spleen"

source
1..318

V_region
1..318
/codon_start=1
BASE COUNT 85 a 77 c 79 g 72 t 5 others
ORIGIN

Query Match 100.0%; Score 21; DB 66; Length 318;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 145 gctgcacccaatctagaatct 165
|||||
Qy 1 GCTGCATCCCAATCTAGAATCT 21

RESULT 19
LOCUS S42888 333 bp DNA ROD 09-NOV-1992
DEFINITION Ig V kappa =immunoglobulin V kappa region [mice, hybridoma 54'CB1,
Genomic, nt].
ACCESSION S42888
NID g254222
KEYWORDS mice hybridoma 54'CB1.
SOURCE Mus sp.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 333)
AUTHORS Matsushita,S., Maeda,H., Kimachi,K., Eda,Y., Maeda,Y., Murakami,T.,
Tokiyoshi,S. and Takatsuki,K.
TITLE Characterization of a mouse/human chimeric monoclonal antibody (C
beta 1) to a principal neutralizing domain of the human
immunodeficiency virus type 1 envelope protein
AIDS Res. Hum. Retroviruses 8 (6), 1107-1115 (1992)

JOURNAL AIDS Res. Hum. Retroviruses 8 (6), 1107-1115 (1992)
MEDLINE 92368728
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 111883] from the original journal article.
This sequence comes from Fig. 2.
FEATURES Location/Qualifiers
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/organism="Mus sp."
/note="mice"
1..333
/partial
/gene="Ig V kappa">
/note="Description: immunoglobulin V kappa region,
antibody C beta 1; This sequence comes from Fig. 2.
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/codon_start=1
/product="immunoglobulin V kappa region"

db_xref="PID:g54223" /translation="DIVLTQSPASVLAVSIGQRATISCKASQSDVDGDSYMMWYQKQP
GQPKLLIYAASNLSCIPARFSGSGRTDFTLNHPVEEDAATYYCQGSNEDPPTF
GSGTKLEIK"
BASE COUNT 91 a 82 c 81 g 79 t
ORIGIN
Query Match 100.0%; Score 21; DB 70; Length 333;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 160 gctgcatccaatctagaatct 180
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Qy 1 GCTGCATCCAATCTAGAATCT 21
RESULT 20
LOCUS MUSIGLSB 333 bp DNA ROD 01-NOV-1991
DEFINITION Mouse IgL chain H2L2 V-region, partial cds.
ACCESSION M80406
NID gl97577
KEYWORDS V-region; immunoglobulin light chain.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) (library:
lambda-gt11) DNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 333)
AUTHORS Matsushita,S., Maeda,H., Kimachi,K., Eda,Y., Maeda,Y., Hattori,T.,
Tokiyoshi,S. and Takatsuki,K.
TITLE Characterization of a mouse/human chimeric monoclonal antibody
(C-beta-1) to a principal neutralizing domain of the human
immunodeficiency virus type I envelope protein
JOURNAL Unpublished (1991)
FEATURES Location/Qualifiers
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/strain="BALB/c"
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/sequenced_mol="DNA"
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/product="immunoglobulin light chain"
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/translation="DIVLTQSPASVLAVSIGQRATISCKASQSDVDGDSYMMWYQKQP
GQPKLLIYAASNLSCIPARFSGSGRTDFTLNHPVEEDAATYYCQGSNEDPPTF
GSGTKLEIK"
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misc_feature 70..114
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/note="CDR2"

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misc_feature 277..303
/gene="0.5 beta-VL"
/note="CDR3"
misc_feature 304..333
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/note="FR4"
BASE COUNT 91 a 82 c 81 g 79 t
ORIGIN
Query Match 100.0%; Score 21; DB 67; Length 333;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 160 gctgcatccaatctagaatct 180
|||||
Qy 1 GCTGCATCCAATCTAGAATCT 21
RESULT 21
LOCUS MMIGLC404 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T404).
ACCESSION X65092
NID g52292
KEYWORDS ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG
REFERENCE 2 (bases 1 to 336)
AUTHORS Weissenhorn,W., Riethmueller,G., Weiss,E.M. and Rieber,E.P.
TITLE Structural characterization of CD4 mAb
JOURNAL Unpublished
FEATURES Location/Qualifiers
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/strain="Balb/c"
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/cell_line="Hybridoma M-T404"
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region"
/db_xref="PID:g52293"
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GQPKLLIYAASNLSCIPARFSGSGTDFTLNHPVEEDAATYYCQGSNEDPPTF
GSGTKLEIK"
BASE COUNT 89 a 90 c 81 g 76 t
ORIGIN
Query Match 100.0%; Score 21; DB 64; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Db 160 gctgcatccaatctagaatct 180
|||||
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 22
LOCUS MUSIGVACP 336 bp mRNA ROD 08-MAR-1993
DEFINITION Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
sequence.
ACCESSION L09040
NID g198038
KEYWORDS V-region; immunoglobulin V region; processed gene.
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 336)
AUTHORS Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
TITLE V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
mice
JOURNAL J. Immunol. 150, 1591-1610 (1993)
MEDLINE 93163585
FEATURES
source
Location/Qualifiers
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/strain="mrl/mp-lpr/lpr"
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BASE COUNT 88 a 81 c 86 g 81 t
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Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcatccaatctagaatct 180
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Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 23
LOCUS MMIGLC413 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T413).
ACCESSION X65093
NID g52298
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

Db 160 gctgcatccaatctagaatct 180
|||||
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 24
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

Db 160 gctgcatccaatctagaatct 180
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Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 25
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG
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REFERENCE 2 (bases 1 to 336)
AUTHORS Weissenhorn,W., Riettmueller,G., Weiss,E.M. and Rieber,E.P.
TITLE Structural characterization of CD4 mAb
JOURNAL Unpublished
FEATURES
source
Location/Qualifiers
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/cell_type="B-cell"
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region"
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GRPKLLIYAASNLIESGIPARFSGSGGTFTLNIRHVEEDAAITYYCQOSTQDPTFE
GGGTLKLEIKR"
BASE COUNT 88 a 87 c 84 g 77 t
ORIGIN
Query Match 100.0%; Score 21; DB 64; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcatccaatctagaatct 180
|||||
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 24
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

Db 160 gctgcatccaatctagaatct 180
|||||
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 25
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

Db 160 gctgcatccaatctagaatct 180
|||||
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 26
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

Db 160 gctgcatccaatctagaatct 180
|||||
Qy 1 GCTGCATCCAACTAGAACT 21

RESULT 27
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Weissenhorn,W.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG
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Mar 19:15:53

US-08-612-929-17.rge

23

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GGGTKLEIKR"

BASE COUNT 89 a 90 c 81 g 76 t
ORIGIN

Query Match 100.0%; Score 21; DB 64; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcacccaatctagaatct 180
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Qy 1 GCTGCATCCAATCTAGAACT 21

RESULT 25 MUSICKABBC 350 bp mRNA ROD 29-OCT-1994
LOCUS Mouse Ig kappa chain mRNA, V-J region from hybridoma MOR8.2.1,
DEFINITION partial cds.
ACCESSION M92401
NID gi196481
KEYWORDS J-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa; morphine specific antibody; processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) B-lymphocyte
cDNA to mRNA.

ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 350)
AUTHORS Sawada,J., Yamazaki,T. and Terao,T.
TITLE Molecular and biochemical analyses of combining sites of monoclonal
anti-morphine antibodies
JOURNAL Mol. Immunol. 30 (1), 77-86 (1993)
MEDLINE 93109376
FEATURES Location/Qualifiers
source
1..350
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/strain="BALB/c"
/sub_species="domesticus"
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GQPPKLLIYAASNLSEGPAPFSGSGTDFTLIHVVEEDAATYYCQSSSEDPPTF
GGGTKLEIKRAAP"

J_segment 297..334
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/map="6"
BASE COUNT 90 a 88 c 89 g 81 t 2 others
ORIGIN chromosome 6.
Query Match 100.0%; Score 21; DB 66; Length 350;
Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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24

Db 160 gctgcacccaatctagaatct 180
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Qy 1 GCTGCATCCAATCTAGAACT 21

RESULT 26 MUSICKABBE 353 bp mRNA ROD 29-OCT-1994
LOCUS Mouse Ig kappa chain mRNA, V-J region from hybridoma MOR35.4.12,
DEFINITION partial cds.
ACCESSION M92403
NID gi196485
KEYWORDS J-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa; morphine specific antibody; processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) B-lymphocyte
cDNA to mRNA.

ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 353)
AUTHORS Sawada,J., Yamazaki,T. and Terao,T.
TITLE Molecular and biochemical analyses of combining sites of monoclonal
anti-morphine antibodies
JOURNAL Mol. Immunol. 30 (1), 77-86 (1993)
MEDLINE 93109376
FEATURES Location/Qualifiers
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/tissue_type="B-lymphocyte"

V_region 1..296
/gene="IgK"
/map="6"
CDS <1..>353
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GQPPKLLIYAASNLSEGPAPFSGSGTDFTLIHVVEEDAATYYCQSSSEDPPTF
GGGTKLEIKRAAPT"

J_segment 297..334
/gene="IgK"
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BASE COUNT 87 a 91 c 91 g 82 t 2 others
ORIGIN chromosome 6.
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 gctgcacccaatctagaatct 180
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Qy 1 GCTGCATCCAATCTAGAACT 21

RESULT 27 MUSL71IGKV 354 bp mRNA ROD 29-OCT-1994
LOCUS Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial
DEFINITION


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cds.
ACCESSION M97875
NID g198677
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c
fusion hybridoma cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 354)
AUTHORS Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.
TITLE Characterization of murine monoclonal anti-CD4; epitope
recognition, idiootope expression, and variable gene sequence
JOURNAL Unpublished (1992)
FEATURES
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V_region
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RESULT 28
LOCUS MUSICKAF 360 bp mRNA ROD 30-AUG-1991
DEFINITION Mouse Ig active kappa chain mRNA V-region (V-D-J).
ACCESSION M61046
NID g196679
KEYWORDS anti-CD4; immunoglobulin light chain; monoclonal antibody.
SOURCE Mouse, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 360)
AUTHORS Attanasio,R., Dilley,D., Buck,D.W., Maino,V.C., Lohman,K.L.,
Kanda,P. and Kennedy,R.C.
TITLE Structural characterization of a cross-reactive idiootype sharedby
monoclonal antibodies specific for the human CD4 molecule
JOURNAL J. Biol. Chem. 266, 14611-14619 (1991)
MEDLINE 91317827
FEATURES
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160..180
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277..303
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RESULT 29
LOCUS MUSL031GKV 363 bp mRNA ROD 29-OCT-1994
DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial
cda.
ACCESSION M97879
NID g198681
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c
fusion hybridoma cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 363)
AUTHORS Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.
TITLE Characterization of murine monoclonal anti-CD4; epitope
recognition, idiootope expression, and variable gene sequence
JOURNAL Unpublished (1992)
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        Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 30
LOCUS MUSL2021GK 363 bp mRNA ROD 29-OCT-1994
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DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial
cde.
ACCESSION M97869
NID g198667
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c
fusion hybridoma cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 363)
AUTHORS Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.
TITLE Characterization of murine monoclonal anti-CD4; epitope
recognition, idiotope expression, and variable gene sequence
JOURNAL Unpublished (1992)
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                specificity)"
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Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 160 gctgcattccaatctagaatct 180
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Qy 1 GCTGCATCCAATCTAGATCT 21

RESULT 31
LOCUS S50265 393 bp mRNA ROD 02-APR-1993
DEFINITION Ig VL=anti-CD4 mAb M-T310 variable region light chain (JL, chimeric
antibody) [mice, hybridoma cells, mRNA Partial, 393 nt].
ACCESSION S50265
NID g260765
KEYWORDS mice hybridoma cells.
SOURCE mice hybridoma cells.
ORGANISM Mus sp.
Unclassified.
REFERENCE 1 (bases 1 to 393)
AUTHORS Weissenhorn,W., Scheuer,W., Kaluza,B., Schwirzke,M., Reiter,C.,
Flieger,D., Lenz,H., Weiss,E.H., Rieber,E.P., Riettmuller,G. et.al.
TITLE Combinatorial functions of two chimeric antibodies directed to
human CD4 and one directed to the alpha-chain of the human
interleukin-2 receptor
JOURNAL Gene 121 (2), 271-278 (1992)
MEDLINE 93077041
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI glibseq 119503] from the original Journal article.
This sequence comes from Fig. 1c.
FEATURES
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        Location/Qualifiers
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                /organism="Mus sp."
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CD5
/notes="mice"
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/partial
/genes="Ig VL"
/notes="Method: conceptual translation supplied by author.
This sequence comes from Fig. 1c."
/codon_start=1
/product="anti-CD4 mAb M-T310 variable region light chain"
/db_xref="PID:g260766"
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BASE COUNT 100 a 105 c 98 g 90 t
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Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 220 gctgcattccaatctagaatct 240
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RESULT 32
LOCUS I08223 900 bp PAT 14-NOV-1994
DEFINITION Sequence 1 from patent EP 0365209.
ACCESSION I08223
NID g589062
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 900)
AUTHORS Hinton,R. and Ol,V.T.
TITLE Anti-leu 3A amino acid sequence
JOURNAL Patent: EP 0365209-A2 1 25-APR-1990;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 5.82e-04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 708 gctgcattccaatctagaatct 728
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Qy 1 GCTGCATCCAATCTAGATCT 21

Search completed: Wed Mar 19 15:55:24 1997
Job time : 71 secs.
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1

WVQSEF (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:21:00 1997; MaePar time 59.78 Seconds
199.194 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-19
Description: (1-27) from US08612929.seq
Perfect Score: 27
N.A. Sequence: 1 CACGACACTATGAGCATCCCGACG 27
Comp: GTGCTTCACTACTCTAGGAGCTGC

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0\$
Listing first 45 summaries

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9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
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141:gneEST2 142:gneEST3 143:gneEST4 144:gneEST5 145:gneEST6
146:gneEST7 147:gneEST8 148:gneEST9 149:gneEST10 150:gneEST11
151:gneEST12 152:gneEST13 153:gneEST14 154:gneEST15
155:gneEST16 156:gneSTS 157:eneEST1 158:eneEST2 159:eneEST3
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169:eneEST13 170:eneEST14 171:eneEST15 172:eneEST16
173:eneSTS1 174:eneSTS2

Statistics: Mean 6.936; Variance 1.332; scale 5.209

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c	1	17	63.0	314	124	T84399	yd45q03.rl Homo sapie	1.11e-04
c	2	16	59.3	408	30	H77752	yu23g11.rl Homo sapie	2.51e-03
c	3	16	59.3	482	128	T98290	ye59g06.sl Homo sapie	2.51e-03
c	4	15	55.6	215	61	N49151	yy84b12.rl Homo sapie	4.99e-02
c	5	15	55.6	236	61	N48736	yy55d11.rl Homo sapie	4.99e-02
c	6	15	55.6	305	168	HSW04100	T1792.WVAT4 bloodstre	4.99e-02
c	7	15	55.6	305	147	W04100	T1792.WVAT4 bloodstre	4.99e-02
c	8	15	55.6	329	170	WM3966	ma67g11.rl Soares mou	4.99e-02
c	9	15	55.6	329	149	W12396	ma67g11.rl Soares mou	4.99e-02
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c	12	15	55.6	361	108	T26512	AB284F11R Homo sapien	4.99e-02
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c	16	15	55.6	368	155	HSPD03654	H.sapiens mitochondri	4.99e-02
c	17	15	55.6	372	155	HSPD04181	H.sapiens mitochondri	4.99e-02
c	18	15	55.6	372	46	HSPD04181	H.sapiens mitochondri	4.99e-02
c	19	15	55.6	372	168	HSPD04181	H.sapiens mitochondri	4.99e-02
c	20	15	55.6	374	99	R95278	SW31C0175SK Onchocerc	4.99e-02
c	21	15	55.6	412	100	R97220	Yq62e11.sl Homo sapie	4.99e-02
c	22	15	55.6	423	168	HSPD03830	H.sapiens mitochondri	4.99e-02
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c	27	15	55.6	455	170	WM4343	ma63a01.rl Soares mou	4.99e-02
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c	30	14	51.9	220	49	HUM571A11B	Human fetal brain cDN	8.55e-01
c	31	14	51.9	284	48	HUM171A11B	Human fetal brain cDN	8.55e-01
c	32	14	51.9	285	164	HS680311	KK2222F Homo sapiens	8.55e-01
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c	35	14	51.9	396	155	HSPD04086	H.sapiens mitochondri	8.55e-01
c	36	14	51.9	401	143	N84913	J1531F Homo sapiens c	8.55e-01
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 44 14 51.9 449 115 T53311 ya88a04.s1 Homo sapie 8.55e-01
 c 45 14 51.9 560 47 HUM093A03B Human fetal brain cdw 8.55e-01

ALIGNMENTS

RESULT 1
 LOCUS T84399 314 bp mRNA EST 16-MAR-1995
 DEFINITION yd45q03.r1 Homo sapiens cDNA clone 111220 5'.
 ACCESSION T84399
 NID g712687

KEYWORDS EST.
 SOURCE human clone=111220 library=Soares fetal liver spleen lNfLS vector=pt7T3D (Pharmacla) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 314)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 207

Source: IMAGE Consortium, L1NL

This clone is available royalty-free through L1NL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
 Location/Qualifiers
 source 1..314

/organism="Homo sapiens"

/clone="111220"

/note="human"

BASE COUNT 90 a 55 c 74 g 91 t 4 others
 ORIGIN

Query Match 63.0%; Score 17; DB 124; Length 314;
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 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 282 ggtggatctactacttgctg 304

|| ||||| ||||| |||||

Cp 23 GGAGGATCCTTACTTTGCTG 1

RESULT 2

Mar 19:08:20

US-08-612-929-19.rst

4

LOCUS H77752 408 bp mRNA EST 09-NOV-1995
 DEFINITION yu23q11.r1 Homo sapiens cDNA clone 234692 5'.
 ACCESSION H77752
 NID g1055841

KEYWORDS EST.
 SOURCE human clone=234692 primer=M13RP1 library=Soares fetal liver spleen lNfLS vector=pt7T3D (Pharmacla) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 408)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 281

Source: IMAGE Consortium, L1NL

This clone is available royalty-free through L1NL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
 Location/Qualifiers

source

1..408

/organism="Homo sapiens"

/clone="234692"

/note="human"

<1..>408

BASE COUNT 116 a 50 c 85 g 154 t 3 others
 ORIGIN

Query Match 59.3%; Score 16; DB 30; Length 408;
 Best Local Similarity 94.4%; Pred. No. 2.51e-03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 155 ggaggatctcttaatt 172

||||| ||||| ||||| ||

Cp 23 GGAGGATCCTCTTACTT 6

RESULT 3

LOCUS T98290 482 bp mRNA EST 31-MAR-1995
 DEFINITION ye39g06.s1 Homo sapiens cDNA clone 122074 3' similar to contains Alu repetitive element;.

ACCESSION T98290

NID 9748027

through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH).

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 236)

REFERENCE

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
High quality sequence stops: 193
Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source 1..236
/organism="Homo sapiens"
/clone="277461"
/notes="human"
mRNA 51 a 44 c 50 g 87 t 4 others
ORIGIN 1..>236

Query Match 55.6%; Score 15; DB 61; Length 236;
Best Local Similarity 85.7%; Pred. No. 4.99e-02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 168 agtactctcatgcttgctg 188
|| ||||| ||||| |||||
Cp 21 AGGATCCTCATTACTTTCTG 1

RESULT

ID HSW04100 standard; RNA; EST; 305 BP.
AC W04100;
DT 30-APR-1996 (Rel. 47, Created)
DT 30-APR-1996 (Rel. 47, Last updated, Version 1)
DE T1792 W04100 bloodstream form of serodeme WRATat1.1 Trypanosoma
DE brucei rhodesiense cDNA 5'.
KW EST.
OS Trypanosoma brucei rhodesiense
OC Eukaryota; Animalia; Protozoa; Sarcostigophora; Mastigophora;
OC Zoomastigophora; Kinetoplastida; Trypanosomatina; Trypanosomatidae.
RN [1]
RP 1-305
RA Majiwa P.A.O.;
RT "Facile identification of genes of the Trypanosoma by single pass
RT cDNA sequence determination";
RL Unpublished.

Contact: Majiwa PAO Molecular Biology Unit International Livestock
Research Institute P.O. Box 30709, Nairobi, Kenya Tel: 254-2 630743
Fax: 254-2 631499 Email: p.majiwa@cnet.com Seq primer: T3 primer.
CC NCBI gi: 1275942
FH Key Location/Qualifiers

FH source 1..305
FT /organism="Trypanosoma brucei rhodesiense"
FT /note="Vector: Lambda ZAP II (Stratagene); Site 1: EcoRI;
FT Site 2: XhoI; The mRNA was purified from a cloned
FT population of bloodstream trypanosomes reexpressing the
FT W04100 metacyclic variant surface glycoprotein (VSG). A
FT unidirectional oligo dT-primed EcoRI/XhoI cDNA library was
FT constructed in Lambda ZAP II (Stratagene).
FT /clone_lib="W04100 bloodstream form of serodeme WRATat1.1"
FT mRNA <1..>305
SQ Sequence 305 BP; 74 A; 71 C; 88 G; 72 T; 0 other;

Query Match 55.6%; Score 15; DB 168; Length 305;
Best Local Similarity 80.0%; Pred. No. 4.99e-02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 182 agcaaatcaatgaggtctactac 206
||||| ||||| || |||||
Qy 2 ACCAAAGTATGAGGATCTCCGAC 26

RESULT

LOCUS W04100 305 bp mRNA EST 22-APR-1996
DEFINITION T1792 W04100 bloodstream form of serodeme WRATat1.1 Trypanosoma
brucei rhodesiense cDNA 5'.

ACCESSION W04100

NID g1275942

KEYWORDS EST.

SOURCE Trypanosoma brucei rhodesiense.

ORGANISM Trypanosoma brucei rhodesiense
Eukaryota; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;
Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 305)

AUTHORS Majiwa, P.A.O.

TITLE Facile identification of genes of the Trypanosoma by single pass
cDNA sequence determination
JOURNAL Unpublished (1996)

COMMENT

Contact: Majiwa PAO
Molecular Biology Unit
International Livestock Research Institute
P.O. Box 30709, Nairobi, Kenya
Tel: 254-2 630743
Fax: 254-2 631499
Email: p.majiwa@cnet.com
Seq primer: T3 primer.

FEATURES

source NCBI gi: 1275942
Location/Qualifiers
1..305
/organism="Trypanosoma brucei rhodesiense"
/note="Vector: Lambda ZAP II (Stratagene); Site 1: EcoRI;
Site 2: XhoI; The mRNA was purified from a cloned
population of bloodstream trypanosomes reexpressing the
W04100 metacyclic variant surface glycoprotein (VSG). A
unidirectional oligo dT-primed EcoRI/XhoI cDNA library was
constructed in Lambda ZAP II (Stratagene)."
/clone_lib="W04100 bloodstream form of serodeme WRATat1.1"

RESULT 11

Livermore National Laboratory, Livermore, CA 94550

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Tel: 5104225711
Fax: 5104233608
Email: greg@medcell.llnl.gov.
Location/Qualifiers

FEATURES

source

1..361
/organism="Homo sapiens"
/clone="LLAB284F11"
/note="human"
<1..>361

mRNA

BASE COUNT
ORIGIN

101 a 124 c 39 g 94 t 3 others

Query Match

55.6%; Score 15; DB 108; Length 361;

Best Local Similarity 89.5%; Pred. No. 4.99e-02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 286 gatctcattactattctg 304

||||| ||||| ||||| |||||

Cp 19 GATCCTCATTACTTTGCTG 1

RESULT 13

LOCUS

T26512 361 bp mRNA EST 15-APR-1996
DEFINITION AB284F11R Homo sapiens cDNA clone LLAB284F11 5'.

ACCESSION

T26512

NID

g773829

KEYWORDS

EST.

SOURCE

human clone=LLAB284F11 primer=M13 Reverse library=Infant brain,

LNHL array of Dr. M. Soares INITB vector=tafmid BA Rsite1=HindIII

Rsite2=NotI Normalized infant brain cDNA library made by Dr. M.

Soares (Columbia University), oligo-dT primed and directionally

cloned between HindIII (5') and NotI (3') sites.

ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 361)

Chisio, N.S., Eveleth, G.G., Lieuallen, K. and Lennon, G.G.

Chromosomal assignment of 20 cDNAs using flow-sorted spot-blot

stamps

Genomics 28 (3), 570-572 (1995)

Contact: Greg G. Lennon

Human Genome Center, J-452

Lawrence Livermore National Laboratory

Livermore CA 94550

Tel: 510 422 8361

Fax: 510 422 2282

Email: info@image.llnl.gov.

FEATURES

source

NCBI gi: 773829
Location/Qualifiers
1..361
/organism="Homo sapiens"
/clone="LLAB284F11"
/note="human"
<1..>361

mRNA

BASE COUNT
ORIGIN

101 a 124 c 39 g 94 t 3 others

Query Match

55.6%; Score 15; DB 143; Length 361;

Best Local Similarity 89.5%; Pred. No. 4.99e-02;

Mar 19 08:20

US-08-612-929-19.rst

14

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 286 gatctcattactattctg 304

||||| ||||| ||||| |||||

Cp 19 GATCCTCATTACTTTGCTG 1

RESULT 14

LOCUS

HSPD03654 368 bp DNA EST 22-DEC-1995
DEFINITION H.sapiens mitochondrial EST sequence (004-X2-28) from skeletal

ACCESSION

F19057

NID

g1135472

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 368)

Lanfranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A.,

Pandolfo, D., Toppo, S., Trevisan, S., Scarso and Valle, G.

Identification of 4,370 expressed sequence tags (ESTs) from a

3'-end specific cDNA library of human skeletal muscle by DNA

sequencing and filter hybridisation

Genome Res. (1996) in press

2 (bases 1 to 368)

Valle, G.

Direct Submission

Submitted (19-DEC-1995) CRIBI Biotechnology Centre, University of

Padua, Via Trieste 75, 35121 Padua, Italy

ABI Chromatograms and other information are available on WWW at

http://eos.bio.unipd.it

Vector: pcDNAII (Invitrogen)

V type: Plasmid

RE_1: EcoRI

RE_2: NotI

PRIMER: PC2R

DESCR: The cDNA was constructed using a biotin-NotI-oligo(dT)

primer,

sonicated and size selected (450-550 BP). The biotinylated 3'-ends

were affinity purified, directionally cloned and sequenced (5' ->

3').

FEATURES

Location/Qualifiers

1..368

/organism="Homo sapiens"

/note="caucasian"

/tissue type="pectoral muscle (after mastectomy)"

/clone_lib="HM1"

/sex="female"

BASE COUNT 108 a 123 c 39 g 89 t 9 others

ORIGIN

Query Match

Best Local Similarity 88.9%; Pred. No. 4.99e-02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 24 atctcattactatnctg 41

||||| ||||| ||||| |||||

Cp 18 ATCCTCATTACTTTGCTG 1

RESULT 15

ID

HSPD03654

standard; DNA; EST; 368 BP.

AC F19057;

Mar 19 08:20

US-08-612-920-19.rst

15

```
DT 22-DEC-1995 (Rel. 46, Created)
DE 06-MAY-1996 (Rel. 47, Last updated, Version 2)
DE H.sapiens mitochondrial EST sequence (004-X2-28) from skeletal
DE muscle.
KW EST.
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RN [1]
RP 1-368
RA Lanfranchi G., Muraro T., Caldara F., Pacchioni B.,
RA Pallavicini A., Pandolfo D., Toppo S., Trevisan S.,
RA Scarso and Valle G.;
RT "Identification of 4,370 expressed sequence tags (ESTs) from a
RT 3'-end specific cDNA library of human skeletal muscle by DNA
RT sequencing and filter hybridisation";
RL Genome Res. 1:35-42 (1996).
RV [2]
RP 1-368
RA Valle G.;
RT ;
RL Submitted (19-DEC-1995) to the EMBL/GenBank/DBJ databases.
RL CRIBI Biotechnology Centre, University of Padua, Via Trieste 75,
RL 35121 Padua, Italy.
CC ABI Chromatograms and other information are available on WWW at
CC http://eos.bio.unipd.it
CC Vector: pcDNAII (Invitrogen)
CC V_type: Plasmid
CC RE_1: EcoRI
CC RE_2: NotI
CC PRIMER: PC2R
CC DESCR: The cDNA was constructed using a biotin-NotI-oligo(dT)
CC primer.
CC sonicated and size selected (450-550 BP). The biotinylated 3'-ends
CC were affinity purified, directionally cloned and sequenced (5' ->
CC 3').
FH Key Location/Qualifiers
FH
FH source 1..368
FH /organism="Homo sapiens"
FH /tissue_type="pectoral muscle (after mastectomy)"
FH /clone_lib="HM1"
FH /note="caucasian"
FH /sex="female"
SQ Sequence 368 BP; 108 A; 123 C; 39 G; 89 T; 9 other;

Query Match 55.6%; Score 15; DB 168; Length 368;
Best Local Similarity 88.9%; Pred. No. 4.99e-02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 24 atccctactactatnctg 41
|||||
Cp 18 ATCCTCATTTACTTTCGTC 1
```

Search completed: Wed Mar 19 08:22:09 1997
Job time : 69 secs.

MUSE (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MParch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:20:26 1997; MasPar time 10.83 Seconds
217.531 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-19

Description: (1-27) from US08612929.seq

Perfect Score: 27

N.A. Sequence: 1 CAGCAAGTAATGAGGATCTCTCGACG 27

Comp: GTCGTTTCATTACTCTAGGAGCTCC

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.665; Variance 3.162; scale 1.792

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	27	100.0	393	14	Q83520	Humanized antibody 3B
2	27	100.0	396	14	Q83490	Mouse MAB 3B9 light c
3	25	92.6	51	14	Q83511	IL-4 CDR3 gene fragment
4	25	92.6	53	14	Q83512	IL-4 CDR3 gene fragment
5	25	92.6	99	9	Q55014	Humanized Ab 60.3 VL
6	25	92.6	334	9	Q55002	Murine anti-CD18 Ab 6
7	25	92.6	334	9	Q55000	Humanized anti-CD18 A
8	25	92.6	393	5	Q30757	p64-k4.

9	25	92.6	393	6	Q36609	Anti-CD4 antibody MT	2.52e-05
10	25	92.6	393	14	Q73986	Humanized antibody 3B	2.52e-05
11	23	85.2	336	2	Q12684	Murine 1B4 light chain	4.32e-04
12	23	85.2	645	13	Q80292	Monoclonal antibody 2	4.32e-04
13	22	81.5	87	9	Q55013	Humanized Ab 60.3 VL	1.75e-03
14	22	81.5	91	9	Q51746	Oligonucleotide probe	1.75e-03
15	22	81.5	900	1	Q04039	Anti-Leu 3a light chain	1.75e-03
16	21	77.8	91	9	Q51746	Oligonucleotide probe	6.93e-03
17	21	77.8	309	9	Q55915	Light chain region of	6.93e-03
18	21	77.8	333	11	Q65554	Mouse anti-HIV mu5.5	6.93e-03
19	21	77.8	333	9	Q55917	Humanized light chain	6.93e-03
20	21	77.8	333	12	Q70372	Anti HIV antibody lig	6.93e-03
21	21	77.8	451	1	Q04694	Light chain variable	6.93e-03
22	20	74.1	41	2	Q12690	Rei light chain varia	2.70e-02
23	20	74.1	45	2	Q12691	Rei light chain varia	2.70e-02
24	20	74.1	334	1	N90492	Gene fragment of immu	2.70e-02
25	20	74.1	396	7	Q42987	Mouse 4C10 anti-idiot	2.70e-02
26	20	74.1	733	4	Q25658	Mouse 0.5beta anti-HI	2.70e-02
27	20	74.1	780	1	N90495	A V chi region gene.	2.70e-02
28	19	70.4	333	12	Q70376	Chimeric anti HIV ant	1.03e-01
29	19	70.4	333	11	Q65558	Mouse-human chimeric	1.03e-01
30	19	70.4	333	14	Q82818	Murine NM-01 variable	1.03e-01
31	19	70.4	334	11	Q73749	Light chain variable	1.03e-01
32	19	70.4	336	2	Q10379	Chimeric MAB 9.2.27 l	1.03e-01
33	19	70.4	363	10	Q56688	Sequence of the monoc	1.03e-01
34	18	66.7	336	16	Q96283	Human IgE receptor-bi	3.84e-01
35	18	66.7	336	16	Q96285	Human IgE receptor-bi	3.84e-01
36	18	66.7	363	6	Q37472	Sequence encoding the	3.84e-01
37	18	66.7	363	10	Q56686	Sequence of the monoc	3.84e-01
38	18	66.7	1014	2	Q10834	Encodes kappa light c	3.84e-01
39	17	63.0	118	4	Q26784	Oligomer ma8 used to	1.39e+00
40	17	63.0	204	1	N81164	Base substituted E.co	1.39e+00
41	17	63.0	333	11	Q63908	Light chain variable	1.39e+00
42	17	63.0	339	18	T04013	Anti-EGFR antibody 11	1.39e+00
43	17	63.0	339	18	T04015	Anti-EGFR antibody 11	1.39e+00
44	17	63.0	632	10	Q56691	Genomic sequence of t	1.39e+00
45	17	63.0	2015	5	Q30455	Sequence of ACP (acyl	1.39e+00

ALIGNMENTS

RESULT 1
ID Q83520 standard; cDNA; 393 BP.
AC Q83520;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW MAb; interleukin-4; IL-4; allergy; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..393
FT /*tag= a
PN WO9507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR P-PSDB; R70202.
DR Chimeric and humanized IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated

Mar 19 08:18

US-08-612-929-19.mg

3

PT and IgE-mediated allergic conditions
PS Disclosure; Page 71-72; 97pp; English.
CC A humanized antibody light chain variable region and signal
CC sequence is given in R75355. The signal sequence is also
CC provided in R70194. The sequences of the 3 CDRs
CC are identical to mouse anti-human IL-4 Mab 3B9 light chain
CC CDRs (given in R70195-97).
SQ Sequence 393 BP; 97 A; 98 C; 105 G; 93 T;

Query Match 100.0%; Score 27; DB 14; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.39e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 334 cagcaagaatgagatcctccgacg 360
|||||
Qy 1 CAGCAAGTAATGAGATCCTCCGACG 27

RESULT 2

ID Q83490 standard; cDNA; 396 BP.

AC Q83490;

DT 20-SEP-1995 (first entry)

DE Mouse Mab 3B9 light chain.

KW Chimeric antibody; humanized antibody; antibody engineering;

KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; ds.

OS Mus sp.

FH Key Location/Qualifiers

FT CDS 1..396

FT /*tag= a

FT sig_peptide 1..60

FT /*tag= b

FT mat_peptide 61..396

FT /*tag= c

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR P-PSDB; R70189.

DR WPI; 95-123387/16.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Fig.1; 97pp; English.

CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only

CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy

CC chains were cloned into pGEM7f+ and transformed into E. coli

CC DH5-alpha. The clones were sequenced (Q83490-91), and used for

CC antibody engineering.

SQ Sequence 396 BP; 99 A; 103 C; 103 G; 91 T;

Query Match 100.0%; Score 27; DB 14; Length 396;

Best Local Similarity 100.0%; Pred. No. 1.39e-06;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 337 cagcaagaatgagatcctccgacg 363

|||||

Qy 1 CAGCAAGTAATGAGATCCTCCGACG 27

Mar 19 08:18

US-08-612-929-19.mg

4

RESULT 3

ID Q83511 standard; DNA; 51 BP.

AC Q83511;

DT 20-SEP-1995 (first entry)

DE IL-4 CDR3 gene fragment.

KW Humanized antibody; antibody engineering; monoclonal antibody;

KW Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;

KW complementarity determining region; ss.

OS Synthetic.

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Example 3; Page 28; 97pp; English.

CC A humanized antibody was designed to contain mouse CDRs (from
CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A

CC synthetic heavy chain was made using the oligonucleotides given

CC in Q83498-502 and amplified by PCR using the primers given in

CC Q83503-04. The construct was ligated into vector pCD, along

CC with a signal sequence (Q83494) and an IgG1 human constant

CC region. The CDR gene regions of a pre-existing light chain

CC framework were replaced with synthetic IL-4 CDR genes constructed

CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),

CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into

CC the vector. The anti-IL4 engineered antibody was expressed in

CC COS and CHO cells.

SQ Sequence 51 BP; 14 A; 11 C; 16 G; 10 T;

Query Match 92.6%; Score 25; DB 14; Length 51;

Best Local Similarity 100.0%; Pred. No. 2.52e-05;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 cagcaagaatgagatcctccgca 35

|||||

Qy 1 CAGCAAGTAATGAGATCCTCCGA 25

RESULT 4

ID Q83512 standard; DNA; 53 BP.

AC Q83512;

DT 20-SEP-1995 (first entry)

DE IL-4 CDR3 gene fragment.

KW Humanized antibody; antibody engineering; monoclonal antibody;

KW Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;

KW complementarity determining region; ss.

OS Synthetic.

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI; 95-123387/16.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

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PT from high affinity mabs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Example 3; Page 28; 97pp; English.
CC A humanized antibody was designed to contain mouse CDRs (from
CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A
CC synthetic heavy chain was made using the oligonucleotides given
CC in Q83498-502 and amplified by PCR using the primers given in
CC Q83503-04. The construct was ligated into vector pCD, along
CC with a signal sequence (Q83494) and an IgG1 human constant
CC region. The CDR gene regions of a pre-existing light chain
CC framework were replaced with synthetic IL-4 CDR genes constructed
CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),
CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into
CC the vector. The anti-IL4 engineered antibody was expressed in
CC COS and CHO cells.
SQ Sequence 53 BP; 9 A; 17 C; 12 G; 15 T;

Query Match 92.6%; Score 25; DB 14; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.52e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 tcggagatctcattactttgctg 45
|||||
Cp 25 TCGGAGATCTCATTACTTTGCTG 1

RESULT 5
ID Q55014 standard; DNA; 99 BP.
AC Q55014;
DT 06-JUL-1994 (first entry)
DE Humanised Ab 60.3 VL oligonucleotide.
KW Monoclonal antibody; Mab; heavy chain; light chain;
KW constant region; variable region; amplification; primer;
KW polymerase chain reaction; PCR; chimera; Ig;
KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.
OS Synthetic.
PN EP-578515-A.
PD 12-JAN-1994.
PF 24-MAY-1993; 401328.
PR 26-MAY-1992; US-888233.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PI Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;
DR WPI; 94-010334/02.
PT Humanised monoclonal antibodies prepn. - using comparative model
PT building, by computer database searching
PS Disclosure; Fig 3; 68pp; English.
CC A humanised monoclonal antibody corresponding to the murine anti-CD18
CC antibody 60.3 was prepared. The variable (V) region sequences from
CC both the heavy (H) and light (L) chains were determined from cDNA
CC (amplified by PCR), and spliced onto human constant (C) regions,
CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected
CC by ELISA), and examined in binding assays. The results from
CC competition and inhibition assays showed that the chimeric Ab was
CC as effective as the murine 60.3 Mab. The deduced murine VH and VL
CC protein sequences were compared to the protein sequence data base,
CC and two human Ig protein sequences were selected to be used as
CC templates. A murine 60.3 Fv was modeled according to the deduced
CC VH and VL protein sequences. Based on the 60.3 Fv model and the two
CC human template sequences selected from the protein data base, a
CC humanised Fv was modeled. Construction of the humanised 60.3 was
CC done by piecing 5 pairs of complementary oligonucleotides together
CC (spanning the entire V region) to form the VH and VL. These were
CC expressed in Aq8.653 cells and binding assays were done. FACS analyses
CC indicated that the humanised Ab recognised cells expressing CD18.
CC About a dozen of the humanised 60.3 Ab master wells were transferred
CC and assayed for Ig.

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CC to form humanised Ab (IgG1, kappa). The humanised proteins were again
CC expressed in Aq8.653 cells and binding assays were done. FACS analyses
CC indicated that the humanised Ab recognised cells expressing CD18.
CC About a dozen of the humanised 60.3 Ab master wells were transferred
CC and assayed for Ig.
SQ Sequence 99 BP; 26 A; 28 C; 19 G; 26 T;

Query Match 92.6%; Score 25; DB 9; Length 99;
Best Local Similarity 96.3%; Pred. No. 2.52e-05;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 64 cgtccgagatctcattactttgctg 90
|||||
Cp 27 CGTCGAGATCTCATTACTTTGCTG 1

RESULT 6
ID Q55002 standard; DNA; 334 BP.
AC Q55002;
DT 06-JUL-1994 (first entry)
DE Murine anti-CD18 Ab 60.3 light chain.
KW Monoclonal antibody; Mab; heavy chain; light chain;
KW constant region; variable region; amplification; primer;
KW polymerase chain reaction; PCR; chimera; Ig;
KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.
OS Mus sp.
PN EP-578515-A.
PD 12-JAN-1994.
PF 24-MAY-1993; 401328.
PR 26-MAY-1992; US-888233.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PI Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;
DR WPI; 94-010334/02.
DR P-PSDB; R47494.
PT Humanised monoclonal antibodies prepn. - using comparative model
PT building, by computer database searching
PS Disclosure; Page 21; 68pp; English.
CC A humanised monoclonal antibody corresponding to the murine anti-CD18
CC antibody 60.3 was prepared. The variable (V) region sequences from
CC both the heavy (H) and light (L) chains were determined from cDNA
CC (amplified by PCR), and spliced onto human constant (C) regions,
CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected
CC by ELISA), and examined in binding assays. The results from
CC competition and inhibition assays showed that the chimeric Ab was
CC as effective as the murine 60.3 Mab. The deduced murine VH and VL
CC protein sequences were compared to the protein sequence data base,
CC and two human Ig protein sequences were selected to be used as
CC templates. A murine 60.3 Fv was modeled according to the deduced
CC VH and VL protein sequences. Based on the 60.3 Fv model and the two
CC human template sequences selected from the protein data base, a
CC humanised Fv was modeled. Construction of the humanised 60.3 was
CC done by piecing 5 pairs of complementary oligonucleotides together
CC (spanning the entire V region) to form the VH and VL. These were
CC then attached onto vectors containing genes for appropriate C regions
CC to form humanised Ab (IgG1, kappa). The humanised proteins were again
CC expressed in Aq8.653 cells and binding assays were done. FACS analyses
CC indicated that the humanised Ab recognised cells expressing CD18.
CC About a dozen of the humanised 60.3 Ab master wells were transferred
CC and assayed for Ig.
SQ Sequence 334 BP; 88 A; 85 C; 81 G; 80 T;

Query Match 92.6%; Score 25; DB 9; Length 334;
Best Local Similarity 96.3%; Pred. No. 2.52e-05;

Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaagaatgagatcctcgagc 303
 |||||
 QY 1 CAGCAAGTAATGAGGATCTCCGAGC 27

RESULT 7

ID Q55000 standard; DNA; 334 BP.
 AC Q55000;
 DT 06-JUL-1994 (first entry)
 DE Humanised anti-CD18 Ab 60.3 light chain.
 KW Monoclonal antibody; Mab; heavy chain; light chain;
 KW constant region; variable region; amplification; primer;
 KW polymerase chain reaction; PCR; chimera; Ig;
 OS Immunoglobulin; humanised antibody; leucocyte; integrin; ss.
 OS Chimeric; Homo sapiens.
 PN EP-578515-A.
 PD 12-JAN-1994.
 PF 24-MAY-1993; 401328.
 PR 26-MAY-1992; US-888233.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;
 DR WPI; 94-010334/02.
 DR P-PSDB; R47492.
 PT Humanised monoclonal antibodies prepn. - using comparative model
 PT building, by computer database searching
 PS Disclosure; Page 18-19; 68pp; English.
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18
 CC antibody 60.3 was prepared. The variable (V) region sequences from
 CC both the heavy (H) and light (L) chains were determined from cDNA
 CC (amplified by PCR), and spliced onto human constant (C) regions,
 CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
 CC expressed in tissue culture (A9.653 mouse myeloma cells, detected
 CC by ELISA), and examined in binding assays. The results from
 CC competition and inhibition assays showed that the chimeric Ab was
 CC as effective as the murine 60.3 Mab. The deduced murine VH and VL
 CC protein sequences were compared to the protein sequence data base,
 CC and two human Ig protein sequences were selected to be used as
 CC templates. A murine 60.3 Fv was modeled according to the deduced
 CC VH and VL protein sequences. Based on the 60.3 Fv model and the two
 CC human template sequences selected from the protein data base, a
 CC humanised Fv was modeled. Construction of the humanised 60.3 was
 CC done by piecing 5 pairs of complementary oligonucleotides together
 CC (spanning the entire V region) to form the VH and VL. These were
 CC then attached onto vectors containing genes for appropriate C regions
 CC to form humanised Ab (IgG1, kappa). The humanised proteins were again
 CC expressed in A9.653 cells and binding assays were done. FACS analyses
 CC indicated that the humanised Ab recognised cells expressing CD18.
 CC About a dozen of the humanised 60.3 Ab master wells were transferred
 CC and assayed for Ig.
 SQ Sequence 334 BP; 90 A; 79 C; 80 G; 85 T;

Query Match 92.6%; Score 25; DB 9; Length 334;
 Best Local Similarity 96.3%; Pred. No. 2.52e-05;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaagaatgagatcctcgagc 303
 |||||
 QY 1 CAGCAAGTAATGAGGATCTCCGAGC 27

RESULT 8

Kaluza 8, Riethmüller G, Scheuer W, Weidle U;

ID Q30757 standard; cDNA; 393 BP.
 AC Q30757;
 DT 30-MAR-1993 (first entry)
 DE p64-k4.
 KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
 KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
 KW plasmid; p64-k4; p64-h2; ss.
 OS Synthetic.

FH Key Location/Qualifiers
 FT sig_peptide 1..60
 FT /*tag= a
 FT mat_peptide 61..393
 FT /*tag= b
 PN W09219759-A.
 PD 12-NOV-1992. J00544.
 PF 24-APR-1992; J00544.
 PR 25-APR-1991; JP-095476.
 PR 19-FEB-1992; JP-032084.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
 DR WPI; 92-398882/48.
 DR P-PSDB; R29008.
 PT Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 PS Disclosure; Page 124-125; 207pp; Japanese.
 CC The sequences given in Q30757-58 were used in example to illustrate
 CC the production of a human antibody which recognises human
 CC interleukin-6 receptor (IL-6R). The antibody comprises light (L)
 CC chain and heavy (H) chain variable regions which were derived from a
 CC mouse monoclonal antibody produced from the hybridoma AUK64-7 which
 CC contained the plasmids p64-k4 and p64-h2.
 SQ Sequence 393 BP; 93 A; 101 C; 100 G; 99 T;

Query Match 92.6%; Score 25; DB 5; Length 393;
 Best Local Similarity 96.3%; Pred. No. 2.52e-05;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 337 cagcaagaatgagatcctcgagc 363
 |||||
 QY 1 CAGCAAGTAATGAGGATCTCCGAGC 27

RESULT 9

ID Q36609 standard; DNA; 393 BP.
 AC Q36609;
 DT 02-JUN-1993 (first entry)
 DE Anti-CD4 antibody MT 3.10 light chain variable region.
 KW immunosuppression; tissue transplantation; graft; L chain; V region;
 KW T-helper cell inhibition; transplant rejection; Mab;
 KW interleukin-2 receptor; ss.

FH Key Location/Qualifiers
 FT sig_peptide 1..60
 FT /*tag= a
 FT mat_peptide 61..393
 FT /*tag= b
 FT /note= "JL region begins at position 361"
 PN DE143214-A.

PD 28-JAN-1993.
 PF 30-DEC-1991; 143214.
 PR 25-JUL-1991; DE-124759.
 PR 30-DEC-1991; DE-143214.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

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DR WP1; 93-037582/05.
DR P-PSDB; R32123.
PT Synergistic antibody compsn. for use as immunosuppressant -
PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
PT alpha- or anti-IL2R beta antibodies
PS Claim 5; Page 11; 18pp; German.
CC This sequence encodes the light chain variable region of a preferred
CC anti-CD4 monoclonal antibody for use in the claimed synergistic
CC composition. Mab MT 3.10 is deposited as clone 3.101/8B10 (ECACC
CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R
CC alpha or beta antibody. Individually the antibodies are strongly
CC inhibiting and when used together their immunosuppressive properties
CC are improved; they synergistically inhibit T-helper cell
CC proliferation to effectively inhibit transplant rejection at low
CC doses without significantly reducing the general immune response.
CC See Q36607-Q36616.
SQ Sequence 393 BP; 100 A; 105 C; 98 G; 90 T;

Query Match 92.6%; Score 25; DB 6; Length 393;
Best Local Similarity 96.3%; Pred. No. 2.52e-05;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 337 cagcaagtagtgaggtctccgacg 363
|||||
QY 1 CAGCAAGTAGTGAGGTCTCCGACG 27

RESULT 10

ID Q73986 standard; cDNA; 393 BP.
AC Q73986;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW Mab; interleukin-4; IL-4; allergy; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..393
FT /*tag= a
FT sig_peptide 1..60
FT /*tag= b
FT mat_peptide 61..393
FT /*tag= c
PN MO9507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WP1; 95-123387/16.
DR P-PSDB; R75355.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.5; 97pp; English.
CC A humanized antibody light chain variable region and signal
CC sequence is given in R75355. The signal sequence is also
CC provided in R70194. The sequences of the first 2 CDRs
CC are identical to mouse anti-human IL-4 Mab 3B9 light chain
CC CDRs (given in R70195-96), but the third (R70201) differs
CC by a single amino acid from the native mouse CDR (R70197).
SQ Sequence 393 BP; 97 A; 96 C; 108 G; 92 T;

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Query Match 92.6%; Score 25; DB 14; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.52e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 334 cagcaagtagtgaggtctccgacg 358
|||||
QY 1 CAGCAAGTAGTGAGGTCTCCGA 25

RESULT 11

ID Q12684 standard; DNA; 336 BP.
AC Q12684;
DT 01-OCT-1991 (first entry)
DE Murine 1B4 light chain-2 variable region.
KW Monoclonal antibody; complementarity determining region; CDR;
KW integrin; hybridoma 1B4; protein REI; Gal/REI; Ig; ss.
PN EP-438312-A.
PN EP-440351-A.
PD 24-JUL-1991.
PF 17-JAN-1991; 300367.
PR 19-JAN-1990; US-467692.
PR 20-DEC-1990; US-627421.
PA (MERI) MERCK & CO INC.
PI Law MF, Mark GE, Schmidt JA, Singer II;
DR WP1; 91-216985/30.
DR P-PSDB; R13089.
PT New recombinant immunoglobulin(s) reactive with leukocyte CD18
PT antigen - comprise human heavy chain framework and murine
PT complementarity regions useful in treatment of inflammation
PS Disclosure; Fig 25; 77pp; English.
CC A recombinant human Ig comprises a human heavy chain framework
CC and murine CDRs (with the heavy chain framework mutated at sites
CC near the CDRs), a human light chain framework and murine CDRs.
CC It has a mean IC50 nearly equal to that of the murine monoclonal
CC antibody from which the CDRs were derived. It is designated
CC mutated Gal/REI. The human Ig is capable of binding to a human
CC CD18 integrin.
CC The murine CDRs are obtd. from murine hybridoma 1B4
CC (ATCC HB 10164). The light chain framework is derived from
CC human myeloma protein REI (EP-239400).
CC See also Q12682-84 and EP-438310.
SQ Sequence 336 BP; 80 A; 87 C; 85 G; 84 T;

Query Match 85.2%; Score 23; DB 2; Length 336;
Best Local Similarity 92.6%; Pred. No. 4.32e-04;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 277 cagcaagtagtgaggtctccgacg 303
|||||
QY 1 CAGCAAGTAGTGAGGTCTCCGACG 27

RESULT 12

ID Q80292 standard; DNA; 645 BP.
AC Q80292;
DT 08-JUL-1995 (first entry)
DE Monoclonal antibody 28C5 light chain.
KW CD14 receptor; monoclonal antibody; 28C5; hybridoma;
KW antiseptic; therapeutic; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT mat_peptide 1..645
FT /*tag= a
PN W09428025-A.

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FT /*tag= b 538..882
FT exon
PN EP-365209-A.
PD 25-APR-1990.
PF 11-OCT-1989; 010415.
PR 17-OCT-1988; US-260558.
PA (BECT) Becton Dickinson Co.
PI Hinton R, OI VT;
DR MPI; 90-126329/17.
DR P-PSDB; R04132.
PT New chimeric variants of murine antibody anti-leucine -
PT contg. human antibody regions, and DNA encoding sequences.
PS Claim 1; Fig 2; 12pp; English.
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
CC used to form chimeric mouse-variable, human-constant region Abs
CC suggested as being useful as a vaccine to HIV.
SQ Sequence 900 BP; 261 A; 206 C; 187 G; 246 T;

Query Match 81.5%; Score 22; DB 1; Length 900;
Best Local Similarity 92.3%; Pred. No. 1.75e-03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 825 caacaaagtatgaggtcctccgac 850
Qy 1 CAGCAAGTAATCAGGATCCTCCGAC 26

Search completed: Wed Mar 19 08:20:40 1997
Job time : 14 secs.

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3

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 195)
AUTHORS Goshorn, S.C., Betzel, E. and Jemerson, R.
TITLE Common structural features among monoclonal antibodies binding the
same antigenic region of cytochrome c
JOURNAL J. Biol. Chem. 266 (4), 2134-2142 (1991)
MEDLINE 91115823

FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/clone="2B5.F8"
/strain="BALB/c"
/sub_species="domesticus"
/cell_line="2B5"
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/sequenced_mol="cDNA to mRNA"
/tissue_type="hybridoma"

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/organism="Mus musculus"
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/strain="BALB/c"
/sub_species="domesticus"
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/db_xref="PID:g196407"
/translation="PKLLIYAASNLESGIPARFSGSGCTFTTNIHPVEEDGATY
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/codon_start=1
/product="Ig kappa chain"
/db_xref="PID:g196407"
/translation="PKLLIYAASNLESGIPARFSGSGCTFTTNIHPVEEDGATY
CQQSNEDPRTFGGGKLEIKR"

misc_feature
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/note="CDR2"
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/gene="IgM"
/map="chromosome 6"
/note="CDR3"
156..195
/gene="IgM"
/map="chromosome 6"
/note="J1"

J_segment
52 a 50 c 51 g 42 t
Chromosome 6.

Query Match 92.6%; Score 25; DB 66; Length 195;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 136 cagcaagtaatgagatcctcgagc 162
|||||
Qy 1 CAGCAAGTAATGAGATCCTCGGACG 27

RESULT 2
LOCUS MMU18577 228 bp mRNA ROD 21-JUN-1995
DEFINITION Mus musculus immunoglobulin kappa light chain, variable region
mRNA, clone BALB/c-51, partial cds.
ACCESSION U18577
NID g619707
KEYWORDS mouse.
SOURCE Mus musculus
ORGANISM Mus musculus

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Eukaryota; mitochondrial eukaryotes; eukaryote crown group;
Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrastoda; Amniota; Mammalia; Theria;
Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Mus.
REFERENCE 1 (bases 1 to 228)
AUTHORS Roark, J.H., Kuntz, C.L., Nguyen, K.A., Caton, A.J. and Erikson, J.
TITLE Breakdown of B cell tolerance in a mouse model of systemic lupus
erythematosus
J. Exp. Med. 181 (3), 1157-1167 (1995)
MEDLINE 95173583
REFERENCE 2 (bases 1 to 228)
AUTHORS Roark, J.H.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Jessica H. Roark, Wistar Institute, 3601
Spruce St., Philadelphia, PA 19104, USA

FEATURES
Location/Qualifiers
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/strain="BALB/c"
/organism="Mus musculus"
/cell_type="splenic B cell hybridoma"
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region"

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BASE COUNT 61 a 57 c 57 g 53 t
ORIGIN

Query Match 92.6%; Score 25; DB 65; Length 228;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 187 cagcaagtaatgagatcctcctacg 213
|||||
Qy 1 CAGCAAGTAATGAGATCCTCGGACG 27

RESULT 3
LOCUS MUS18KCM1 273 bp mRNA ROD 15-MAR-1989
DEFINITION Mouse Ig rearranged kappa-chain V-region mRNA from hybridoma
H37-63, partial cds.
ACCESSION M21525
NID g196987
KEYWORDS C-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa; rearranged gene.
SOURCE Mouse (strain BALB/c) hybridoma H37-63, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 273)
AUTHORS Clarke, S.H., Huppi, K., Ruzinsky, D., Staudt, L., Gerhard, W. and
Weigert, M.
TITLE Inter- and intracolon diversity in the antibody response to
influenza hemagglutinin
J. Exp. Med. 161, 687-704 (1985)
MEDLINE 85159415
FEATURES Location/Qualifiers
source
1..273
/organism="Mus musculus"

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CDS

<1..>273

/note="Ig kappa-chain VJ-regions"

/codon_start=1

/db_xref="PID:q196988"

/translation="SCRASESVDYXGSLMHVYQKQGPQPKLLISRASNLSEGIPAR
FSGVGRDFTLTINVEADVDATYYCOQSNEDPPTFGAGTKLEKR"

BASE COUNT 69 a 72 c 66 g 65 t 1 others

ORIGIN Chromosome 6.

Query Match 92.6%; Score 25; DB 67; Length 273;

Best Local Similarity 96.3%; Pred. No. 5.58e-07;

Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 214 cagcaagaatgagatctccacg 240

Qy 1 CAGCAAGTAATGAGATCTCCGACG 27

RESULT 4

LOCUS MMIGLA 307 bp RNA ROD 05-AUG-1994

DEFINITION Mus musculus (DBA/1) mRNA for immunoglobulin gamma light chain

ACCESSION 226771

NID g436888

KEYWORDS immunoglobulin; immunoglobulin gamma; light chain joining region;

SOURCE house mouse.

ORGANISM

Eukaryota; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 307)

AUTHORS Mo,J.A., Scheynius,A., Nilsson,S. and Holmdahl,R.

TITLE Germline encoded IgG antibodies bind mouse cartilage in vivo

JOURNAL epitope- and idiotype specific binding and inhibition

REFERENCE 2 (bases 1 to 307)

AUTHORS Mo,J.A.

TITLE Direct Submission

JOURNAL Submitted (30-SEP-1993) to the EMBL/GenBank/DBSJ databases. John A

Mo, Department of Medical and Physiological, Department of, Medical

and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden

REFERENCE 3 (bases 1 to 307)

AUTHORS Mo,J.A., Scheynius,A., Nilsson,S. and Holmdahl,R.

TITLE Germline-encoded IgG antibodies bind mouse cartilage in vivo:

epitope- and idiotype-specific binding and inhibition

JOURNAL Scand. J. Immunol. 39 (2), 122-130 (1994)

MEDLINE 9412659

FEATURES Location/Qualifiers

source 1..307

/organism="Mus musculus"

/strain="DBA/1"

/dev_stage="Adult"

/tissue_type="Lymph node"

/cell_type="B cell hybridoma"

/cell_line="CIIF4 hybridoma"

/chromosome="6"

V_segment 1..272

/note="Light chain variable region"

J_segment 273..307

/note="Joining region JK2"

BASE COUNT 81 a 77 c 77 g 72 t

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ORIGIN

Query Match 92.6%; Score 25; DB 64; Length 307;

Best Local Similarity 96.3%; Pred. No. 5.58e-07;

Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 250 cagcaagaatgagatctccacg 276

Qy 1 CAGCAAGTAATGAGATCTCCGACG 27

RESULT 5

LOCUS MUSICKCK 336 bp mRNA ROD 15-MAR-1989

DEFINITION Mouse Ig rearranged kappa-chain V-region mRNA from hybridoma

ACCESSION M21524

NID g196985

KEYWORDS C-region; V-region; immunoglobulin light chain;

immunoglobulin-kappa; rearranged gene.

SOURCE Mouse (strain BALB/c) hybridoma H37-77, cDNA to mRNA.

ORGANISM

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 336)

AUTHORS Clarke,S.H., Huppi,K., Ruzinsky,D., Staudt,L., Gerhard,W. and

Weigert,M.

TITLE Inter- and intracolon diversity in the antibody response to

JOURNAL influenza hemagglutinin

MEDLINE 85159415

FEATURES Location/Qualifiers

source 1..336

/organism="Mus musculus"

<1..>336

/note="Ig kappa-chain VJ-regions"

/codon_start=1

/db_xref="PID:q196986"

/translation="DIELTQSPASLAVSLQPRATISCRASESVYSGKSPMHVYQKRP

GQPKLLIYRASNLSEGIPAREFGSGSRDFTLTINVEADVDATYYCOQSNEDPPTF

CAGTKLEKR"

BASE COUNT 84 a 88 c 84 g 80 t

ORIGIN Chromosome 6.

Query Match 92.6%; Score 25; DB 67; Length 336;

Best Local Similarity 96.3%; Pred. No. 5.58e-07;

Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaagaatgagatctccacg 303

Qy 1 CAGCAAGTAATGAGATCTCCGACG 27

RESULT 6

LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992

DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310).

ACCESSION X65091

NID g52288

KEYWORDS Ig light chain; VJ domain.

SOURCE house mouse.

ORGANISM

Eukaryota; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

Eukaryota; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

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REFERENCE
AUTHORS      1 (bases 1 to 336)
TITLE        Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
JOURNAL      Weissenhorn, Institut fuer Immunologie, Goethestraasse 31, W-8000
              Muenchen 2, FRG

REFERENCE
AUTHORS      2 (bases 1 to 336)
TITLE        Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
JOURNAL      Weissenhorn, Institut fuer Immunologie, Goethestraasse 31, W-8000
              Muenchen 2, FRG

FEATURES
  source      1..336
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              /strain="Balb/c"
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              /cell_line="Hybridoma M-T310"
              <1..>336
              /codon_start=1
              /product="alpha CD4 mAb immunoglobulin light chain VJ
              region"
              /db_xref="PID:g52289"
              /translation="DIVLTQSPASLPMSIGQRAITISCKASQSLDYDGDSYMNWYQKRP
              GQPKLLIYAASNLSESGIPARFSGSGCTDFTLNHPVEEDAATYYCQSSSEDPPTF
              GGGTKLEIKR"

BASE COUNT   89 a   90 c   81 g   76 t
ORIGIN
Query Match   92.6%; Score 25; DB 64; Length 336;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaaatagtgagatcctccgacg 303
|||||
QY 1 CAGCAAGTAATGAGGATCCTCCGACG 27
|||||

LOCUS          MMIGLC404      336 bp      RNA      ROD      07-MAY-1992
DEFINITION     M.musculus mRNA for IG light chain VJ region (M-T404).
ACCESSION      X65092
NID            g52292
KEYWORDS       Ig light chain; VJ domain.
SOURCE          house mouse.
ORGANISM       Mus musculus
               Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
               Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
               Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
               Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
               Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE
AUTHORS        1 (bases 1 to 336)
TITLE          Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
JOURNAL        Weissenhorn, Institut fuer Immunologie, Goethestraasse 31, W-8000
                Muenchen 2, FRG

REFERENCE
AUTHORS        2 (bases 1 to 336)
TITLE          Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
JOURNAL        Weissenhorn, Institut fuer Immunologie, Goethestraasse 31, W-8000
                Muenchen 2, FRG

FEATURES
  source      1..336
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              /strain="Balb/c"
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              /cell_line="Hybridoma M-T310"
              <1..>336
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              /product="alpha CD4 mAb immunoglobulin light chain VJ
              region"
              /db_xref="PID:g52289"
              /translation="DIVLTQSPASLPMSIGQRAITISCKASQSLDYDGDSYMNWYQKRP
              GQPKLLIYAASNLSESGIPARFSGSGCTDFTLNHPVEEDAATYYCQSSSEDPPTF
              GGGTKLEIKR"

BASE COUNT   89 a   90 c   81 g   76 t
ORIGIN
Query Match   92.6%; Score 25; DB 64; Length 336;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaaatagtgagatcctccgacg 303
|||||
QY 1 CAGCAAGTAATGAGGATCCTCCGACG 27
|||||

LOCUS          MMIGLC404      336 bp      RNA      ROD      07-MAY-1992
DEFINITION     M.musculus mRNA for IG light chain VJ region (M-T404).
ACCESSION      X65092
NID            g52292
KEYWORDS       Ig light chain; VJ domain.
SOURCE          house mouse.
ORGANISM       Mus musculus
               Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
               Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
               Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
               Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
               Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE
AUTHORS        1 (bases 1 to 336)
TITLE          Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
JOURNAL        Weissenhorn, Institut fuer Immunologie, Goethestraasse 31, W-8000
                Muenchen 2, FRG

REFERENCE
AUTHORS        2 (bases 1 to 336)
TITLE          Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
JOURNAL        Weissenhorn, Institut fuer Immunologie, Goethestraasse 31, W-8000
                Muenchen 2, FRG

FEATURES
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              /strain="Balb/c"
              /cell_type="B-cell"
              /cell_line="Hybridoma M-T310"
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              /codon_start=1
              /product="alpha CD4 mAb immunoglobulin light chain VJ
              region"
              /db_xref="PID:g52289"
              /translation="DIVLTQSPASLPMSIGQRAITISCKASQSLDYDGDSYMNWYQKRP
              GQPKLLIYAASNLSESGIPARFSGSGCTDFTLNHPVEEDAATYYCQSSSEDPPTF
              GGGTKLEIKR"

BASE COUNT   89 a   90 c   81 g   76 t
ORIGIN
Query Match   92.6%; Score 25; DB 64; Length 336;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaaatagtgagatcctccgacg 303
|||||
QY 1 CAGCAAGTAATGAGGATCCTCCGACG 27
|||||

LOCUS          MMIGLC404      336 bp      RNA      ROD      07-MAY-1992
DEFINITION     M.musculus mRNA for IG light chain VJ region (M-T404).
ACCESSION      X65092
NID            g52292
KEYWORDS       Ig light chain; VJ domain.
SOURCE          house mouse.
ORGANISM       Mus musculus
               Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
               Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
               Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
               Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
               Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE
AUTHORS        1 (bases 1 to 336)
TITLE          Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
JOURNAL        Weissenhorn, Institut fuer Immunologie, Goethestraasse 31, W-8000
                Muenchen 2, FRG

REFERENCE
AUTHORS        2 (bases 1 to 336)
TITLE          Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
JOURNAL        Weissenhorn, Institut fuer Immunologie, Goethestraasse 31, W-8000
                Muenchen 2, FRG

FEATURES
  source      1..336
              /organism="Mus sp."
              /notes="mice"
              /partial
              /genes="Ig VL"
              /note="Method: conceptual translation supplied by author.
              This sequence comes from Fig. 1c."
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              /product="anti-CD4 mAb M-T310 variable region light chain"
              /db_xref="PID:g260766"
              /translation="METDTLLWLLWPGSTGDIVLTQSPASLPMSIGQRAITISCK
              ASQSLDYDGDSYMNWYQKRPQPKLLIYAASNLSESGIPARFSGSGCTDFTLNHPV
              EEEDAATYYCQSSSEDPPTFGGGTKLEIK"

BASE COUNT   100 a  105 c   98 g   90 t
ORIGIN
Query Match   92.6%; Score 25; DB 70; Length 393;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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CDS
/cell_type="B-cell"
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region"
/db_xref="PID:g52293"
/translation="DIVLTQSPASLPMSIGQRAITISCKASQSLDYDGDSYMNWYQKRP
GQPKLLIYAASNLSESGIPARFSGSGCTDFTLNHPVEEDAATYYCQSSSEDPPTF
GGGTKLEIKR"

BASE COUNT   89 a   90 c   81 g   76 t
ORIGIN
Query Match   92.6%; Score 25; DB 64; Length 336;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaaatagtgagatcctccgacg 303
|||||
QY 1 CAGCAAGTAATGAGGATCCTCCGACG 27
|||||

LOCUS          S50265      393 bp      mRNA      ROD      02-APR-1993
DEFINITION     Ig VI-anti-CD4 mAb M-T310 variable region light chain [J1, chimeric
antibody] [mice, hybridoma cells, mRNA Partial, 393 nt].
ACCESSION      S50265
NID            g260765
KEYWORDS       mice hybridoma cells.
SOURCE          Mus sp.
ORGANISM       Unclassified.

REFERENCE
AUTHORS        1 (bases 1 to 393)
              Weissenhorn, W., Scheuer, W., Kaluza, B., Schwirzke, M., Reiter, C.,
              Flieger, D., Lenz, H., Weiss, E.H., Rieber, E.P., Riethmuller, G. et.al.
              Combinatorial functions of two chimeric antibodies directed to
              human CD4 and one directed to the alpha-chain of the human
              interleukin-2 receptor
              Gene 121 (2), 271-278 (1992)
              93077041
REMARK         GenBank staff at the National Library of Medicine created this
              entry [NCBI gibbsq 119503] from the original journal article.
              This sequence comes from Fig. 1c.

FEATURES
  source      Location/Qualifiers
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              /notes="mice"
              1..393
              /partial
              /genes="Ig VL"
              /note="Method: conceptual translation supplied by author.
              This sequence comes from Fig. 1c."
              /codon_start=1
              /product="anti-CD4 mAb M-T310 variable region light chain"
              /db_xref="PID:g260766"
              /translation="METDTLLWLLWPGSTGDIVLTQSPASLPMSIGQRAITISCK
              ASQSLDYDGDSYMNWYQKRPQPKLLIYAASNLSESGIPARFSGSGCTDFTLNHPV
              EEEDAATYYCQSSSEDPPTFGGGTKLEIK"

BASE COUNT   100 a  105 c   98 g   90 t
ORIGIN
Query Match   92.6%; Score 25; DB 70; Length 393;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 337 cagcaagtagtgaggtactctcgagc 363
|||||
Qy 1 CAGCAAGTAATGAGGATCTCCGAGC 27

RESULT 9
LOCUS MMU01973 394 bp mRNA ROD 24-SEP-1993
DEFINITION Mus musculus Balb/c anti-CD18 Ig light chain variable region mRNA,
partial cds.
ACCESSION U01973
NID g403071
KEYWORDS .
SOURCE mouse.
ORGANISM Mus musculus
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Rodentia; Myomorpha; Muridae; Mus.
REFERENCE 1 (bases 1 to 394)
AUTHORS Heiao,K., Bajorath,J. and Harris,L.J.
TITLE Humanization of 60.3, an anti-CD18 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 394)
AUTHORS Harris,L.J.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1993) Linda J. Harris, Molecular Immunology,
Bristol-Myers Squibb, Pharmaceutical Research Institute, 3005 First
Avenue, Seattle, WA 98121 USA
FEATURES
source
location/Qualifiers
1..394
/strain="Balb/c"
/organism="Mus musculus"
/cell_line="60.3 hybridoma"
/cell_type="hybridoma (B-cell)"
/tissue_type="spleen"
/dev_stage="adult"
1..60
/notes="nucleotides 1-29 derived from PCR primer and may
not reflect mRNA sequence"
1..49
/number=1
/product="partial signal peptide"
1..394
/partial
/notes="V gene is identical to VK21c germline gene; uses
Jk1"
/codon_start=1
/product="Ig variable region, light chain"
/db_xref="PID:g403072"
/translation="METDTLLVLLVPGSTGDIVLTQSPASIVSLQQRATISCR
ASESVDSYGNFPMHWYQKPKQLLYRASNLGSGIPARSGSGSRDTFTLTNPV
EADDVATYYCCQSNEDPRTFGGTKLEIK"
50..394
/number=2
/product="carboxyl end of signal peptide and mature heavy
chain"
61..135
/standard_name="FR1"
61..393
/product="Ig variable region, light chain"
136..168
/standard_name="CDR1"
169..219
/standard_name="FR2"
220..228
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misc_feature 229..339 /standard_name="CDR2"
misc_feature 340..357 /standard_name="FR3"
misc_feature 358..393 /standard_name="CDR3"
BASE COUNT 99 a 100 c 98 g 97 t
ORIGIN
Query Match 92.6%; Score 25; DB 64; Length 394;
Best Local Similarity 96.3%; Pred. No. 5.58e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 337 cagcaagtagtgaggtactctcgagc 363
|||||
Qy 1 CAGCAAGTAATGAGGATCTCCGAGC 27

RESULT 10
LOCUS MUSIGKVR3 841 bp DNA ROD 14-APR-1994
DEFINITION Mouse Ig germline kappa V-region 9.5kb-V-kappa, V-kappa-21C.
ACCESSION K02161
NID g197492
KEYWORDS C-region; V-region; germline; immunoglobulin light chain;
immunoglobulin-kappa; immunoglobulin-kappa subgroup vk-21.
SEGMENT 3 of 3
SOURCE Mouse BALB/c embryo DNA, clones KM23 and KE5e.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 841)
AUTHORS Heinrich,G., Traunecker,A. and Tonegawa,S.
TITLE Somatic mutation creates diversity in the major group of mouse
immunoglobulin kappa-light chains
JOURNAL J. Exp. Med. 159, 417-435 (1984)
MEDLINE 84113346
FEATURES
source
location/Qualifiers
1..841
/organism="Mus musculus"
<198..246
/notes="Ig kappa V-region 9.5kb-V-kappa"
/number=1
198..246
/notes="Ig kappa V-region 9.5kb-V-kappa signal peptide,
exon 1; putative"
join(198..246,486..793)
/partial
/notes="Ig kappa V-region 9.5kb-V-kappa"
/codon_start=1
/db_xref="PID:g197496"
/translation="METDTLLVLLVPGSTGDIVLTQSPASIVSLQQRATISCR
ASESVDSYGNFPMHWYQKPKQLLYRASNLGSGIPARSGSGSRDTFTLTNPV
EADDVATYYCCQSNEDP"
198..246
/notes="Ig kappa V-region 9.5kb-V-kappa signal peptide"
/codon_start=1
198..246
/notes="Ig kappa V-region 9.5kb-V-kappa, exon 1; putative"
join(198..246,486..496)
/notes="Ig kappa V-region 9.5kb-V-kappa signal peptide"
/codon_start=1
247..485
/notes="VK9.5 intron A"
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exon          486..793
              /note="Ig kappa V-region 9.5kb-V-kappa, exon 2; putative"
sig_peptide   486..496
              /note="Ig kappa V-region 9.5kb-V-kappa signal peptide"
              /codon_start=1
exon          486..794
              /note="Ig kappa V-region 9.5kb-V-kappa"
              /number=2
exon          486..496
              /note="Ig kappa V-region 9.5kb-V-kappa signal peptide,
              exon 2; putative"
              /codon_start=1
              /partial
mat_peptide   /note="Ig kappa V-region 9.5kb-V-kappa mature peptide"
              /codon_start=1
idna          795..841
              /note="V-J intervening DNA (5' end +/- 1 bp)"
misc_signal   796..823
              /note="putative recombination recognition sequence;
              putative"
BASE COUNT   218 a 196 c 191 g 236 t
ORIGIN        About 39 kb after segment 2; chromosome 6.

Query Match   88.9%; Score 24; DB 67; Length 841;
Best Local Similarity 96.2%; Pred. No. 4.14e-06;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 773 cagcaagaatgagatctctccac 798
   |||||||
Qy 1 CAGCAAGTAATGAGATCTCTCCGAC 26

RESULT 11
LOCUS      MUSIGKABK 312 bp mRNA ROD 15-SEP-1990
DEFINITION Mouse Ig kappa-chain (anti-insulin Ab 127) mRNA V region, partial
            cds.
ACCESSION  M34529
NID        g196507
KEYWORDS   V-region; immunoglobulin heavy chain; immunoglobulin-kappa;
            processed gene.
SOURCE      Mouse (strain Balb/c), cDNA to mRNA.
ORGANISM    Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1 (bases 1 to 312)
AUTHORS     Ewulonu,U.K., Nell,L.J. and Thomas,J.W.
TITLE       V-H and V-L gene usage by murine IgG antibodies that bind
            autologous insulin
JOURNAL     J. Immunol. 144, 3091-3098 (1990)
MEDLINE     90217518
FEATURES     Location/Qualifiers
              source
              1..312
              /organism="Mus musculus"
              <1..>312
              /note="Ig kappa-chain V-region"
              /codon_start=1
              /db_xref="PID:g196508"
              /translation="DIVLTQSPASLAIVLQQRATISCRASEVDSYGNSEFMHWYQKRP
              GQPKLLIYRASNLIESGIPARFSGSGRTDITINPEADDVASVYCCQSNEEPTF
              GG"
BASE COUNT   78 a 81 c 77 g 76 t
ORIGIN

Query Match   85.2%; Score 23; DB 66; Length 312;
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Best Local Similarity 92.6%; Pred. No. 2.97e-05;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 277 cagcaagaatgaggaacccaccac 303
   |||||||
Qy 1 CAGCAAGTAATGAGGATCTCTCCGAC 27

RESULT 12
LOCUS      MWVL2D4 318 bp RNA ROD 16-MAY-1995
DEFINITION M.musculus mRNA for immunoglobulin light chain variable region
            (VL2D4) .
ACCESSION  X86545
NID        g809058
KEYWORDS   immunoglobulin; immunoglobulin light chain; kappa chain;
            light chain; variable region.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1 (bases 1 to 318)
AUTHORS     Cerato,E., Birkle,S., Portoukalian,J. and Aubry,J.
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 318)
AUTHORS     Cerato,E.M.
TITLE       Direct Submission
JOURNAL     Submitted (24-APR-1995) to the EMBL/GenBank/DBSJ databases. E.M.
            Cerato, INSERM U211, Institut de Biologie, 9 qual Moncoueu, 44035
            Nantes Cedex 01, FRANCE
FEATURES     Location/Qualifiers
              source
              1..318
              /organism="Mus musculus"
              /strain="BALB/c"
              /dev_stage="adult"
              /tissue_type="spleen"
              /cell_type="B cell hybridoma"
              /cell_line="2D4 hybridoma"
              /chromosome="12"
              /rearranged
              V_region
              16..318
              /note="anti-ganglioside asialo CM2 immunoglobulin"
              /product="immunoglobulin light chain variable region VL
              2D4"
BASE COUNT   75 a 84 c 80 g 79 t
ORIGIN

Query Match   85.2%; Score 23; DB 65; Length 318;
Best Local Similarity 92.6%; Pred. No. 2.97e-05;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 262 cagcaagaatgagatctctccac 288
   |||||||
Qy 1 CAGCAAGTAATGAGGATCTCTCCGAC 27

RESULT 13
LOCUS      MDIGKVBV 333 bp RNA ROD 05-NOV-1994
DEFINITION M.domesticus Igk variable region.
ACCESSION  Z22133
NID        g297695
KEYWORDS   anti-DNA antibody; IgK gene; IgK variable region; immunoglobulin.
            western European house mouse.
SOURCE      Mus musculus domesticus
            Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
```


Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonadata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 333)

Tilman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.

Both IgM and IgG anti-DNA antibodies are the products of clonally

selective B cell stimulation in (NZB x NZW)F1 mice

J. Exp. Med. 176 (3), 761-779 (1992)

MEDLINE

92381444

2 (bases 1 to 333)

Marion,T.N.

Direct Submission

Submitted (23-MAR-1993) to the EMBL/GenBank/DBJ databases. Tony N.

Marion, Microbiology and Immunology, University of Tennessee,

Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA

Location/Qualifiers

1..333

/organism="Mus domesticus"

/strain="(NZB x NZW)F1"

/dev stage="somatic variant"

/tissue_type="spleen"

/cell_type="hybridoma"

/cell_line="202p.38"

/isolate="mouse #202"

/chromosome="6"

/sex="Female"

<1..>333

/gene="Igk"

/codon start=1

/function="kappa light chain variable region for anti-DNA

antibody; VK21 family"

/product="immunoglobulin variable region"

/db xref="PID:g297696"

/translation="DIVLTQSPASIVSLGQRATISCRASEVDNYGLSFMMWFQKRP

GQPKLIYANSGSQVPARFSGSGTDFSIHPMEEDDTAMFCQSQKEVPTTF

GGGKLEIK"

84 a 86 c 84 g 78 t 1 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 85.2%; Score 23; DB 63; Length 333;

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 277 cagcaagaaggaaggtcttcgcgacg 303

||||| ||||| ||||| ||||| |||||

QY 1 CAGCAAGTATCAGGATCTCCGACG 27

RESULT 14

LOCUS MUSL93IGKV 363 bp mRNA ROD 29-OCT-1994

DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial

cds.

ACCESSION M97879

NTID g198681

KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;

processed gene.

SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c

fusion hybridoma cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 363)

Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.

TITLE Characterization of murine monoclonal anti-CD4; epitope recognition, idiotope expression, and variable gene sequence

JOURNAL

Unpublished (1992)

FEATURES

source

1..363

/organism="Mus musculus"

/strain="BALB/c"

/sub_species="domesticus"

/sequenced_mol="cDNA to mRNA"

/tissue_type="SP20-BALB/c fusion hybridoma"

1..363

/gene="Igk"

/standard_name="L93; monoclonal antibody (CD4 antigen

specificity)"

/map="6"

BASE COUNT 94 a 97 c 89 g 83 t

ORIGIN

Query Match

Best Local Similarity 85.2%; Score 23; DB 67; Length 363;

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 277 cagcaagaatcaggatcttcgcgacg 303

||||| ||||| ||||| ||||| |||||

QY 1 CAGCAAGTATCAGGATCTCCGACG 27

RESULT 15

LOCUS MUSL34IGKV 363 bp mRNA ROD 29-OCT-1994

DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial

cds.

ACCESSION M97871

NTID g198669

KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;

processed gene.

SOURCE Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c

fusion hybridoma cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 363)

Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.

Characterization of murine monoclonal anti-CD4; epitope

recognition, idiotope expression, and variable gene sequence

Unpublished (1992)

Location/Qualifiers

1..363

/organism="Mus musculus"

/strain="BALB/c"

/sub_species="domesticus"

/sequenced_mol="cDNA to mRNA"

/tissue_type="SP20-BALB/c fusion hybridoma"

1..363

/gene="Igk"

/standard_name="L34; monoclonal antibody (CD4 antigen

specificity)"

/map="6"

BASE COUNT 92 a 95 c 90 g 86 t

ORIGIN

Query Match

Best Local Similarity 85.2%; Score 23; DB 67; Length 363;

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 277 cagcaactatgaggatcctccgacg 303
||||||| || |||||||||||||||
Qy 1 CAGCAACTATGAGGATCCTCCGACG 27

Search completed: Wed Mar 19 08:20:08 1997
Job time : 60 secs.

Query Match 78.6%; Score 44; DB 5; Length 111;
 Best Local Similarity 88.9%; Pred. No. 8.48e-01;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 93 qgsnedp 101
 |||||
 Qy 1 QQSNEPPT 9

RESULT 2
 ID KV3M MOUSE STANDARD; PRT; 111 AA.
 AC P01665;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (PC 7043).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 DR PIR; A01937; KVM543.
 DR HSP; P01679; IGGB.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12002 MW; ADC728CA CRC32;

Query Match 76.8%; Score 43; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.50e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsnedp 99
 |||||
 Qy 1 QQSNEP 7

RESULT 3
 ID KV3O MOUSE STANDARD; PRT; 111 AA.
 AC P01667;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (PC 6308).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 DR PIR; C01937; KVM508.

DR HSP; P01679; IGGB.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12071 MW; F7865271 CRC32;

Query Match 76.8%; Score 43; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.50e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsnedp 99
 |||||
 Qy 1 QQSNEP 7

RESULT 4
 ID KV3L MOUSE STANDARD; PRT; 111 AA.
 AC P01664;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (CBPC 101).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 79012520.
 RA MCKEAN D.J., BELL M., POTTER M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
 CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

DR HSP; A01936; KVM5C1.
 DR HSP; P01679; IGGB.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 11964 MW; A2AC84C7 CRC32;

Query Match 76.8%; Score 43; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.50e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsnedp 99
 |||||
 Qy 1 QQSNEP 7

RESULT 5
 ID KV3H MOUSE STANDARD; PRT; 111 AA.
 AC P01660;

Mar 18 10:10

US-08-612-929-20.rsp

5

DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (PC 3741 AND TEPC 111).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE (PC 3741).
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 RN [2]
 RP SEQUENCE (TEPC 111).
 RX MEDLINE; 79012520.
 RA MCKEAN D.J., BELL M., POTTER M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
 CC -/- THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
 DR PIR; A01934; KVM537.
 DR HSP; P01679; IGGB.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12099 MW; 76502E89 CRC32;

Query Match 76.8%; Score 43; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.50e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsndp 99
 |||||
 Qy 1 QQSNDP 7

RESULT 6
 ID KV3Q MOUSE STANDARD; PRT; 111 AA.
 AC P01669;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (PC 7769).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 79073152.
 RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 DR PIR; E01937; KVM569.
 DR HSP; P01679; IACY.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT FRAMEWORK 1.
 FT FRAMEWORK 2.
 FT FRAMEWORK 3.

Mar 18 10:10

US-08-612-929-20.rsp

6

FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 111 FRAMEWORK 4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12011 MW; 9CB705B9 CRC32;
 Query Match 76.8%; Score 43; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.50e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgsndp 99
 |||||
 Qy 1 QQSNDP 7

RESULT 7
 ID KV3F MOUSE STANDARD; PRT; 132 AA.
 AC P01658;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 321).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE OF 1-37.
 RX MEDLINE; 78235887.
 RA BURSTEIN Y., SCHECHTER I.;
 RL BIOCHEMISTRY 17:2392-2400(1978).
 RN [2]
 RP SEQUENCE OF 21-132.
 RX MEDLINE; 73140224.
 RA MCKEAN D.J., POTTER M., HOOD L.E.;
 RL BIOCHEMISTRY 12:749-759(1973).
 CC -/- THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN
 CC WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE
 CC MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.
 DR PIR; A01933; KVM532.
 DR HSP; P01679; IGGB.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 132 IG KAPPA CHAIN V-III REGION (MOPC 321).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 59 73 FRAMEWORK 2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 81 112 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 113 121 FRAMEWORK 3.
 FT DOMAIN 122 131 FRAMEWORK 4.
 FT DISULFID 43 112 BY SIMILARITY.
 FT NON TER 132 132
 SQ SEQUENCE 132 AA; 14523 MW; E572F824 CRC32;

Query Match 76.8%; Score 43; DB 5; Length 132;
 Best Local Similarity 28.6%; Pred. No. 1.50e+00;
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 113 zszbzbp 119
 :::::|
 Qy 1 QQSNDP 7

RESULT 8

ID GLHR ANTEL STANDARD; PRT; 925 AA.
AC P35409;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE PROBABLE GLYCOPROTEIN HORMONE G-PROTEIN COUPLED RECEPTOR PRECURSOR.
OS ANTHOLEURA ELEGANTISSIMA (SEA ANEMONE).
OC EUKARYOTA; METAZOA; CNIDARIA; ANTHOZOA; ZOANTHARIA; ACTINOTARIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94107299.
RA NOTHACKER H.-P., GRIMMELIKHUIJZEN C.J.P.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 197:1062-1069 (1993).
CC -/- FUNCTION: PROBABLE RECEPTOR FOR A GLYCOPROTEIN HORMONE.
CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -/- SIMILARITY: HIGHLY SIMILAR TO FSH, LSH AND TSH RECEPTORS.
CC -/- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; Z28332; G452811; -;
DR PIR; S41908; S41908.
DR PIR; JC2033; JC2033.
DR GCRDB; GCR 0876; -;
DR PROSITE; PS00237; G-PROTEIN RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL;
KW ALTERNATIVE SPLICING; REPEAT.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 925 PROBABLE GLYCOPROTEIN HORMONE G-PROTEIN COUPLED RECEPTOR.
FT DOMAIN 28 529 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 530 551 1 (POTENTIAL).
FT DOMAIN 552 561 2 (POTENTIAL).
FT TRANSMEM 562 584 2 (POTENTIAL).
FT DOMAIN 585 606 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 607 628 3 (POTENTIAL).
FT DOMAIN 629 651 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 652 673 4 (POTENTIAL).
FT DOMAIN 674 691 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 692 712 5 (POTENTIAL).
FT DOMAIN 713 739 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 740 763 6 (POTENTIAL).
FT DOMAIN 764 774 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 775 795 7 (POTENTIAL).
FT DOMAIN 796 925 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 925 925 5 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 333 349 1 (INCOMPLETE).
FT REPEAT 350 384 2.
FT REPEAT 385 419 3.
FT REPEAT 420 453 4.
FT REPEAT 454 461 5 (INCOMPLETE).
FT VARSPLIC 235 925 MISSING (IN SPLICED VARIANT).
FT CARBOHYD 61 61 POTENTIAL.
FT CARBOHYD 152 152 POTENTIAL.
FT CARBOHYD 212 212 POTENTIAL.
FT CARBOHYD 435 435 POTENTIAL.
FT CARBOHYD 495 495 POTENTIAL.
FT CARBOHYD 558 558 POTENTIAL.
SQ SEQUENCE 925 AA; 100059 MW; 168E8B81 CRC32;

Query Match 75.0%; Score 42; DB 4; Length 925;
Best Local Similarity 66.7%; Pred. No. 2.62e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 477 hqstdpdt 485

QY 1 QQSNEPPT 9

RESULT 9
ID KY3K MOUSE STANDARD; PRT; 111 AA.
AC P01663;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 4050).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790 (1978).
DR PIR; A01935; KVM5M6.
DR HSSP; P01679; LACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 5EBF3264 CRC32;

Query Match 73.2%; Score 41; DB 5; Length 111;
Best Local Similarity 77.8%; Pred. No. 4.55e+00;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 93 qgmndpdt 101

QY 1 QQSNEPPT 9

RESULT 10
ID YFK7 YEAST STANDARD; PRT; 557 AA.
AC P43609;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 63.2 KD PROTEIN IN CDC26-YMR31 INTERGENIC REGION.
GN YFK037C.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYTES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA MURAKAMI Y., NAITOU M., HAGIWARA H., SHIBATA T., OZAWA M.,
RA SASANUMA S.-I., SASANUMA M., TSUCHIYA Y., SOEDA E., YOKOYAMA K.,
RA YAMAZAKI M., TASHIRO H., EKI T.;
RL NAT. GENET. 10:261-268 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA EKI T., NAITOU M., HAGIWARA H., ABE M., OZAWA M., SASANUMA S.-I.,
RA SASANUMA M., TSUCHIYA Y., SHIBATA T., WTANABE K., ONO A.,
RA YAMAZAKI M.-A., TASHIRO H., HANAOKA F., MURAKAMI Y.;
RL YEAST 12:177-190 (1996).

CC -!- SIMILARITY: TO YEAST TRANSCRIPTION REGULATORY PROTEIN SW13.

DR EMBL; D50617; G836792; -.

DR EMBL; D44602; G893432; -.

KW HYPOTHETICAL PROTEIN.

SQ SEQUENCE 557 AA; 63168 MW; D2C310A3 CRC32;

Query Match 73.2%; Score 41; DB 10; Length 557;

Best Local Similarity 44.4%; Pred. No. 4.55e+00;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 16 heateeppt 24

|||||

Qy 1 QOSNEDPPT 9

RESULT 11

ID ERG7 YEAST STANDARD; PRT; 730 AA.

AC P38604;

DT 01-OCT-1994 (REL. 30, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE LANOSTEROL SYNTHASE (EC 5.4.99.7) (OXIDOSQUALENE--LANOSTEROL CYCLASE)

DE (2,3-EPOXY)SQUALENE--LANOSTEROL CYCLASE) (OSC).

GN ERG7 OR YHR072M.

OS SACHAROMYCES CEREVISIAE (BAKER'S YEAST).

OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.

RX MEDLINE; 94181562.

RA COREY E.J., MATSUDA S.P.T., BARTEL B.;

RL PROC. NATL. ACAD. SCI. U.S.A. 91:2211-2215 (1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE; 94316697.

RA SHI Z., BUNTEL C.J., GRIFFIN J.H.;

RL PROC. NATL. ACAD. SCI. U.S.A. 91:7370-7374 (1994).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C / AB972;

RX MEDLINE; 94378003.

RA JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,

RA DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,

RA KUCABA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,

RA LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER L.,

RA NHAN M., RIFKIN L., RILES L., ST-PETER H., TREVASKIS E., VAUGHAN K.,

RA VIGNATI D., WILCOX L., WORLDMAN P., WATERSTON R., WILSON R.,

RA VAUDIN M.;

RL SCIENCE 265:2077-2082 (1994).

CC -!- FUNCTION: CATALYZES THE CYCLIZATION OF (S)-2,3 OXIDOSQUALENE TO

CC LANOSTEROL, A REACTION THAT FORMS THE STEROL NUCLEUS.

CC -!- CATALYTIC ACTIVITY: (S)-2,3-EPOXY)SQUALENE = LANOSTEROL.

CC -!- PATHWAY: EARLY STAGES OF ERGOSTEROL BIOSYNTHESIS.

CC -!- SIMILARITY: BELONGS TO THE FAMILY OF TERPENE CYCLASES/MUTASES.

DR EMBL; U04841; G465105; -.

DR EMBL; U23488; G733000; -.

DR EMBL; U10556; G500834; -.

DR PIR; A53493; A53493.

DR LISTA; SC00322; ERG7.

DR SGD; L0000573; ERG7.

DR PROSITE; PS01074; TERPENE SYNTHASES.

KW ISOMERASE; STEROID BIOSYNTHESIS.

FT INIT MET 0 0

FT CONFLICT 60 60 H -> N (IN REF. 3).

FT CONFLICT 529 529 N -> D (IN REF. 1).

SQ SEQUENCE 730 AA; 83329 MW; 22EB7C8C CRC32;

Query Match 73.2%; Score 41; DB 3; Length 730;

Best Local Similarity 55.6%; Pred. No. 4.55e+00;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 36 qqandpps 44

|||||

Qy 1 QOSNEDPPT 9

RESULT 12

ID ACVS CEPAC STANDARD; PRT; 3712 AA.

AC P25464;

DT 01-MAY-1992 (REL. 22, CREATED)

DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

DE DELTA-(L-ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE SYNTHETASE

DE (EC 6.-.-.-) (ACV SYNTHETASE) (ACVS).

GN PCBAB.

OS CEPHALOSPORIUM ACREMONIUM (ACREMONIUM CHRYSOGENUM).

OC EUKARYOTA; FUNGI; ASCOMYCOTINA; PLECTOMYCETES; EUROTIALES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 91177827.

RA GUTIERREZ S., DIEZ B., MONTENEGRO E., MARTIN J.F.;

RL J. BACTERIOL. 173:2354-2365 (1991).

RN [2]

RP PARTIAL SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=ATCC 11550;

RX MEDLINE; 91168300.

RA HOSKINS J.A., O'CALLAGHAN N., QUEENER S.W., CANTWELL C.A., WOOD J.S.,

RA CHEN V.J., SKATRUD P.L.;

RL CURR. GENET. 18:523-530 (1990).

CC -!- FUNCTION: EACH OF THE CONSTITUENT AMINO ACIDS OF THE TRIPEPTIDE

CC ACV ARE ACTIVATED AS AMONACYL-ADENYLATES WITH PEPTIDE BONDS

CC FORMED THROUGH THE PARTICIPATION OF AMINO ACID THIOLESTER

CC INTERMEDIATES.

CC -!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF PENICILLIN AND

CC CEPHALOSPORIN.

CC -!- COFACTOR: CONTAINS THREE COVALENTLY BOUND PHOSPHOPANTHETHEINES

CC (POTENTIAL).

CC -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT

CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.

DR PIR; A38531; YGCEVC.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE.

DR PROSITE; PS00455; AMP BINDING.

KW LIGASE; ANTIBIOTIC BIOSYNTHESIS; MULTIFUNCTIONAL ENZYME;

KW REPEAT; PHOSPHOPANTHETHEINE.

FT REPEAT 234 1062

FT REPEAT 1335 2162 DOMAIN 1 (ADIPATE-ACTIVATING).

FT REPEAT 2409 3387 DOMAIN 2 (CYSTEINE-ACTIVATING).

FT BINDING 827 827 DOMAIN 3 (VALINE-ACTIVATING).

FT BINDING 1916 1916 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT BINDING 2990 2990 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT ACT SITE 3568 3568 THIOESTERASE (BY SIMILARITY).

SQ SEQUENCE 3712 AA; 414767 MW; D6048F12 CRC32;

Query Match 73.2%; Score 41; DB 1; Length 3712;

Best Local Similarity 66.7%; Pred. No. 4.55e+00;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 2569 qqskentptt 2577

|||||

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Qy 1 QQSNDPPT 9

RESULT 13

ID KV3J MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (ABPC 22 AND PC 9245).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
[2]
RP SEQUENCE (PC 9245).
RX MEDLINE; 79073152.
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
CC -!- THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KVM56.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; 711C554A CRC32;

Query Match 71.4%; Score 40; DB 5; Length 111;
Best Local Similarity 85.7%; Pred. No. 7.83e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 93 qgmndp 99

|||||

Qy 1 QQSNDP 7

RESULT 14

ID KV3I MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 63).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE; 78235887.
RA BURSTEIN Y., SCHECHTER I.;
RL BIOCHEMISTRY 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.

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RX MEDLINE; 73140225.
RA MCKEAN D.J., POTTER M., HOOD L.E.;
RL BIOCHEMISTRY 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE; 79012520.
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KVM56.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION (MOPC 63).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; 9D55A06B CRC32;

Query Match 71.4%; Score 40; DB 5; Length 131;
Best Local Similarity 85.7%; Pred. No. 7.83e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 113 qgmndp 119

|||||

Qy 1 QQSNDP 7

RESULT 15

ID LMP2 EBV STANDARD; PRT; 497 AA.
AC P13285;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE GENE TERMINAL PROTEIN (MEMBRANE PROTEIN LMP-2A/LMP-2B).
OS EBSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; GAMMAHERPESVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88283646.
RA LAUX G., PERRICAUDET M., FARRELL P.J.;
RL EMBO J. 7:769-774(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89095024.
RA SAMPLE J., LIEBOWITZ D., KIEFF E.;
RL J. VIROL. 63:933-937(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84270667.
RA BAER R., BANKIER A.T., BIGGIN M.D., DEININGER P.L., FARRELL P.J.,
RA GIBSON T.J., HATFULL G., HUDSON G.S., SATCHWELL S.C., SEGUIN C.,
RA TUFFNELL P.S., BARRELL B.G.;
RL NATURE 310:207-211(1984).
CC -!- FUNCTION: MAY BE IMPORTANT FOR IMMORTALIZATION OF CELLS BY EBV.
CC -!- SUBCELLULAR LOCATION: MEMBRANE (PROBABLE).
DR EMBL; M24212; G522187; -.
DR EMBL; Y00835; G59184; -.
DR EMBL; V01555; -; NOT_ANNOTATED_CDS.

DR PIR; A30178; MWBEIM.
KW TRANSMEMBRANE.
FT CHAIN 1 497 MEMBRANE PROTEIN LMP-2A.
FT CHAIN 120 497 MEMBRANE PROTEIN LMP-2B.
FT TRANSMEM 122 141 POTENTIAL.
FT TRANSMEM 150 168 POTENTIAL.
FT TRANSMEM 178 198 POTENTIAL.
FT TRANSMEM 208 235 POTENTIAL.
FT TRANSMEM 242 259 POTENTIAL.
FT TRANSMEM 267 288 POTENTIAL.
FT TRANSMEM 300 316 POTENTIAL.
FT TRANSMEM 321 339 POTENTIAL.
FT TRANSMEM 355 373 POTENTIAL.
FT TRANSMEM 392 411 POTENTIAL.
FT TRANSMEM 419 443 POTENTIAL.
FT TRANSMEM 450 470 POTENTIAL.
SQ SEQUENCE 497 AA; 53011 MW; 6F2B2E7D CRC32;

Query Match 71.4%; Score 40; DB 5; Length 497;
Best Local Similarity 62.5%; Pred. No. 7.83e+00;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 50 resnepp 57
::|||::
Qy 1 QOSNEDPP 8

Search completed: Tue Mar 18 10:12:11 1997
Job time : 10 secs.

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Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Db 93 qqsedpdt 101
|||||
Qy 1 QQSNEDPPT 9

RESULT 2
ENTRY #type fragment
TITLE Ig kappa chain precursor V region (M-T310) - human (fragment)
ORGANISM #formal name Homo sapiens #common name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
30-Apr-1995

ACCESSIONS PH1226
REFERENCE PH1224
#authors Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.;
Reiter, C.; Flieger, D.; Lenz, H.; Weiss, E.H.; Rieber,
E.P.; Riethmüller, G.; Weidle, U.H.
#journal Gene (1992) 121:271-278
#title Combinatorial functions of two chimeric antibodies directed
to human CD4 and one directed to the alpha-chain of the
human interleukin-2 receptor.
#accession PH1226
##molecule_type mRNA
##residues 1-131 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
1-20 #domain signal sequence #status predicted #label SIG\
21-131 #product Ig light chain V region #status predicted
#label MAT
SUMMARY #length 131 #checksum 4648

Query Match 92.9%; Score 52; DB 5; Length 131;
Best Local Similarity 88.9%; Pred. No. 8.89e-02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 113 qqsedpdt 121
|||||
Qy 1 QQSNEDPPT 9

RESULT 3
ENTRY #type fragment
TITLE Ig kappa chain V region (2B5) - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change
23-Mar-1993

ACCESSIONS C38601
REFERENCE A38601
#authors Goshorn, S.C.; Retzel, E.; Jermerson, R.
#journal J. Biol. Chem. (1991) 266:2134-2142
#title Common structural features among monoclonal antibodies
binding the same antigenic region of cytochrome c.
#cross-references M01D:91115823
#accession C38601
##status preliminary
##molecule_type mRNA
##residues 1-65 ##label GOS
#cross-references CB:M57980
SUMMARY #length 65 #checksum 8125

Query Match 83.9%; Score 47; DB 12; Length 65;
Best Local Similarity 88.9%; Pred. No. 1.13e+00;
```

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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Db 46 qqsedpdt 54
|||||
Qy 1 QQSNEDPPT 9

RESULT 4
ENTRY #type fragment
TITLE Ig light chain V region (50.1) - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995

ACCESSIONS B49442
REFERENCE A49442
#authors Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.;
Roguska, M.; Hincapie, L.M.; Simmerman, H.K.B.; Profy,
A.T.; Wilson, I.A.
#journal Proteins (1992) 14:499-508
#title Crystallization, sequence, and preliminary crystallographic
data for an antipeptide Fab 50.1 and peptide complexes with
the principal neutralizing determinant of HIV-1 gp120.
#accession B49442
##status preliminary; not compared with conceptual translation
##molecule_type DNA
##residues 1-96 ##label STU
SUMMARY #length 96 #checksum 7322

Query Match 78.6%; Score 44; DB 12; Length 96;
Best Local Similarity 88.9%; Pred. No. 4.85e+00;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 85 qqsedpdt 93
|||||
Qy 1 QQSNEDPPT 9

RESULT 5
ENTRY #type complete
TITLE Ig kappa chain V region (PC7183) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
30-Sep-1993

ACCESSIONS B01937; A01937
REFERENCE A93204
#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce
immunoglobulin diversity.
#cross-references M01D:79073152
#accession B01937
##molecule_type protein
##residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
23-92 #disulfide bonds #status predicted
SUMMARY #length 111 #molecular-weight 11952 #checksum 9

Query Match 78.6%; Score 44; DB 2; Length 111;
Best Local Similarity 88.9%; Pred. No. 4.85e+00;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 93 qqsedpdt 101
```


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Qy 1 QQSNEPPT 9
||||||| I

RESULT 6

ENTRY D45722 #type fragment
TITLE anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 109) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
ACCESSIONS D45722
REFERENCE A45722
#authors Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez, M.; Britt, W.J.; Coelingh, K.L.
#journal J. Virol. (1993) 67:489-496
#title Neutralizing monoclonal antibodies that distinguish three antigenic sites on human cytomegalovirus glycoprotein H have conformationally distinct binding sites.
#cross-references MUID:93100833
#accession D45722
##status preliminary; not compared with conceptual translation
##molecule_type nucleic acid
##residues 1-111 ##label SIM
##cross-references NCBIP:120592
##note sequence extracted from NCBI backbone
SUMMARY #length 111 #checksum 811

Query Match 78.6%; Score 44; DB 12; Length 111;
Best Local Similarity 77.8%; Pred. No. 4.85e+00;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 93 qnnedprt 101
||||||| I
Qy 1 QQSNEPPT 9

RESULT 7

ENTRY S42193 #type fragment
TITLE Ig kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
ACCESSIONS S42193
REFERENCE S42176
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal Eur. J. Immunol. (1993) 23:2503-2510
#title Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen.
#accession S42193
##status preliminary
##molecule_type DNA
##residues 1-81 ##label MOJ
##cross-references EMBL:225456
##note the authors translated the codon GTT for residue 36 as Ala
SUMMARY #length 81 #checksum 9746

Query Match 76.8%; Score 43; DB 12; Length 81;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 75 qgsnedp 81
||||||| I
Qy 1 QQSNEDP 7

RESULT 8

ENTRY S42189 #type fragment
TITLE Ig kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jul-1995
ACCESSIONS S42189
REFERENCE S42176
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal Eur. J. Immunol. (1993) 23:2503-2510
#title Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen.
#accession S42189
##status preliminary
##molecule_type DNA
##residues 1-85 ##label MOJ
##cross-references EMBL:225448
SUMMARY #length 85 #checksum 7866

Query Match 76.8%; Score 43; DB 12; Length 85;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 79 qgsnedp 85
||||||| I
Qy 1 QQSNEDP 7

RESULT 9

ENTRY S42190 #type fragment
TITLE Ig kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
ACCESSIONS S42190
REFERENCE S42176
#authors Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal Eur. J. Immunol. (1993) 23:2503-2510
#title Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen.
#accession S42190
##status preliminary
##molecule_type DNA
##residues 1-87 ##label MOJ
##cross-references EMBL:225450
SUMMARY #length 87 #checksum 2354

Query Match 76.8%; Score 43; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 81 qgsnedp 87
||||||| I
Qy 1 QQSNEDP 7

RESULT 10

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```
ENTRY          S42194      #type fragment
TITLE          Ig kappa chain V region - mouse (fragment)
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
                21-Jul-1995
ACCESSIONS
REFERENCE
#authors       Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal       Eur. J. Immunol. (1993) 23:2503-2510
#title         Variable region gene selection of immunoglobulin G-expressing
                B cells with specificity for a defined epitope on type II
                collagen.
#accession     S42194
#status        preliminary
#molecule_type DNA
#residues      1-88 #label MOJ
#cross-references EMBL:Z25458
SUMMARY        #length 88 #checksum 4364
```

Query Match 76.8%; Score 43; DB 12; Length 88;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 82 qgsndp 88
|||||||
Qy 1 QQSNEDP 7

```
RESULT 11
ENTRY          S42187      #type fragment
TITLE          Ig kappa chain V region - mouse (fragment)
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change
                21-Jul-1995
ACCESSIONS
REFERENCE
#authors       Mo, J.A.; Bona, C.A.; Holmdahl, R.
#journal       Eur. J. Immunol. (1993) 23:2503-2510
#title         Variable region gene selection of immunoglobulin G-expressing
                B cells with specificity for a defined epitope on type II
                collagen.
#accession     S42187
#status        preliminary
#molecule_type DNA
#residues      1-90 #label MOJ
#cross-references EMBL:Z25444
SUMMARY        #length 90 #checksum 9303
```

Query Match 76.8%; Score 43; DB 12; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 84 qgsndp 90
|||||||
Qy 1 QQSNEDP 7

```
RESULT 12
ENTRY          S26344      #type complete
TITLE          Ig kappa chain V region - mouse
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                12-Apr-1995
ACCESSIONS
```

S26344

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8

```
REFERENCE
#authors       Stark, S.E.; Caton, A.J.
#journal       J. Exp. Med. (1991) 174:613-624
#title         Antibodies that are specific for a single amino acid
                interchange in a protein epitope use structurally distinct
                variable regions.
#accession     S26344
#status        preliminary
#molecule_type mRNA
#residues      1-107 #label STA
#cross-references EMBL:X59209
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY        #length 107 #molecular-weight 11646 #checksum 6789
```

Query Match 76.8%; Score 43; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 92 qgsndp 98
|||||||
Qy 1 QQSNEDP 7

```
RESULT 13
ENTRY          S26343      #type complete
TITLE          Ig kappa chain V region - mouse
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                12-Apr-1995
ACCESSIONS
REFERENCE
#authors       Stark, S.E.; Caton, A.J.
#journal       J. Exp. Med. (1991) 174:613-624
#title         Antibodies that are specific for a single amino acid
                interchange in a protein epitope use structurally distinct
                variable regions.
#accession     S26343
#status        preliminary
#molecule_type mRNA
#residues      1-107 #label STA
#cross-references EMBL:X59207
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY        #length 107 #molecular-weight 11660 #checksum 6543
```

Query Match 76.8%; Score 43; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 92 qgsndp 98
|||||||
Qy 1 QQSNEDP 7

```
RESULT 14
ENTRY          KYMS08      #type complete
TITLE          Ig kappa chain V region (PC6308) - mouse
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
                30-Sep-1993
ACCESSIONS     C01937; A01937
REFERENCE       A93204
#authors       Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal       Nature (1978) 276:785-790
#title         Rearrangement of genetic information may produce
```


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9

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#cross-references MUID:79073152
#accession C01937
#molecule_type protein
#residues 1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
23-92
SUMMARY #disulfide bonds #status predicted
#length 111 #molecular-weight 12071 #checksum 2195
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Query Match 76.8%; Score 43; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 93 qqsndp 99
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Oy 1 QQSNEDP 7
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RESULT 15
ENTRY A33936 #type fragment
TITLE Ig kappa chain V region (VM201) - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
12-Apr-1995
ACCESSIONS A33936
REFERENCE A33936
#authors Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:4664-4668
#title Nucleotide changes in sequential variants of influenza virus
hemagglutinin genes and molecular structures of
corresponding monoclonal antibodies specific for each
variant.
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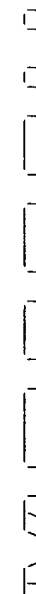
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#cross-references MUID:89282831
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#status preliminary
#molecule_type mRNA
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#cross-references GB:J04575
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 111 #checksum 1618
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Query Match 76.8%; Score 43; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 7.80e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 93 qqsndp 99
|||||
Oy 1 QQSNEDP 7
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Search completed: Tue Mar 18 10:12:34 1997
Job time : 6 secs.

(TUL)



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```

MPsrch_pp      protein - protein database search, using Smith-Waterman algorithm
Run on:        Tue Mar 18 10:12:52 1997;  MacPar time 1.71 Seconds
               54.031 Million cellupdates/sec

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>US-08-612-929-20
Title:
Description: (1-9) from US08612929, pep
Perfect Score: 56
Sequence: 1 QQSNEDPPT 9
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Scoring table: PAM 150
Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Database:
a-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
```

Statistics: Mean 13.130: Variance 39.761: scale 0.330

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB ID	Description	Pred. No.	
		Match	Length				
1	56	100.0	9	13	R70197	MAB 3B9 light chain C	1.78e+00
2	56	100.0	131	13	R70202	Humanized antibody 3B	1.78e+00
3	56	100.0	131	6	R29008	p64-k4 protein produc	1.78e+00
4	56	100.0	132	13	R70189	Mouse Mab 3B9 light c	1.78e+00
5	52	92.9	131	6	R32123	Anti-CD4 antibody MT	5.29e+00
6	51	91.1	9	13	R70201	Humanized antibody 3B	6.92e+00
7	51	91.1	131	13	R75355	Humanized antibody 3B	6.92e+00
8	49	87.5	17	12	R66145	CD-4 antibody variabl	1.18e+01
9	49	87.5	103	9	R47933	Light chain region of	1.18e+01
10	49	87.5	111	9	R47935	Humanised light chain	1.18e+01
11	49	87.5	115	1	R04134	Anti-Leu 3a light cha	1.18e+01
12	49	87.5	131	1	R04133	Anti-Leu 3a light cha	1.18e+01

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3

CC encoded the protein given in R70189. 3 CDRs (R70195-97) were
 CC identified.
 SQ Sequence 9 AA;

Query Match 100.0%; Score 56; DB 13; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.78e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qgsnedppt 9
 |||||
 Qy 1 QQSNEDEPT 9

RESULT 2

ID R70202 standard; Protein; 131 AA.
 AC R70202;
 DT 20-SEP-1995 (first entry)
 DE Humanized antibody 3B9 light chain.
 KW Humanized antibody; antibody engineering; monoclonal antibody;
 KW Mab; interleukin-4; IL-4; allergy.
 OS Homo sapiens.
 PN W09507301-A.
 PD 16-MAR-1995.
 PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR N-PSDB; Q83520.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Page 71-72; 97pp; English.
 CC A humanized antibody light chain variable region and signal
 CC sequence is given in R75355. The signal sequence is also
 CC provided in R70194. The sequences of the 3 CDRs
 CC are identical to mouse anti-human IL-4 Mab 3B9 light chain
 CC CDRs (given in R70195-97).
 SQ Sequence 131 AA;

Query Match 100.0%; Score 56; DB 13; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.78e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 112 qgsnedppt 120
 |||||
 Qy 1 QQSNEDEPT 9

RESULT 3

ID R29008 standard; Protein; 131 AA.
 AC R29008;
 DT 30-MAR-1993 (first entry)
 DE p64-k4 protein product.
 KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
 KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
 KW plasmid; p64-k4; p64-h2.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "Signal peptide"
 FT Protein 21..131

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FT /note= "Mature peptide"
 PN W09219759-A.
 PD 12-NOV-1992.
 PF 24-APR-1992; J00544.
 PR 25-APR-1991; JP-095476.
 PR 19-FEB-1992; JP-032084.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
 DR WPI; 92-398882/48.
 DR N-PSDB; Q30757.
 PT Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 PS Disclosure; Page 124-125; 207pp; Japanese.
 CC The sequences given in R29008-09 were encoded by plasmids which were
 CC used in example to illustrate the production of a human antibody which
 CC recognises human interleukin-6 receptor (IL-6R). The antibody
 CC comprises light (L) chain and heavy (H) chain variable regions which
 CC were derived from a mouse monoclonal antibody produced from the
 CC hybridoma AUK64-7 which contained the plasmids p64-k4 and p64-h2.
 SQ Sequence 131 AA;

Query Match 100.0%; Score 56; DB 6; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.78e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 113 qgsnedppt 121
 |||||
 Qy 1 QQSNEDEPT 9

RESULT 4

ID R70189 standard; Protein; 132 AA.
 AC R70189;
 DT 20-SEP-1995 (first entry)
 DE Mouse Mab 3B9 light chain.
 KW Chimeric antibody; humanized antibody; antibody engineering;
 KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= sig_peptide
 FT /label= CDR 44..58
 FT /note= "complementarity determining region"
 FT Region 74..80
 FT /label= CDR
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT Region 113..121
 FT /label= CDR
 FT /note= "complementarity determining region"
 PN W09507301-A.
 PD 16-MAR-1995.
 PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR N-PSDB; Q83490.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions

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PS Disclosure; Fig.1; 97pp; English.
CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 MAB secretion. Only
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC chains were cloned into pGEMTf+ and transformed into E. coli
CC DH5-alpha. The clones were sequenced (083490-91), and used for
CC antibody engineering.
SQ Sequence 132 AA;

Query Match 100.0%; Score 56; DB 13; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.78e+00;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 113 qqsnedpdt 121
|||||
Qy 1 QQSNEDPPT 9

RESULT 5
ID R32123 standard; Protein; 131 AA.
AC R32123;
DT 02-JUN-1993 (first entry)
DE Anti-CD4 antibody MT 3.10 light chain variable region.
KW Immunosuppression; tissue transplantation; graft; L chain; V region;
KW T-helper cell inhibition; transplant rejection; MAB;
KW Interleukin-2 receptor.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /Label= signal
FT Region 21..120
FT /Label= Variable
FT Region 121..131
FT /Label= J1
PN DE4143214-A.
PD 28-JAN-1993.
PF 30-DEC-1991; 143214.
PR 25-JUL-1991; DE-124759.
PR 30-DEC-1991; DE-143214.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
PI Kaluza B, Riethmuller G, Scheuer W, Weidle U;
DR WPI; 93-037582/05.
DR N-PSDB; Q36609.
PT Synergistic antibody compsn. for use as immunosuppressant -
PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
PT alpha- or anti-IL2R beta antibodies
PS Claim 5; Page 11; 18pp; German.
CC This sequence is the light chain variable region of a preferred
CC anti-CD4 monoclonal antibody for use in the claimed synergistic
CC composition. MAB MT 3.10 is deposited as clone 3.101/sB10 (ECACC
CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R
CC alpha or beta antibody. Individually the antibodies are strongly
CC inhibiting and when used together their immunosuppressive properties
CC are improved; they synergistically inhibit T-helper cell
CC proliferation to effectively inhibit transplant rejection at low
CC doses without significantly reducing the general immune response.
CC See also Q36608-Q36616.
SQ Sequence 131 AA;

Query Match 92.9%; Score 52; DB 6; Length 131;
Best Local Similarity 88.9%; Pred. No. 5.29e+00;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 113 qqsnedpdt 121
|||||

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Qy 1 QQSNEDPPT 9

RESULT 6
ID R70201 standard; Protein; 9 AA.
AC R70201;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain CDR.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW MAB; interleukin-4; IL-4; allergy; CDR;
KW complementarity determining region.
OS Homo sapiens.
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Page 28; 97pp; English.
CC A humanized antibody light chain variable region and signal
CC sequence is given in R75355. The signal sequence is also
CC provided in R70194. The sequences of the first 2 CDRs
CC are identical to mouse anti-human IL-4 MAB 3B9 light chain
CC CDRs (given in R70195-96), but the third (R70201) differs
CC by a single amino acid from the native mouse CDR (R70197).
SQ Sequence 9 AA;

Query Match 91.1%; Score 51; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.92e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qqsnedpdt 8
|||||
Qy 1 QQSNEDPPT 8

RESULT 7
ID R75355 standard; Protein; 131 AA.
AC R75355;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW MAB; interleukin-4; IL-4; allergy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /Label= Sig_peptide
FT Region 43..57
FT /Label= CDR
FT /note= "complementarity determining region"
FT Region 73..79
FT /Label= CDR
FT /note= "complementarity determining region"
FT Region 112..120
FT /Label= CDR
FT /note= "complementarity determining region"
PN W09507301-A.
PD 16-MAR-1995.

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PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvestre DR;
 WP1; 95-123387/16.
 DR N-PSDB; Q73986.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAb), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Fig.5; 97pp; English.
 CC A humanized antibody light chain variable region and signal
 CC sequence is given in R75355. The signal sequence is also
 CC provided in R70194. The sequences of the first 2 CDRs
 CC are identical to mouse anti-human IL-4 Mab 3B9 light chain
 CC CDRs (given in R70195-96), but the third (R70201) differs
 CC by a single amino acid from the native mouse CDR (R70197).
 SQ Sequence 131 AA;

Query Match 91.1%; Score 51; DB 13; Length 131;
 Best Local Similarity 100.0%; Pred. No. 6.92e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 112 qqsndpp 119
 |||||
 Qy 1 QQSNEPPT 8

RESULT 8

ID R66145 standard; peptide; 17 AA.
 AC R66145;
 DE 12-JUL-1995 (first entry)
 DE CD-4 antibody variable region complementary peptide.
 KW CD-4 antibody variable region; complementary peptide;
 KW extra-corporeal blood circulation; cell filter material.
 OS Synthetic.
 PN J06269663-A.
 PD 27-SEP-1994.
 PF 17-MAR-1993; 057206.
 PR 17-MAR-1993; JP-057206.
 PA (TOYM) TOYOBO KK.
 DR WP1; 94-346316/43.
 PT Material for collecting cells positive for CD-4 antibody -
 PT comprises nonwoven fabric having keto-alkyl halide functional gp
 PS Example 3; Page 8; 9pp; Japanese.
 CC R66140-R66146 are peptides complementary to the variable region
 CC of the CD-4 antibody, these peptides are fixed onto a claimed
 CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with
 CC keto-alkyl halide functional groups. This material can be used
 CC as a filter for CD-4 positive cells in a medical treatment
 CC involving the extra-corporeal circulation of blood.
 SQ Sequence 17 AA;

Query Match 87.5%; Score 49; DB 12; Length 17;
 Best Local Similarity 88.9%; Pred. No. 1.18e+01;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 9 qqsyedp 17
 |||||
 Qy 1 QQSNEPPT 9

RESULT 9

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ID R47933 standard; Protein; 103 AA.
 AC R47933;
 DT 24-JUL-1994 (first entry)
 DE Light chain region of 23F2G.
 KW Amplification; 23F2G; humanised antibody; heavy chain; light chain;
 KW hybridoma; inflammation; CD18; human leukocyte integrins; mAb 60.3;
 KW monoclonal antibody; LFA-1; adhesion; migration; multiple
 KW sclerosis; MS.
 PN W09402175-A.
 PD 03-FEB-1994.
 PF 16-JUL-1993; U06734.
 PR 16-JUL-1992; US-915068.
 PR 10-MAY-1993; US-060699.
 PA (ICOS-) ICOS CORP.
 PA (UNIW) UNIV WASHINGTON.
 PI Rose LM;
 DR WP1; 94-048551/06.
 DR N-PSDB; Q55915.

PT Antibodies immunologically reactive with the CD18 of human
 PT leukocyte integrins and/or competing with mAb 60.3 for binding to
 PT human LFA-1 - for alleviating symptoms associated with
 PT inflammatory disease states
 PS Example 6; Page 43; 58pp; English.
 CC Total RNA was isolated from the hybridoma cell line 23F2G and first
 CC strand cDNA was synthesised using the total RNA as a template. The
 CC first strand cDNA was used as a template for PCR to obtain double
 CC stranded DNA fragments encoding the variable regions of both the
 CC heavy and light chains of monoclonal antibody 23F2G. The sequence
 CC shown is that of the light chain variable region of Mab 23F2G
 CC The humanised form of Mab 23F2G may be administered to
 CC for the inhibition of inflammatory processes associated with
 CC multiple sclerosis. The Mab blocks leukocyte adhesion and
 CC migration to inflammatory sites. The Mab is an anti-CD18 integrin
 CC antibody which competes with Mab 60.3 for binding to LFA-1.
 CC See also R47931-6.
 SQ Sequence 103 AA;

Query Match 87.5%; Score 49; DB 9; Length 103;
 Best Local Similarity 77.8%; Pred. No. 1.18e+01;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 85 hqndp 93
 :| |||||
 Qy 1 QQSNEPPT 9

RESULT 10

ID R47935 standard; Protein; 111 AA.
 AC R47935;
 DT 24-JUL-1994 (first entry)
 DE Humanised light chain region of 23F2G.
 KW Amplification; 23F2G; humanised antibody; heavy chain; light chain;
 KW hybridoma; inflammation; CD18; human leukocyte integrins; mAb 60.3;
 KW monoclonal antibody; LFA-1; adhesion; migration; multiple
 KW sclerosis; MS.
 PN W09402175-A.
 PD 03-FEB-1994.
 PF 16-JUL-1993; U06734.
 PR 16-JUL-1992; US-915068.
 PR 10-MAY-1993; US-060699.
 PA (ICOS-) ICOS CORP.
 PA (UNIW) UNIV WASHINGTON.
 PI Rose LM;

DR WPI; 94-048551/06.
 DR N-PSDB; Q55917.
 PT Antibodies immunologically reactive with the CD18 of human
 PT leukocyte integrins and/or competing with mAb 60.3 for binding to
 PT human LFA-1 - for alleviating symptoms associated with
 PT inflammatory disease states
 PS Example 6; Page 45; 58pp; English.
 CC Total RNA was isolated from the hybridoma cell line 23F2G and first
 CC strand cDNA was synthesised using the total RNA as a template. The
 CC first strand cDNA was used as a template for PCR to obtain double
 CC stranded DNA fragments encoding the variable regions of both the
 CC heavy and light chains of monoclonal antibody 23F2G. The sequence
 CC shown is a humanised form of the light chain variable region of MAb
 CC 23F2G. The humanised form of MAb 23F2G may be administered to
 CC alleviate symptoms associated with inflammatory disease states, esp.
 CC for the inhibition of inflammatory processes associated with
 CC multiple sclerosis. The MAb blocks leukocyte adhesion and
 CC migration to inflammatory sites. The MAb is an anti-CD18 integrin
 CC antibody which competes with MAb 60.3 for binding to LFA-1.
 CC See also R47931-6.
 SQ Sequence 111 AA;

Query Match 87.5%; Score 49; DB 9; Length 111;
 Best Local Similarity 77.8%; Pred. No. 1.18e+01;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 93 hqnedpdt 101
 : |||||
 Qy 1 QQSNEPDPT 9

RESULT 11

ID R04134 standard; protein; 115 AA.
 AC R04134;
 DT 06-SEP-1990 (first entry)
 DE Anti-Leu 3a light chain variable region gene product, KOL/206 VL.
 KW HIV; AIDS; anti-Leu3A; vaccine; ds.
 OS Mus musculus.
 PN EP-365209-A.
 PD 25-APR-1990.
 PF 11-OCT-1989; 010415.
 PR 17-OCT-1988; US-260558.
 PA (BECT) Becton Dickinson Co.
 PI Hinton R, Oi VT;
 DR WPI; 90-126329/17.
 DR N-PSDB; Q04041.
 PT New chimeric variants of murine antibody anti-leucine -
 PT contg. human antibody regions, and DNA encoding sequences.
 PS Claim 4; Fig 4; 12pp; English.
 CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
 CC used to form chimeric mouse-variable, human-constant region Abs
 CC suggested as being useful as a vaccine to HIV.
 SQ Sequence 115 AA;

Query Match 87.5%; Score 49; DB 1; Length 115;
 Best Local Similarity 88.9%; Pred. No. 1.18e+01;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 96 qgsyedpdt 104
 : |||||
 Qy 1 QQSNEPDPT 9

RESULT 12

ID R04132 standard; protein; 131 AA.
 AC R04132;
 DT 06-SEP-1990 (first entry)
 DE Anti-Leu 3a light chain variable region gene product, 206 Vx.
 KW HIV; AIDS; anti-Leu3A; vaccine; ds.
 OS Mus musculus.
 PN EP-365209-A.
 PD 25-APR-1990.
 PF 11-OCT-1989; 010415.
 PR 17-OCT-1988; US-260558.
 PA (BECT) Becton Dickinson Co.
 PI Hinton R, Oi VT;
 DR WPI; 90-126329/17.
 DR N-PSDB; Q04039.
 PT New chimeric variants of murine antibody anti-leucine -
 PT contg. human antibody regions, and DNA encoding sequences.
 PS Claim 1; Fig 2; 12pp; English.
 CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
 CC used to form chimeric mouse-variable, human-constant region Abs
 CC suggested as being useful as a vaccine to HIV.
 SQ Sequence 131 AA;

Query Match 87.5%; Score 49; DB 1; Length 131;
 Best Local Similarity 88.9%; Pred. No. 1.18e+01;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 113 qgsyedpdt 121
 : |||||
 Qy 1 QQSNEPDPT 9

RESULT 13

ID R47494 standard; Protein; 111 AA.
 AC R47494;
 DT 06-JUL-1994 (first entry)
 DE Murine anti-CD18 Ab 60.3 light chain.
 KW Monoclonal antibody; MAb; heavy chain; light chain;
 KW constant region; variable region; amplification; primer;
 KW polymerase chain reaction; PCR; chimera; Ig;
 KW immunoglobulin; humanised antibody; leucocyte; integrin.
 OS Mus sp.
 PN EP-578515-A.
 PD 12-JAN-1994.
 PF 24-MAY-1993; 401328.
 PR 26-MAY-1992; US-888233.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;
 DR WPI; 94-010334/02.
 DR N-PSDB; Q55002.
 PT Humanised monoclonal antibodies prepn. - using comparative model
 PT building, by computer database searching
 PS Disclosure; Page 21; 68pp; English.
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18
 CC antibody 60.3 was prepared. The variable (V) region sequences from
 CC both the heavy (H) and light (L) chains were determined from cDNA
 CC (amplified by PCR), and spliced onto human constant (C) regions,
 CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
 CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected
 CC by ELISA), and examined in binding assays. The results from
 CC competition and inhibition assays showed that the chimeric Ab was
 CC as effective as the murine 60.3 MAb. The deduced murine VH and VL
 CC protein sequences were compared to the protein sequence data base,
 CC and two human Ig protein sequences were selected to be used as
 CC templates. A murine 60.3 Fv was modeled according to the deduced

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CC VH and VL protein sequences. Based on the 60.3 Fv model and the two
CC human template sequences selected from the protein data base, a
CC humanised Fv was modeled. Construction of the humanised 60.3 was
CC done by piecing 5 pairs of complementary oligonucleotides together
CC (spanning the entire V region) to form the VH and VL. These were
CC then attached onto vectors containing genes for appropriate C regions
CC to form humanised Ab (IgG1, kappa). The humanised proteins were again
CC expressed in Aq8.653 cells and binding assays were done. FACS analyses
CC indicated that the humanised Ab recognised cells expressing CD18.
CC About a dozen of the humanised 60.3 Ab master wells were transferred
CC and assayed for Ig.
SQ Sequence 111 AA;

Query Match 83.9%; Score 47; DB 9; Length 111;
Best Local Similarity 88.9%; Pred. No. 2.01e+01;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 93 qgsnedprt 101
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Qy 1 QQSNEPPT 9

RESULT 14

ID R47492 standard; Protein; 111 AA.
AC R47492;
DT 06-JUL-1994 (first entry)
DE Humanised anti-CD18 Ab 60.3 light chain.
KW Monoclonal antibody; MAb; heavy chain; light chain;
KW constant region; variable region; amplification; primer;
KW polymerase chain reaction; PCR; chimera; Ig;
KW immunoglobulin; humanised antibody; leucocyte; integrin.
OS Chimeric; Homo sapiens.
PN EP-578515-A.
PD 12-JAN-1994.
PR 24-MAY-1993; 401328.
PR 26-MAY-1992; US-888233.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PI Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;
DR WPI: 94-010334/02.
DR N-PSDB; Q55000.
PT Humanised monoclonal antibodies prepn. - using comparative model
PT building, by computer database searching
PS Disclosure; Page 19; 68pp; English.
CC A humanised monoclonal antibody corresponding to the murine anti-CD18
CC antibody 60.3 was prepared. The variable (V) region sequences from
CC both the heavy (H) and light (L) chains were determined from cDNA
CC (amplified by PCR), and spliced onto human constant (C) regions,
CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected
CC by ELISA), and examined in binding assays. The results from
CC competition and inhibition assays showed that the chimeric Ab was
CC as effective as the murine 60.3 MAb. The deduced murine VH and VL
CC protein sequences were compared to the protein sequence data base,
CC and two human Ig protein sequences were selected to be used as
CC templates. A murine 60.3 Fv was modeled according to the deduced
CC VH and VL protein sequences. Based on the 60.3 Fv model and the two
CC human template sequences selected from the protein data base, a
CC humanised Fv was modeled. Construction of the humanised 60.3 was
CC done by piecing 5 pairs of complementary oligonucleotides together
CC (spanning the entire V region) to form the VH and VL. These were
CC then attached onto vectors containing genes for appropriate C regions
CC to form humanised Ab (IgG1, kappa). The humanised proteins were again
CC expressed in Aq8.653 cells and binding assays were done. FACS analyses

Mar 18 10:11

US-08-612-929-20.rag

12

CC Indicated that the humanised Ab recognised cells expressing CD18.
CC About a dozen of the humanised 60.3 Ab master wells were transferred
CC and assayed for Ig.
SQ Sequence 111 AA;

Query Match 83.9%; Score 47; DB 9; Length 111;
Best Local Similarity 88.9%; Pred. No. 2.01e+01;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 93 qgsnedprt 101
|||||||
Qy 1 QQSNEPPT 9

RESULT 15

ID R74781 standard; peptide; 215 AA.
AC R74781;
DT 26-JUN-1995 (first entry)
DE Light chain of 59.1 an anti-HIV antibody.
KW Identifying compounds; anti-HIV antibodies; HIV treatment;
KW peptide RPI42; antibody 59.1.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified site 8
FT /label= OTHER
FT /note= "CPR no further definition"
FT Modified site 81
FT /label= OTHER
FT /note= "CPR no further definition"
FT Modified site 99
FT /label= OTHER
FT /note= "CPR no further definition"
FT Modified site 145
FT /label= OTHER
FT /note= "CPR no further definition"
PN WO9418232-A.
PD 18-AUG-1994.
PF 09-FEB-1994; U01458.
PR 12-FEB-1993; US-017485.
PA (REPK) REPLIGEN CORP.
PA (SCRI) SCRIPPS RES INST.
PI Profy AT, Wilson IA;
DR WPI: 94-332662/41.
PT Identifying cpds. which elicit, or bind to, anti-HIV antibodies -
PT and new antibodies which neutralise a broad range of HIV strains
PS Disclosure; Page 78; 137pp; English.
CC R74781 describes the amino acid sequence of the light chain of
CC 59.1 an anti-HIV antibody (Ab), it was used in the development of
CC the peptide RPI42 (R74783). This peptide can bind to anti-HIV Abs or
CC elicit new Abs effective against a broad range of HIV strains,
CC that can be used in the treatment of HIV infection.
SQ Sequence 215 AA;

Query Match 80.4%; Score 45; DB 12; Length 215;
Best Local Similarity 77.8%; Pred. No. 3.40e+01;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 93 qgsnedprt 101
|||||||
Qy 1 QQSNEPPT 9

Search completed: Tue Mar 18 10:13:00 1997
Job time : 8 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:22:29 1997; MasPar time 52.87 Seconds
327.119 Million cell updates/sec

Tabular output not generated.

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>US-08-612-929-21
Description: (1-21) from US08612929.seq
Perfect Score: 21
N.N.A. Sequence: 1 ACTTCTGGTATGGGTGTGAGC 21
Comp: TGAAGACCATCCACACTCG

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Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0: Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: **embl-new5**
1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI
10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

Database: genbank94

16:BCR1	17:BCR2	18:BCR3	19:BCY4	20:BCY5	21:BCY6	22:BCY7
23:BCR8	24:BCY9	25:INV1	26:INV2	27:INV3	28:INV4	29:INV5
30:INV6	31:INV7	32:MAM1	33:MAM2	34:MAM3	35:VRT1	36:VRT2
37:VRT3	38:PAT1	39:PAT2	40:PAT3	41:PHG	42:PLN1	43:PLN2
44:PLN3	45:PLN4	46:PLN5	47:PLN6	48:PLN7	49:PLN8	50:PR11
51:PR12	52:PR13	53:PR14	54:PR15	55:PR16	56:PR17	57:PR18
58:PR19	59:PR110	60:PR111	61:PR112	62:PR113	63:ROD1	
64:ROD2	65:ROD3	66:ROD4	67:ROD5	68:ROD6	69:ROD7	70:ROD8
71:STR	72:SYN	73:UNA	74:VR1	75:VR2	76:VR3	77:VR14
78:VR15	79:VR16	80:VR17	81:VR18			

Database: genbank-new5
82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG
89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL
Database: u-emb146_94
96:part1

Statistics: Mean 6.886; Variance 2.651; scale 2.598

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

2.87 Seconds
on cell updates/sec

Result No.	Score	Query Match	Length	DB	ID	Description	SUMMARIES	
							Pred.	No.
1	21	100.0	286	65	MMU223019	Mus musculus C57BL/6	1.35e-03	
2	21	100.0	306	66	MDSB	Mus musculus immunogl	1.35e-03	
3	21	100.0	318	65	MMU22990	Mus musculus CB17 SCI	1.35e-03	
4	21	100.0	318	12	MMU22990	Mus musculus CB17 SCI	1.35e-03	
5	21	100.0	318	91	MMU22990	Mus musculus CB17 SCI	1.35e-03	
6	21	100.0	320	65	MMU22991	Mus musculus CB17 SCI	1.35e-03	
7	21	100.0	320	91	MMU22991	Mus musculus CB17 SCI	1.35e-03	
8	21	100.0	320	12	MMU22991	Mus musculus CB17 SCI	1.35e-03	
9	21	100.0	326	91	MMU22986	Mus musculus CB17 SCI	1.35e-03	
10	21	100.0	326	12	MMU22986	Mus musculus CB17 SCI	1.35e-03	
11	21	100.0	330	91	MMU22975	Mus musculus CB17 SCI	1.35e-03	
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13	21	100.0	353	91	MMU22995	Mus musculus CB17 SCI	1.35e-03	
14	21	100.0	353	12	MMU22995	Mus musculus CB17 SCI	1.35e-03	
15	21	100.0	358	65	MMU223000	Mus musculus CB17 SCI	1.35e-03	
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20	21	100.0	360	65	MMU223010	Mus musculus CB17 SCI	1.35e-03	
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26	21	100.0	360	91	MMU22988	Mus musculus CB17 SCI	1.35e-03	
27	21	100.0	360	91	MMU22984	Mus musculus CB17 SCI	1.35e-03	
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29	21	100.0	360	65	MMU22992	Mus musculus CB17 SCI	1.35e-03	
30	21	100.0	360	12	MMU22977	Mus musculus CB17 SCI	1.35e-03	
31	21	100.0	360	65	MMU22988	Mus musculus CB17 SCI	1.35e-03	
32	21	100.0	360	12	MMU22997	Mus musculus CB17 SCI	1.35e-03	
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34	21	100.0	360	65	MMU22979	Mus musculus CB17 SCI	1.35e-03	
35	21	100.0	360	63	MHCVR3	M.musculus (A-SW) m5N	1.35e-03	
36	21	100.0	360	91	MMU22994	Mus musculus CB17 SCI	1.35e-03	
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38	21	100.0	360	65	MMU22999	Mus musculus CB17 SCI	1.35e-03	
39	21	100.0	360	12	MMU22992	Mus musculus CB17 SCI	1.35e-03	
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41	21	100.0	360	65	MMU223005	Mus musculus CB17 SCI	1.35e-03	
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43	21	100.0	360	12	MMU22981	Mus musculus CB17 SCI	1.35e-03	
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ALIGNMENTS

RESULT	1
LOCUS	MU23019 286 bp DNA ROD
DEFINITION	Mus musculus C57BL/6 immunoglobulin heavy chain V region mRNA, clone CB17H-1, partial cds.
ACCESSION	U23019
KEYWORDS	NID g780640
SOURCE	.
ORGANISM	house mouse. Mus musculus

Mar 19 08:21

US-08-612-999-21.rge

3

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Young,D.C. and Kearney,J.F.
TITLE Sequence analysis and antigen binding characteristics of immunoglobulins from SCID Ig+ mice

JOURNAL

Int. Immunol. 7 (1995) In press

AUTHORS

Young,D.C.

TITLE

Direct Submission

JOURNAL

Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

FEATURES

source

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/organism="Mus musculus"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 92 acctctgtatgggtgagc 112

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Qy 1 ACTTCTGGTATGGGTGACG 21

RESULT

2

LOCUS

MUSB 306 bp mRNA ROD 14-MAR-1994

DEFINITION Mus musculus immunoglobulin heavy chain (Igh) mRNA, VDJ4 region, partial cds.

ACCESSION

L22743

NID

g348959

KEYWORDS

Ig heavy chain; diversity region; immunoglobulin; joining region; variable region.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE

1 (bases 1 to 306)

Sheehan,K.M., Mainville,C.A., Willert,S. and Brodeur,P.H.

J. Immunol. 151 (10), 5364-5375 (1993)

JOURNAL

94044761

FEATURES

source

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Mar 19 08:21

US-08-612-999-21.rge

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BASE COUNT

72 a 80 c 75 g 79 t

ORIGIN

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 34 acctctgtatgggtgagc 54

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Qy 1 ACTTCTGGTATGGGTGACG 21

RESULT

3

LOCUS

MU022990 318 bp mRNA ROD 26-APR-1995

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA, clone 45-24h, partial cds.

ACCESSION

U22990

NID

g780582

KEYWORDS

house mouse.

ORGANISM

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 318)

Young,D.C. and Kearney,J.F.

Sequence analysis and antigen binding characteristics of immunoglobulins from SCID Ig+ mice

Int. Immunol. 7 (1995) In press

JOURNAL

2 (bases 1 to 318)

REFERENCE

Young,D.C.

Direct Submission

Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

FEATURES

source

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/sub_species="domesticus"

/cell_type="lymphocyte"

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Mar 19:08:21

US-08-612-929-21.rge

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BASE COUNT 74 a 84 c 79 g 81 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatggtgtgagc 111

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Qy 1 ACTTCTGGTATGGGTGTGAGC 21

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Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatggtgtgagc 111

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Qy 1 ACTTCTGGTATGGGTGTGAGC 21

Mar 19:08:21

US-08-612-929-21.rge

6

RESULT 4

ID MM22990 standard; RNA; ROD; 318 BP.

AC U72990;

DT 29-APR-1995 (Rel. 43, Created)

DT 09-APR-1996 (Rel. 47, Last updated, Version 2)

DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,

DE clone 45-24h, partial cds.

KW .

OS Mus musculus (mouse)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

RN [1]

RP 1-318

RA Young D., Kearney J.F.;

RT "Sequence analysis and antigen binding characteristics of Ig SCID

RT Ig+ mice";

RL Int. Immunol. 7:807-819(1995).

RN [2]

RP 1-318

RA Young D.C.;

RT ;

RL Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.

RL David C. Young, University of Texas Health Science Center, Houston,

RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

CC NCBI gi: 780582

FH Key Location/Qualifiers

FH source

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FT /organism="Mus musculus"

FT /strain="CB17 SCID"

FT /sub_species="domesticus"

FT /clone="45-24h"

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FT S

FT Ty*

SQ Sequence 318 BP; 74 A; 84 C; 79 G; 81 T; 0 other;

Query Match 100.0%; Score 21; DB 12; Length 318;

RESULT 5

LOCUS MMU22990 318 bp mRNA 09-APR-1996

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,

clone 45-24h, partial cds.

ACCESSION U72990

NID g780582

KEYWORDS .

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;

Murinae; Mus.

REFERENCE 1 (bases 1 to 318)

AUTHORS Young, D. and Kearney, J.F.

TITLE Sequence analysis and antigen binding characteristics of Ig SCID

IG+ mice

JOURNAL Int. Immunol. 7 (5), 807-819 (1995)

MEDLINE 96053543

REFERENCE 2 (bases 1 to 318)

AUTHORS Young, D.C.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

COMMENT NCBI gi: 780582

FEATURES

source

Location/Qualifiers

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BASE COUNT 74 a 84 c 79 g 81 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ACTTCTGGTATGGGTGTGAGC 21

RESULT 6

LOCUS MMU22991 320 bp mRNA 26-APR-1995

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,

clone 45-24h, partial cds.

ACCESSION U72990

NID g780582

KEYWORDS .

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;

Murinae; Mus.

REFERENCE 1 (bases 1 to 318)

AUTHORS Young, D. and Kearney, J.F.

TITLE Sequence analysis and antigen binding characteristics of Ig SCID

IG+ mice

JOURNAL Int. Immunol. 7 (5), 807-819 (1995)

MEDLINE 96053543

REFERENCE 2 (bases 1 to 318)

AUTHORS Young, D.C.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

COMMENT NCBI gi: 780582

FEATURES

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Location/Qualifiers

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FT GLEWLTHYWDGDKRYNPSLKSLRTISKDTSRNQVFLRITSVDTDATTYYCARRALG

FT S

FT Ty*

SQ Sequence 318 BP; 74 A; 84 C; 79 G; 81 T; 0 other;

Query Match 100.0%; Score 21; DB 12; Length 318;

RESULT 6

LOCUS MMU22991 320 bp mRNA 26-APR-1995

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,

clone 45-24h, partial cds.

ACCESSION U72990

NID g780582

KEYWORDS .

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;

Murinae; Mus.

REFERENCE 1 (bases 1 to 318)

AUTHORS Young, D. and Kearney, J.F.

TITLE Sequence analysis and antigen binding characteristics of Ig SCID

IG+ mice

JOURNAL Int. Immunol. 7 (5), 807-819 (1995)

MEDLINE 96053543

REFERENCE 2 (bases 1 to 318)

AUTHORS Young, D.C.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

COMMENT NCBI gi: 780582

FEATURES

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Location/Qualifiers

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FT GSTY*

BASE COUNT 74 a 84 c 79 g 81 t

ORIGIN

Query Match 100.0%; Score 21; DB 91; Length 318;

Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatggtgtgagc 111

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Qy 1 ACTTCTGGTATGGGTGTGAGC 21

Mar 19 08:21

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7

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clone 45-25h, partial cds.
ACCESSION   U22991
NID         g780584
KEYWORDS    .
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
            Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
            Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonadata;
            Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
            Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 320)
AUTHORS    Young, D.C. and Kearney, J.F.
TITLE      Sequence analysis and antigen binding characteristics of
            immunoglobulins from SCID Ig+ mice
JOURNAL    Int. Immunol. 7 (1995) In press
REFERENCE   2 (bases 1 to 320)
AUTHORS    Young, D.C.
TITLE      Direct Submission
JOURNAL    Submitted (17-MAR-1995) David C. Young, University of Texas Health
            Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
            Houston, TX 77030, USA
FEATURES    source
            Location/Qualifiers
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            /organism="Mus musculus"
            /sub_species="domesticus"
            /cell_type="lymphocyte"
            /tissue type="spleen"
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            /db_xref="PID:g780585"
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BASE COUNT  72 a 86 c 78 g 84 t
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Best Local Similarity 100.0%; Pred. No. 1.35e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 acctctggtatgggtgtgagc 111
|||||
Qy 1 ACTTCTGGTATGGGTGTGACC 21

RESULT 7
LOCUS       MM022991 320 bp mRNA ROD 09-APR-1996
DEFINITION  Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
            clone 45-25h, partial cds.
ACCESSION   U22991
NID         g780584
KEYWORDS    .
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
            Murinae; Mus.
REFERENCE   1 (bases 1 to 320)
AUTHORS    Young, D. and Kearney, J.F.
TITLE      Sequence analysis and antigen binding characteristics of Ig SCID

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Ig+ mice
JOURNAL    Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE    96053543
REFERENCE   2 (bases 1 to 320)
AUTHORS    Young, D.C.
TITLE      Direct Submission
JOURNAL    Submitted (17-MAR-1995) David C. Young, University of Texas Health
            Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
            Houston, TX 77030, USA
COMMENT     NCBI gi: 780584
FEATURES    source
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            /tissue type="spleen"
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            /codon start=1
            /product="immunoglobulin heavy chain"
            /db_xref="PID:g780585"
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            AITY"
BASE COUNT  72 a 86 c 78 g 84 t
ORIGIN
Query Match      100.0%; Score 21; DB 91; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.35e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 acctctggtatgggtgtgagc 111
|||||
Qy 1 ACTTCTGGTATGGGTGTGACC 21

RESULT 8
ID          MM02991 standard; RNA; ROD; 320 BP.
AC          U22991;
DT          29-APR-1995 (Rel. 43, Created)
DT          09-APR-1996 (Rel. 47, Last updated, Version 2)
DE          Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
            DE clone 45-25h, partial cds.
KW          .
OS          Mus musculus (mouse)
OC          Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN          [1]
RP          1-320
RA          Young D., Kearney J.F.;
RT          "Sequence analysis and antigen binding characteristics of Ig SCID
            RT Ig+ mice";
            RL Int. Immunol. 7:807-819(1995).
            RN [2]
            RP 1-320
            RA Young D.C.;
            RT ;
            RL Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.
            RL David C. Young, University of Texas Health Science Center, Houston,
            RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
            CC NCBI gi: 780584
            FH Key Location/Qualifiers

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FT /strain="CB17 SCID"
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FT /tissue_type="spleen"
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FT /db_xref="PID:g780575"
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TYX"
SQ Sequence 320 BP; 72 A; 86 C; 78 G; 84 T; 0 other;

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatgggtgtgagc 111
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Qy 1 ACTTCTGATGGGTGTGAGC 21

RESULT 9
LOCUS MMU22986 326 bp mRNA ROD 09-APR-1996
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-20h, partial cds.
ACCESSION U22986
NID g780574
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE
1 (bases 1 to 326)
Young, D. and Kearney, J.F.
Sequence analysis and antigen binding characteristics of Ig SCID
Igf mice
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
REFERENCE 2 (bases 1 to 326)
Young, D.C.
Direct Submission
AUTHORS David C. Young, University of Texas Health
JOURNAL Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
NCBI gi: 780574
COMMENT Location/Qualifiers
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BASE COUNT 76 a 82 c 81 g 87 t
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actctcgtatgggtgtgagc 111
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Qy 1 ACTTCTGATGGGTGTGAGC 21

RESULT 10
ID MM22986 standard; RNA; ROD; 326 BP.
AC U22986;
DT 29-APR-1995 (Rel. 43, Created)
DT 09-APR-1996 (Rel. 47, Last updated, Version 2)
DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-20h, partial cds.
KW Mus musculus (mouse)
OS Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-326
RA Young D., Kearney J.F.;
RT "Sequence analysis and antigen binding characteristics of Ig SCID
Igf mice";
RL Int. Immunol. 7:807-819(1995).
RN [2]
RP 1-326
RA Young D.C.;
RT ;
RL Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.
RL David C. Young, University of Texas Health Science Center, Houston,
RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
CC NCBI gi: 780574
FH Key Location/Qualifiers
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FT /strain="CB17 SCID"
FT /sub_species="domesticus"
FT /clone="45-20h"
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FT <1..>326
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SQ Sequence 326 BP; 76 A; 82 C; 81 G; 87 T; 0 other;

Query Match 100.0%; Score 21; DB 12; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.35e-03;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actcttgatggtgtgagc 111
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Qy 1 ACTTCTGCTATGGGTGTGAGC 21

RESULT 11

LOCUS MMU22975 330 bp mRNA ROD 09-APR-1996
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-10h, partial cds.

ACCESSION U22975

NID g780552

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.

REFERENCE 1 (bases 1 to 330)

AUTHORS Young, D. and Kearney, J.F.

TITLE Sequence analysis and antigen binding characteristics of Ig SCID
Ig+ mice

JOURNAL Int. Immunol. 7 (5), 807-819 (1995)

MEDLINE 96053543

REFERENCE 2 (bases 1 to 330)

AUTHORS Young, D.C.

Direct Submission

TITLE Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

COMMENT NCBI gi: 780552

FEATURES

source Location/Qualifiers

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/strain="CB17 SCID"

/sub_species="domesticus"

/clone="45-10h"

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/product="immunoglobulin heavy chain"

/db_xref="PID:g780553"

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BASE COUNT 76 a 86 c 81 g 87 t

ORIGIN

Query Match 100.0%; Score 21; DB 91; Length 330;

Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 actcttgatggtgtgagc 111
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RESULT 12

LOCUS MMU22995 353 bp mRNA ROD 26-APR-1995

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-28h, partial cds.

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ACCESSION U22995

NID g780592

KEYWORDS

SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 353)

AUTHORS Young, D.C. and Kearney, J.F.

TITLE Sequence analysis and antigen binding characteristics of

immunoglobulins from SCID Ig+ mice

Int. Immunol. 7 (1995) In press

JOURNAL 2 (bases 1 to 353)

AUTHORS Young, D.C.

Direct Submission

TITLE Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

FEATURES Location/Qualifiers

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BASE COUNT 81 a 96 c 87 g 89 t

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Best Local Similarity 100.0%; Pred. No. 1.35e-03;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 85 actcttgatggtgtgagc 105

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Qy 1 ACTTCTGCTATGGGTGTGAGC 21

RESULT 13

LOCUS MMU22995 353 bp mRNA ROD 09-APR-1996

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-28h, partial cds.

ACCESSION U22995

NID g780592

KEYWORDS

SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.

REFERENCE 1 (bases 1 to 353)

AUTHORS Young, D. and Kearney, J.F.

TITLE Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice

JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
REFERENCE 2 (bases 1 to 353)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

COMMENT NCBI gi: 780592

FEATURES Location/Qualifiers

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FFDYWGQGTTLTVSG"

BASE COUNT 81 a 96 c 87 g 89 t
ORIGIN

Query Match 100.0%; Score 21; DB 91; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.35e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 85 actctgtgtatgggtgtgagc 105
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QY 1 ACTTCTGATGGGTGTGACC 21

RESULT 14
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AC U72995;
DT 29-APR-1995 (Rel. 43, Created)
DT 09-APR-1996 (Rel. 47, Last updated, Version 2)
DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-28h, partial cds.
KW Mus musculus (mouse)
OS Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-353
RA Young D., Kearney J.F.;

RT "Sequence analysis and antigen binding characteristics of Ig SCID
Ig⁺ mice";
RL Int. Immunol. 7:807-819(1995).
RN [2]
RP 1-353
RA Young D.C.;

RT ;
RL Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.
RL David C. Young, University of Texas Health Science Center, Houston,
RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
CC NCBI gi: 780592
FH Key Location/Qualifiers

FT source 1..353
FT /organism="Mus musculus"
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FT /translation="SERVWPDIAVLDPQSDLFFLWVTEHFHWGCELDSSAFRKGS
G
FT VAGTHYWDKRYNPSLKSLRTISKDTSRQVFLKITSVDIADTATYYCARRVLGSSF
F
FT DYYWGQGTTLTVSG"
SQ Sequence 353 BP; 81 A; 96 C; 87 G; 89 T; 0 other;

Query Match 100.0%; Score 21; DB 12; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.35e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 85 actctgtgtatgggtgtgagc 105
|||||
QY 1 ACTTCTGATGGGTGTGACC 21

RESULT 15
LOCUS MMU23000 358 bp mRNA ROD 26-APR-1995
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-32h, partial cds.

ACCESSION U73000

NID g780602

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM

Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 358)
AUTHORS Young, D.C. and Kearney, J.F.
TITLE Sequence analysis and antigen binding characteristics of
immunoglobulins from SCID Ig⁺ mice

JOURNAL Int. Immunol. 7 (1995) In press

REFERENCE 2 (bases 1 to 358)

AUTHORS Young, D.C.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

FEATURES Location/Qualifiers

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/cell_type="lymphocyte"

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/product="immunoglobulin heavy chain"

/db_xref="PID:g780603"

CDS

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15

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BASE COUNT 81 a 95 c 87 g 95 t
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Best Local Similarity 100.0%; Pred. No. 1.35e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 acttcggtatgggtgtgagc 109
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Qy 1 ACTTCTGTATGGGTGTGAGC 21

Search completed: Wed Mar 19 08:23:25 1997
Job time : 56 secs.

MASSIVE (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:24:19 1997; MasPar time 57.38 Seconds
161.419 Million cell updates/sec

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Description: (1-21) from US08612929.seq
Perfect Score: 21
N.A. Sequence: 1 ACTTCTGGTATGGGTGACG 21
Comp: TGAAGACCATACCCACATCG

Scoring table:
Gap 10
TABLE default

Rmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS
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9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
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130:STS52 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7
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161:STS33 162:STS34 163:STS35 164:STS36 165:STS37
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Statistics: Mean 6.550; Variance 1.345; scale 4.869

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	16	76.2	273	148	W09417	ma08f03.r1 Soares mou	1.46e-03	
3	16	76.2	352	132	G08125	human STS CHLC.GATA10	1.46e-03	
4	16	76.2	392	96	R83741	yp16a07.s1 Homo sapie	1.46e-03	
5	16	76.2	402	159	HS154322	zc67f05.s1 Soares fet	1.46e-03	
6	16	76.2	402	146	W02154	zc67f05.s1 Soares fet	1.46e-03	
7	16	76.2	486	83	R42566	yo01dl1.s1 Homo sapie	1.46e-02	
8	15	71.4	313	19	H42722	yo71h05.r1 Homo sapie	2.69e-02	
9	15	71.4	316	5	CELK083A1R	C.elegans cDNA clone	2.69e-02	
10	15	71.4	397	13	H23221	yo52f07.s1 Homo sapie	2.69e-02	
11	15	71.4	431	20	H46104	yo17d06.r1 Homo sapie	2.69e-02	
12	15	71.4	556	16	H32803	EST108258 Rattus sp.	2.69e-02	
13	14	66.7	232	50	H0WGS02742	Human adult lung 3'di	4.37e-01	
14	14	66.7	254	133	G13411	human STS WI-3806.	4.37e-01	
c 15	14	66.7	295	44	HSC3AE011	H. sapiens partial cD	4.37e-01	
c 16	14	66.7	296	104	T03263	FB7B1 Homo sapiens cD	4.37e-01	
c 17	14	66.7	305	44	HSC31F122	H. sapiens partial cD	4.37e-01	
c 18	14	66.7	305	81	R36147	yh92f08.s1 Homo sapie	4.37e-01	
19	14	66.7	342	123	T79663	yd71a12.r1 Homo sapie	4.37e-01	
20	14	66.7	361	21	H50853	yp86d10.r1 Homo sapie	4.37e-01	
21	14	66.7	365	25	H61789	yu39g11.r1 Homo sapie	4.37e-01	
22	14	66.7	371	15	H28742	yp03b02.r1 Homo sapie	4.37e-01	
23	14	66.7	376	117	T59282	yc02c04.r1 Homo sapie	4.37e-01	
24	14	66.7	382	90	R64035	yi19h03.r1 Homo sapie	4.37e-01	
c 25	14	66.7	385	75	R12253	yf33f11.r1 Homo sapie	4.37e-01	
c 26	14	66.7	393	22	H53654	yu38b03.r1 Homo sapie	4.37e-01	
c 27	14	66.7	399	154	W24372	zb50b06.r1 Soares fet	4.37e-01	
c 28	14	66.7	399	161	H5372330	zb50b06.r1 Soares fet	4.37e-01	
29	14	66.7	403	127	T94984	yf38h05.r1 Homo sapie	4.37e-01	
30	14	66.7	421	75	R14317	yf80e06.r1 Homo sapie	4.37e-01	
31	14	66.7	422	25	H62080	yu40b03.r1 Homo sapie	4.37e-01	
32	14	66.7	442	15	H30175	yo58h11.r1 Homo sapie	4.37e-01	
33	14	66.7	446	25	H62101	yu40e07.r1 Homo sapie	4.37e-01	
34	14	66.7	456	25	H62106	yu40f07.r1 Homo sapie	4.37e-01	
35	14	66.7	457	113	T44386	7649 Arabidopsis tha	4.37e-01	
36	14	66.7	458	59	N41612	yw67c02.r1 Homo sapie	4.37e-01	
c 37	14	66.7	466	29	H76545	18250 Arabidopsis tha	4.37e-01	
c 38	14	66.7	467	172	OS37943	Oryza sativa clone pF	4.37e-01	
39	14	66.7	477	21	H49110	yo21c06.r1 Homo sapie	4.37e-01	
40	14	66.7	508	19	H44369	yp18e11.r1 Homo sapie	4.37e-01	
c 41	14	66.7	524	121	T74507	yc83b01.r1 Homo sapie	4.37e-01	
42	14	66.7	537	20	H45847	yp22c02.r1 Homo sapie	4.37e-01	

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3

43 14 66.7 537 107 T21646 3654 Arabidopsis thal 4.37e-01
 44 14 66.7 589 147 W04275 za49a10.r1 Soares fet 4.37e-01
 45 14 66.7 589 168 H5W04275 za49a10.r1 Soares fet 4.37e-01

ALIGNMENTS

RESULT 1
 ID MM4172 standard; RNA; EST; 273 BP.
 AC W09417;
 DT 29-APR-1996 (Rel. 47, Created)
 DT 29-APR-1996 (Rel. 47, Last updated, Version 1)
 DE ma08f03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA 5' .
 KW EST.
 OS Mus musculus (mouse)
 OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 RN {}
 RP 1-273
 RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
 RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
 RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
 RA Moore B., Theising B., Wyllie T., Lennon G., Soares B., Wilson R.,
 RA Waterston R.;
 RT "The WashU-HHMI Mouse EST Project";
 RL Unpublished.
 CC Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
 CC Washington University School of Medicine 4444 Forest Park Parkway,
 CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
 CC Email: mouseest@wustl.edu This clone is available
 CC royalty-free through LNL ; contact the IMAGE Consortium
 CC (info@image.llnl.gov) for further information. Seq primer:
 CC mob.REGA+ET High quality sequence stop: 261. NCBI gi: 1283734
 FH Key Location/Qualifiers
 FT 1..273
 FT /organism="Mus musculus"
 FT /note="Vector: pT73D (Pharmacia) with a modified
 FT polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 FT was primed with a Not I - oligo(dT) primer [5'
 FT TCTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'] ,
 FT double-stranded cDNA was size selected, ligated to Eco RI
 FT adapters (Pharmacia), digested with Not I and cloned into
 FT the Not I and Eco RI sites of a modified pT73 vector
 FT (Pharmacia). Library went through one round of
 FT normalization to a Cot = 5. Library constructed by Bento
 FT Soares and M.Fatima Bonaldo."
 FT /clone lib="Soares mouse p3NMF19.5"
 FT /dev stage="19 weeks"
 FT /lab_host="DH10B (ampicillin resistant)"
 FT <1..>273
 FT mRNA
 FT Sequence 273 BP; 81 A; 60 C; 73 G; 59 T; 0 other;

Query Match 76.2%; Score 16; DB 170; Length 273;
 Best Local Similarity 94.4%; Pred. No. 1.46e-03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 126 tctggatgggtgagc 143
 ||||| ||||| |||||
 QY 4 TCTGGTATGGGTGTGAGC 21

RESULT 2
 LOCUS W09417 273 bp mRNA EST 26-APR-1996

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DEFINITION ma08f03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA 5' .
 ACCESSION W09417
 NID g1283734
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
 Murinae; Mus.
 REFERENCE 1 (bases 1 to 273)
 AUTHORS Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
 Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
 Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
 Theising B., Wyllie T., Lennon G., Soares B., Wilson R. and
 Waterston R.
 TITLE The WashU-HHMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT

Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: mob.REGA+ET
 High quality sequence stop: 261.

NCBI gi: 1283734
 Location/Qualifiers
 1..273
 /organism="Mus musculus"
 /note="Vector: pT73D (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TCTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'] ,
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo."
 /clone lib="Soares mouse p3NMF19.5"
 /dev stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 <1..>273
 BASE COUNT 81 a 60 c 73 g 59 t
 ORIGIN

Query Match 76.2%; Score 16; DB 148; Length 273;
 Best Local Similarity 94.4%; Pred. No. 1.46e-03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 126 tctggatgggtgagc 143
 ||||| ||||| |||||
 QY 4 TCTGGTATGGGTGTGAGC 21

RESULT 3
 LOCUS G08125 352 bp DNA STS 08-AUG-1995
 DEFINITION human STS CHLC.GATA10H05.P7044 clone GATA10H05.
 ACCESSION G08125

9938675
NID
KEYWORDS
STS sequence; primer; sequence tagged site.
human vector=pcp1 host=E.coli dut+ung+ (DH10B) Marker Selected
genomic DNA prepared from XY individual of French nationality.
ORGANISM
Homo Sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominoidea; Homo.
1 (bases 1 to 352)
Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.
Cooperative Human Linkage Center
Unpublished (1995)
Synonyms: GATA10H05, CHLC.GATA10H05.#P7043
Contact: Dr. Jeffrey C. Murray
UofI
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu
Primer A: CCTAAATTGTGAGAAATCTTTTATC
Primer B: TTTTCTAGACTACCCCTTACC
STS size: 216
PCR Profile:

denature:	30 seconds at 94 degrees C
annealing:	75 seconds at 55 degrees C
extension:	15 seconds at 72 degrees C
PCR cycles:	27
extension:	6 minutes at 72 degrees C
Protocol:	
Template:	30ng genomic DNA
Primer:	each 1.5 pmole
dNTPs:	each 200 uM
Taq Polymerase:	0.3 units
Total Vol:	10 ul

```

Buffer:
MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3.
Location/Qualifiers
1..352
/organism="Homo Sapiens"
/note="human"

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FEATURES
  source      Location/Qualifiers
              1..352
                /organism="Homo Sapiens"
                /note="human"
  STS
    primer_bind  2..217
    primer_bind  2..217
    complement(195..217)
  BASE_COUNT    109 a 47 c 65 g 128 t 3 others
  ORIGIN
    Query Match      76.2%; Score 16; DB 132; Length 35
    Best Local Similarity 94.4%; Pred. No. 1.46e-03;
    Matches 17; Conservative 0; Mismatches 1; Indels

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Query Match 76.2%; Score 16; DB 132; Length 352;
Best Local Similarity 94.4%; Pred. No. 1.46e-03;
Matches 17; Conservative 0; Mismatches 1; Indels

Db 327 ttcaggtatgggtgtgag 344
 ||| |||||
QY 3 TTCTGGTATCGGTGTGAG 20

QY 3 TTCTGGTATGGGTGTGAC 20

RESULT	4	R83741	392 bp	mRNA	EST	04-AUG-1995
LOCUS						

DEFINITION	human clone=187572 library=Soares breast 3NbHbSt vector=pT7T3D (Pharmacia) with a modified polylinker host=DRI0B (ampicillin resistant) primer=T3 Reitel=Not I Reite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACAACTCAGATGGAGCGGCCCTTTTCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.
ACCESSION	Y16A07.s1 Homo sapiens cDNA clone 187572 3'.
NID	R83741
KEYWORDS	g928618
SOURCE	EST.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 392)

REFERENCE 1 (bases 1 to 392)

AUTHORS
 Hillier, L., Clark, N., Dubucq, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
TITLE
 The WashU-Merck EST Project
JOURNAL
 Unpublished (1995)

TITLE	COMMENT
The WashU-Merck EST Project	
Unpublished (1995)	

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence stops: 319
Source: IMAGE Consortium LINL

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

```

FEATURES
  Location/Qualifiers
    1..392
      /organism="Homo sapiens"
      /clone="187572"
      /note="human"

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BASE COUNT	87 a	96 c	101 g	101 t	7 others
ORIGIN					
Query Match		76.2%	Score 16;	DB 96;	Length 392;
Best local Similarity		90.0%;	Pred. 1.46e-03;		
Matches	18:	Conservative	0:	Mismatches	2: Indels
					Gaps 0:

Db 254 cttctgatatggatgtgagc 273
||||| ||||| |||||
Qv 2 CTTCTGTATGGGTGTGACC 21

RESULT	5
ID	HS154322
AC	W02154;
	standard; RNA; EST; 402 BP.

DT 25-APR-1996 (Rel. 47, Created)
DT 25-APR-1996 (Rel. 47, Last updated, Version 1)
DE zc67f05.sl Soares fetal heart NBHH19W Homo sapi
DE 327393 3'.
KW EST.

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411 Japan

Phone: 0559-81-6854

Fax : 0559-81-6855

Email: ykohara@dbj.nig.ac.jp.

Location/Qualifiers

1..316

/organism="Caenorhabditis elegans"

/strain="N2"

/dev_stage="embryo"

/sequenced_mol="cDNA to mRNA"

/sex="Hermaphrodite"

/tissue_type="embryo"

/clone_lib="Yuji Kohara unpublished cDNA"

120 a 45 c 49 g 97 t 5 others

ORIGIN

Query Match 71.4%; Score 15; DB 5; Length 316;

Best Local Similarity 84.2%; Pred. No. 2.69e-02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 282 ttctgntgntgttgac 300

||||| t t t t t t t t

Qy 3 TTCTGGTATGGTGTGAC 21

RESULT 10

LOCUS H23221 397 bp mRNA EST 06-JUL-1995

DEFINITION ym52107.s1 Homo sapiens cDNA clone 51884 3'.

ACCESSION H23221

NID g891916

KEYWORDS EST.

SOURCE human clones-51884 library=Soares infant brain IN1B vector=Iafmid BA host=DH10B (ampicillin resistant) primer=Promega -2lm13 Rsite1=Not I Rsite2=Hind III Whole brain from a 73 days post natal female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAGAAATTCGCGCCGACGAGAAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Iafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Choanata; Tetrápoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 397)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson.R.

The WashU-Merck EST Project

Unpublished (1995)

GDB: G00-424-820

Contact: Wilson RK

WashU-Merck EST Project

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Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 353

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Source: IMAGE Consortium, L1NL

This clone is available royalty-free through L1NL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

Location/Qualifiers

1..397

/organism="Homo sapiens"

/clone="51884"

/note="human"

BASE COUNT 96 a 85 c 88 g 121 t 7 others

ORIGIN

Query Match 71.4%; Score 15; DB 13; Length 397;

Best Local Similarity 85.0%; Pred. No. 2.69e-02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 307 ctctgatatggtgtgac 326

||||| t t t t t t t t

Qy 2 CTCTGGTATGGTGTGAC 21

RESULT 11

LOCUS H46104 431 bp mRNA EST 31-JUL-1995

DEFINITION y017d06.r1 Homo sapiens cDNA clone 178187 5'.

ACCESSION H46104

NID g922156

KEYWORDS EST.

SOURCE Homo sapiens clone=178187 library=Soares adult brain N2b5HB55Y vector=pf7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI 55-year old male. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATTCGAGTGGAGCGCGCGCTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Choanata; Tetrápoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 431)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

The WashU-Merck EST Project

Unpublished (1995)

JOURNAL

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

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Tel: 314 286 1800

Fax: 314 286 1810

Mar 19:08:23

US-08-612-929-21.rst

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Email: est@watson.wustl.edu
High quality sequence stops: 238
Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL; contact the
IMAGE Consortium (info@image.l1nl.gov) for further information.

FEATURES

source

1..431
/organism="Homo sapiens"
/clone="178187"

BASE COUNT 106 a 104 c 101 g 116 t 4 others

ORIGIN

Query Match 71.4%; Score 15; DB 20; Length 431;
Best Local Similarity 85.7%; Pred. No. 2.69e-02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 364 actgcggcatgggtgtgggc 384

Qy 1 ACTTCTGGTATGGGTGTGAGC 21

RESULT 12

LOCUS H32803 556 bp mRNA EST 08-SEP-1995

DEFINITION EST108258 Rattus sp. cDNA 5' end.

ACCESSION H32803

NID g978220

KEYWORDS EST.

SOURCE

rat primer=M13 Reverse library=Rat PC-12 cells, untreated
vector=phuescript SK- RsaI=I-EcoRI RsaI=2-XhoI poly(A)+ RNA was
purified from untreated PC12 cells cultured for 9 days. cDNA was
constructed using an oligo-dT primer and directionally cloned using
the Lambda ZAP II Vector Kit by Stratagene.

ORGANISM

Rattus sp.
Eukaryota; Eukaryotes; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha;
Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 556)
Lee,N.H., Weinstock,K.G., Kirkness,E.F., Earle-Hughes,J.A.,
Fuldner,R.A., Marmaras,S., Glodek,A., Gocayne,J.D., Adams,M.D.,
Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
Comparative expressed sequence tag analysis of differential gene
expression profiles in PC-12 cells before and after nerve growth
factor treatment

JOURNAL Proc. Natl. Acad. Sci. USA 92, 8303-8307 (1995)

COMMENT

Contact: Lee NH
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: nhlee@tigr.org

For clone availability please contact the TIGR Database
(tdbinfo@tdb.tigr.org).

FEATURES

source

1..556
/organism="Rattus sp."
/note="rat"

BASE COUNT 128 a 134 c 150 g 140 t 4 others

ORIGIN

Query Match 71.4%; Score 15; DB 16; Length 556;
Best Local Similarity 85.0%; Pred. No. 2.69e-02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Mar 19:08:23

US-08-612-929-21.rst

14

Db 469 acatcgmtatgggtgtgag 488

Qy 1 ACTTCTGGTATGGGTGTGAG 20

RESULT 13

LOCUS HUMGS02742 232 bp mRNA EST 20-FEB-1995

DEFINITION Human adult lung 3'directed MboI cDNA, HUMGS02742, clone lq0864.

ACCESSION D45555

NID g662509

KEYWORDS EST(expressed sequence tag); gene signature(GS); lung.

SOURCE Homo sapiens (library: Human adult lung 3'directed MboI cDNA) Adult

Lung cDNA to mRNA.

ORGANISM

Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Homiidae.

REFERENCE

1 (bases 1 to 232)

AUTHORS Kohichi Ito, Kousaku O., Junji Y., Hideoki Y. and Kenichi M.

TITLE An expression profile of active genes in human lung

JOURNAL DNA Research 1, 279-287 (1994)

COMMENT

PROJECT = 'bodymapping'

Submitted (02-FEB-1995) to DDBJ by:

Kohichi Itoh

Institute for Molecular and Cellular Biology

Osaka University

3-1, Yamadaoka

Suita, Osaka, 565

Japan

Phone: 06-877-5111 x3910

Fax : 06-877-1922.

Location/Qualifiers

1..232

/organism="Homo sapiens"

/dev_stage="Adult"

/sequenced_mol="cDNA to mRNA"

/tissue_type="lung"

/clone_lib="Human adult lung 3'directed MboI cDNA"

BASE COUNT 49 a 63 c 64 g 56 t

ORIGIN

Query Match 66.7%; Score 14; DB 50; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.37e-01;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 174 gtatgggtgtgagc 187

Qy 8 GTATGGGTGTGAGC 21

RESULT 14

LOCUS G13411 254 bp DNA STS 20-DEC-1995

DEFINITION human STS WI-3806.

ACCESSION G13411

NID g1127520

KEYWORDS STS sequence; primer; sequence tagged site.

SOURCE human STSs derived from random genomic DNA.

ORGANISM

Homo sapiens
Eukaryota; Eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 254)

AUTHORS Hudson,T.

Mar 19 08:23

US-08-612-929-21.rst

15

TITLE Whitehead Institute/MIT Center for Genome Research; Physically

JOURNAL Mapped STSs
COMMENT Unpublished (1995)

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TACTCTGGAATGGGTGTGG
Primer B: CTTCGTCTTTCATGCAGAA
STS size: 200
PCR Profile:

Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
Protocol:

Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 mM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

Random genome wide STS.

FEATURES
source Location/Qualifiers
1..254
/organism="Homo sapiens"
/note="human"

STS
52..251
/map="373.9 cR from top of Chr11 linkage group"
primer_bind 52..71
/map="373.9 cR from top of Chr11 linkage group"
primer_bind complement(230..251)
/map="373.9 cR from top of Chr11 linkage group"

BASE COUNT 81 a 50 c 55 g 68 t
ORIGIN

Query Match 66.7%; Score 14; DB 133; Length 254;
Best Local Similarity 88.9%; Pred. No. 4.37e-01;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 53 acctctggaatgggtgtg 70
|| ||||| |||||
Qy 1 ACTTCTGCTATGGGTGTC 18

RESULT 15

LOCUS HSC3AE011 295 bp RNA EST 21-SEP-1995
DEFINITION H. sapiens partial cDNA sequence; clone c-3ae01.
ACCESSION F12473
NTD g708465
KEYWORDS partial cDNA sequence; transcribed sequence fragment.

Mar 19 08:23

US-08-612-929-21.rst

16

SOURCE human.

ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 295)
AUTHORS Genexpress.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France
and Genetique Moleculaire et Biologie du developpement, CNRS UPR420
B.P. 8, 94801 Villejuif Cedex France. E-mail:
genexpress@genethon.fr

REFERENCE 2 (bases 1 to 295)

AUTHORS Genexpress.
TITLE The Genexpress cDNA program
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 295)

AUTHORS Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,
Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B.,
Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,
Sebastiani-Kabaktchis, C. and Tessier, A.

TITLE IMAGE: molecular integration of the analysis of the human genome
and its expression
JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE 95277534

COMMENT Cloning method: total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the laimid BA
vector;

Sequencing method: single read, full automatic;

Primer: M13 reverse

cDNA sequence colinear to mRNA

Stretch removed: nothing

Normalization method: Bento Soares, P.N.A.S. 91:9228-9232 (1994);

Genexpress library_id: G;

Genexpress_sequence_id: y1c-3ae01.

FEATURES
Location/Qualifiers

source

1..295
/organism="Homo sapiens"
/isolate="muscular atrophy patient"
/clone_lib="normalized infant brain cDNA from B.Souares,
Psychiatry Dept. Columbia University USA"
/sex="female"
/tissue_type="total brain"
/dev_stage="3 months old"

BASE COUNT 104 a 71 c 56 g 62 t 2 others
ORIGIN

Query Match 66.7%; Score 14; DB 44; Length 295;
Best Local Similarity 93.8%; Pred. No. 4.37e-01;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 33 cacacccacaccagaa 48
||||| |||||

Cp 18 CACACCCATACCAGAA 3

Search completed: Wed Mar 19 08:25:25 1997
Job time : 66 secs.

WATERMAN

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:23:44 1997; MasPar time 10.31 Seconds
177.715 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-21
Description: (1-21) from US08612929.seq
Perfect Score: 21
N.A. Sequence: 1 ACTCTGCTATGGGTGAGC 21
Comp: TGAAGACCATACCCACATCG

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0\$
Listing first 45 summaries

Database: n-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.273; Variance 3.101; scale 1.700

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.
1	21	100.0	423 14	Q83492 Chimeric antibody 3B9	5.62e-03
2	21	100.0	483 14	Q83491 Mouse MAb 3B9 heavy c	5.62e-03
3	21	100.0	738 12	Q70612 IL-6 binding inhibito	5.62e-03
c	4	20	95.2	91 9 Q51746 Oligonucleotide probe	2.11e-02
5	19	90.5	366 11	Q68709 Humanised MAb H-chain	7.80e-02
6	17	81.0	45 4	Q24650 PCR Primer C for ampl	9.99e-01
7	17	81.0	139 4	Q24653 Fragment CD of HUMDXC	9.99e-01
8	17	81.0	207 4	Q24652 Fragment AB of HUMDXC	9.99e-01

9	17	81.0	265 4	Q24654 Fragment AD of HUMDXC	9.99e-01
10	17	81.0	360 19	T09300 Murine anti-Protein C	9.99e-01
11	17	81.0	417 19	T09299 Murine anti-Protein C	9.99e-01
12	16	76.2	429 11	Q64166 Sequence of mouse VH	3.45e+00
13	16	76.2	630 13	Q78948 Human immunoglobulin	3.45e+00
14	15	71.4	812 6	Q37056 Rat immunoglobulin H	1.16e+01
15	15	71.4	2352 1	Q04729 Xylene oxygenase gene	1.16e+01
c	16	14	66.7	25 10 Q56540 Nucleic acid detectio	3.76e+01
c	17	14	66.7	25 10 Q57121 Chromosomal transloc	3.76e+01
c	18	14	66.7	232 19 T21378 Human gene signature	3.76e+01
c	19	14	66.7	789 6 Q36376 NDP kinase gene.	3.76e+01
c	20	14	66.7	1159 7 Q40592 JSC1 precursor DNA.	3.76e+01
c	21	14	66.7	1422 16 Q95109 Human papillomavirus	3.76e+01
c	22	14	66.7	1564 21 T36701 Plasmid pNHK101.	3.76e+01
c	23	14	66.7	1650 13 Q74684 Early Ripening Tomato	3.76e+01
c	24	14	66.7	2438 1 N80408 Plasmid pRAJ220 iner	3.76e+01
c	25	14	66.7	2457 1 N81451 Sequence encoding fus	3.76e+01
c	26	14	66.7	2476 21 T18377 Plasmid pMKH1.	3.76e+01
c	27	14	66.7	2511 1 N92113 Polynucleotide encodi	3.76e+01
c	28	14	66.7	2673 1 N81449 Sequence encoding fus	3.76e+01
c	29	14	66.7	4284 12 Q74259 Stress-induced tobacc	3.76e+01
c	30	14	66.7	5406 1 N93197 Fragment of clone lam	3.76e+01
c	31	14	66.7	5642 8 Q51193 pDE4; plasmid DNA rep	3.76e+01
c	32	14	66.7	7050 7 Q40419 Sequence of pTE4.	3.76e+01
c	33	13	61.9	43 9 Q50622 Canine coronavirus 1-	1.18e+02
c	34	13	61.9	97 21 T24468 Human gene signature	1.18e+02
c	35	13	61.9	370 20 T21289 Human gene signature	1.18e+02
c	36	13	61.9	382 8 Q59352 Human brain Expressed	1.18e+02
c	37	13	61.9	1191 14 Q85439 FCV DNA insert of clo	1.18e+02
c	38	13	61.9	2246 4 Q25541 Consensus sequence fo	1.18e+02
c	39	13	61.9	4074 20 T13950 B. thuringiensis VIP2	1.18e+02
c	40	13	61.9	4359 9 Q52447 Canine coronavirus 1-	1.18e+02
c	41	13	61.9	4365 4 Q25536 S gene of TS FIPV.	1.18e+02
c	42	13	61.9	4565 1 Q03704 Gene encoding plant e	1.18e+02
c	43	13	61.9	4669 9 Q52726 Sequence of human mul	1.18e+02
c	44	13	61.9	4800 4 N81533 Sequence of the peplo	1.18e+02
c	45	13	61.9	6785 3 Q20065 Plasmid pAZ112.	1.18e+02

ALIGNMENTS

RESULT 1
ID Q83492 standard; cDNA; 423 BP.
AC Q83492;
DT 20-SEP-1995 (first entry)
DE Chimeric antibody 3B9 heavy chain.
KW Chimeric antibody; antibody engineering; monoclonal antibody;
KW MAb; interleukin-4; IL-4; allergy; ds.
OS Homo sapiens; Mus sp.
FH Key Location/Qualifiers
FT CDS 1..423
FT /*tag= a
FT sig_peptide 1..57
FT /*tag= b
FT mat_peptide 58..423
FT /*tag= c
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;

DR WPI1; 95-123387/16.
DR P-PSDB; R70191.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions
PS Disclosure; Fig.3; 9/pp; English.
CC A human/mouse chimeric antibody heavy chain variable region was constructed (given in R70191) that contained the mouse anti-human IL-4 MAb 3B9 variable region including 3 CDRs (R70198-200) and a CC human antibody signal peptide (R70193). The construct was used CC for humanized antibody production.
SQ Sequence 423 BP; 87 A; 115 C; 110 G; 111 T;

Query Match 100.0%; Score 21; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 5.62e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 151 actctggtatgggtgtgagc 171
|||||
Qy 1 ACTTCTGATGGGTGTGAGC 21

RESULT 2
ID Q83491 standard; cDNA; 483 BP.
AC Q83491;
DT 20-SEP-1995 (first entry)
DE Mouse MAb 3B9 heavy chain.
KW Monoclonal antibody; humanized antibody; antibody engineering;
KW Monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 64..483
FT /*tag= a
FT sig_peptide 64..120
FT /*tag= b
FT mat_peptide 121..483
FT /*tag= c
PN W09507301-A.
PD 16-MAR-1995.
PE 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI1; 95-123387/16.
DR P-PSDB; R70190.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions
PS Disclosure; Fig.2; 9/pp; English.
CC Spleen cells from mice immunized with human IL-4 were used to prepare CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy CC chains were cloned into pGEM7f+ and transformed into E. coli CC DH5-alpha. The clones were sequenced (Q83490-91), and used for CC antibody engineering.
SQ Sequence 483 BP; 108 A; 130 C; 124 G; 121 T;

Query Match 100.0%; Score 21; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 5.62e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 211 actctggtatgggtgtgagc 231

Qy 1 ACTTCTGATGGGTGTGAGC 21
|||||
RESULT 3
ID Q70612 standard; DNA; 738 BP.
AC Q70612;
DT 28-APR-1995 (first entry)
DE IL-6 binding inhibitor DNA.
KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
KW septic shock; multiple myeloma; ss.
OS Homo sapiens.
PN EP-617126-A.
PD 28-SEP-1994.
PF 16-FEB-1994; 102346.
PR 17-FEB-1993; JP-028173.
PA (AJIN) AJINOMOTO KK.
PI Hamuro J, Nakazawa H, Shimamura T;
DR WPI1; 94-295777/37.
DR P-PSDB; R58612.
PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to PT its receptor - useful for treating auto:immune disease induced PT or aggravated by IL-6
PS Claim 9; Page 19; 26pp; English.
CC Q70612 codes for human interleukin-6 binding inhibitor, the CC polypeptide described in R58612. This polypeptide inhibits the CC binding of human IL-6 to its receptor, and can therefore be CC useful in the treatment of a variety of autoimmune diseases;
CC specifically in the treatment of rheumatoid arthritis, septic CC shock due to bacterial infection and multiple myeloma.
SQ Sequence 738 BP; 187 A; 189 C; 180 G; 182 T;

Query Match 100.0%; Score 21; DB 12; Length 738;
Best Local Similarity 100.0%; Pred. No. 5.62e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 457 actctggtatgggtgtgagc 477
|||||
Qy 1 ACTTCTGATGGGTGTGAGC 21

RESULT 4
ID Q51746 standard; cDNA; 91 BP.
AC Q51746;
DT 31-MAY-1994 (first entry)
DE Oligonucleotide probe MK14-A
KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
KW ss.
OS Synthetic.
PN EP-571911-A.
PD 01-DEC-1993.
PF 24-MAY-1993; 108325.
PR 26-MAY-1992; US-889651.
PA (BECT) BECTON DICKINSON CO.
PI Shank DD, Spears PA;
DR WPI1; 93-378844/48.
PT New oligo:nucleotide probes specific for Mycobacteria - used for PT detection and amplification of Mycobacteria nucleic acid in PT samples
PS Claim 3; Page 14; 23pp; English.
CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 CC (Q51735). It hybridized to all spp. of mycobacteria tested, but CC cross reacted to a few non-mycobacterial spp. The probe may CC be useful as an initial screen for mycobacterial infection.


```

CC See also Q51735-45 and Q51747-59.
SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 95.2%; Score 20; DB 9; Length 91;
Best Local Similarity 0.0%; Pred.No. 2.11e-02;
Matches 0; Conservative 20; Mismatches 0; Indels 0; Gaps 0;

Db 22 vshhsvhvhhvvhvsvvv 41
      ::::~::~~::::~:::
Cp 21 GCTCACACCATACCAGGAG 2

RESULT 5
ID Q68709 standard; cDNA to mRNA; 366 BP.
AC Q68709;
DT 08-FEB-1995 (first entry)
DE Humanised MAb H-chain coding sequence.
KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
KW complementarity determining region; CDR; IgG; kappa; IIGB; IIIMN; ds.
OS Chimeric - Mus musculus.
PN J06141885-A.
PD 24-MAY-1994.
PF 05-NOV-1992; 322476.
PR 05-NOV-1992; JP-322476.
PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
DR WPI; 94-205040/25.
PT P-P5DB; R54101.
PT Recombinant anti-HIV monoclonal antibody - capable of
PT neutralising strains which can not be neutralised by anti-IIIB
PS PT and IIIMN antibodies
PS Disclosure; Page 13; 23pp; Japanese.
CC The sequences given in Q68709-10 encode the heavy and light chains
CC respectively of the humanised monoclonal antibody (MAB) of the
CC invention. The antibody has the ability to neutralise human
CC immunodeficiency virus. The antibody is classified as IgG kappa and
CC has the sequence RTGPCR or RVGPCR in the principal neutralising
CC domain. The antibody may be used to neutralise the clinically
CC separate strains which cannot be neutralised by the neutralising
CC antibodies against IIIB and IIIMN strains.
SQ Sequence 366 BP; 85 A; 98 C; 84 G; 99 T;

Query Match 90.5%; Score 19; DB 11; Length 366;
Best Local Similarity 95.2%; Pred.No. 7.80e-02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 91 acttttggtggtgtgcac 111
      ||||| |~~~~~|~~~~~|
Qy 1 ACTTCTGGTAGCGGTGAGC 21

RESULT 6
ID Q24650 standard; DNA; 45 BP.
AC Q24650;
DT 10-NOV-1992 (first entry)
DE PCR Primer C for amplifying HUMDXCH.23.
KW Polymerase chain reaction; CAMPATH-1H; rat anti-digoxin MAb; DX48;
KW human IgG1 heavy chain; humanised antibody; PCR grafting; ss.
OS Synthetic.
PN W09207075-A.
PD 30-APR-1992.
PF 08-OCT-1991; G01744.
PR 10-OCT-1990; GB-022011.
PA (WELL ) WELLCOME FOUND LTD.

```

PI Crowe JS, Lewis AP;
WPI; 92-167155/20.

PT Prepn. of chimeric humanised antibodies - using a new polymerase
chain reaction technique

PS Example 1; Page 33; 67pp; English.

CC Primer C is made up of the positive strand sequence of DX48 CDRH1,
complementary to the CDRH1 region of primer B (Q24649), running
into the 5' end of the CAMPATH-1H FRH2. Primer C was used with
Primer D (Q24651) to PCR-amplify fragment CD (Q24653) of HUMDXCH.23
which contains the DX48 CDRH1 sequence. A second fragment (AB) was
generated from the same template, but using primers A and B
(Q24648-9), which also contained the DX48 CDRH1 sequence such that
on denaturation and reannealing the overlapping sequences of AB and
CD can anneal.

SQ Sequence 45 BP; 9 A; 8 C; 18 G; 10 T;

Query Match 81.0%; Score 17; DB 4; Length 45;
Best Local Similarity 90.5%; Pred. No. 9.99e-01;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 acttatgtatgggtcgtgggc 21
|||||
Qy 1 ACTTCTGGTATGGGTGAGC 21

RESULT 7

ID Q24653 standard; DNA; 139 BP.

AC Q24653; 10-NOV-1992 (first entry)

DE Fragment CD of HUMDXCH.23 humanised antibody.

KW Polymerase chain reaction; CAMPATH-1H; rat anti-digoxin Mab; DX48;

KW human IgG1 heavy chain; humanised antibody; PCR grafting; ds.

OS Synthetic.

FT Key Location/Qualifiers

FT misc_feature 1..48

FT /*tag= a

FT /*note= "DX48 CDRH1"

FT misc_feature 49..108

FT /*tag= b

FT /*note= "represents insert of 117bp"

FT misc_feature 109..139

FT /*tag= c

FT /*note= "3' terminus of CAMPATH-H1 CH3"

PN W09207075-A.

PD 30-APR-1992.

PD 08-OCT-1991; G01744.

PR 10-OCT-1990; GB-022011.

PA (WELL) WELLCOME FOUND LTD.

PI Crowe JS, Lewis AP;

DR WPI; 92-167155/20.

PT Prepn. of chimeric humanised antibodies - using a new polymerase
chain reaction technique

PS Example 1; Page 36; 67pp; English.

CC Fragment CD was generated by PCR using the humanised antibody
HUMDXCH.23 as template (see Q29298). Primers C and D were used
in the PCR reaction; Primer C is made up of the positive strand
sequence of DX48 CDRH1, complementary to the CDRH1 region of
primer B (Q24649), running into the 5' end of the CAMPATH-1H FRH2
and Primer D corresponds to a negative strand oligonucleotide
incorporating the HindIII site at the 3' terminus of HUMDXCH.23.

CC Fragment CD overlaps with fragment AB (Q24652) and the two
fragments were annealed to form a template for secondary PCR.

SQ Sequence 139 BP; 17 A; 14 C; 31 G; 17 T;

Query Match 81.0%; Score 17; DB 4; Length 139;
 Best Local Similarity 90.5%; Pred. No. 9,99e-01;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 acttatggtatgggtgtgggc 21
 |||| ||||||||||||| ||
 Qy 1 ACTTCTGGTATGGGTGTGAGC 21

RESULT 8

ID Q24652 standard; DNA; 207 BP.
 AC Q24652;
 DT 10-NOV-1992 (first entry)
 DE Fragment AB of HUMDXCH.23 humanised antibody.
 KW Polymerase chain reaction; CAMPATH-1H; rat anti-digoxin MAb; DX48;
 KW human IgG1 heavy chain; humanised antibody; PCR grafting; ds.
 OS Synthetic.

FH Key Location/Qualifiers
 FT misc_feature 1..42
 FT /*tag= a
 FT /note= "5' end of HUMDXCH.23, including start codon"
 FT of CAMPATH-1H leader sequence"
 FT misc_feature 160..186
 FT /*tag= b
 FT /note= "3' 27bp of CAMPATH-1H FRH1"
 FT misc_feature 187..207
 FT /*tag= c
 FT /note= "DX48 CDRH1 sequence"
 PN W09207075-A.

PD 30-APR-1992.
 PF 08-OCT-1991; G01744.
 PR 10-OCT-1990; GB-022011.
 PA (WELL) WELLCOME FOUND LTD.
 PI Crowe JS, Lewis AP;
 DR WPI; 92-167155/20.
 PT Prepn. of chimeric humanised antibodies - using a new polymerase
 PT chain reaction technique
 PS Example 1; Page 34 and Fig 2; 67pp; English.
 CC Fragment AB was generated by PCR using the humanised antibody
 CC HUMDXCH.23 as template (see Q29298). Primers A and B were used
 CC in the PCR reaction; Primer A corresponds to a positive strand
 CC of HUMDXCH.23 and Primer B possesses negative strand sequence from
 CC oligonucleotide incorporating the HindIII site at the 5' terminus
 CC the 3' end of the CAMPATH-1H FRH1 region (with point mutations to
 CC convert Phe 27 and Thr 30 of CAMPATH-1H back to the Ser residues
 CC present in the NEW FRH1) together with the CDRH1 sequence of DX48
 CC in place of the CAMPATH-1H CDRH1. Fragment AB overlaps with
 CC fragment CD (Q24653) and the two fragments were annealed to form a
 CC template for secondary PCR.
 SQ Sequence 207 BP; 20 A; 24 C; 24 G; 22 T;

Query Match 81.0%; Score 17; DB 4; Length 207;
 Best Local Similarity 90.5%; Pred. No. 9,99e-01;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 187 acttatggtatgggtgtgggc 207
 |||| ||||||||||||| ||
 Qy 1 ACTTCTGGTATGGGTGTGAGC 21

RESULT 9

ID Q24654 standard; DNA; 265 BP.
 AC Q24654;
 DT 10-NOV-1992 (first entry)

DE Fragment AD of HUMDXCH.23 humanised antibody.
 KW Polymerase chain reaction; CAMPATH-1H; rat anti-digoxin MAb; DX48;
 KW human IgG1 heavy chain; humanised antibody; PCR grafting; ss.
 OS Synthetic.

FH Key Location/Qualifiers
 FT misc_feature 1..42
 FT /*tag= a
 FT /note= "5' end of HUMDXCH.23, including start codon"
 FT of CAMPATH-1H leader sequence"
 FT misc_feature 43..102
 FT /*tag= b
 FT /note= "represents 117bp insert"

FT misc_feature 103..129
 FT /*tag= c
 FT /note= "3' 27bp of CAMPATH-1H FRH1 in which
 FT point mutations convert Phe 27 and Thr 30
 FT of CAMPATH-1H back to the Ser residues
 FT present in NEW FRH1"
 FT misc_feature 130..150
 FT /*tag= d
 FT /note= "DX48 CDRH1"

FT misc_feature 151..174
 FT /*tag= e
 FT /note= "CAMPATH-1H FRH2"
 FT misc_feature 175..234
 FT /*tag= f
 FT /note= "represents insert of 1206bp"
 FT misc_feature 235..265
 FT /*tag= g
 FT /note= "3' terminus of CAMPATH-1H CH3"
 PN W09207075-A.
 PD 30-APR-1992.
 PF 08-OCT-1991; G01744.
 PR 10-OCT-1990; GB-022011.
 PA (WELL) WELLCOME FOUND LTD.
 PI Crowe JS, Lewis AP;
 DR WPI; 92-167155/20.

PT Prepn. of chimeric humanised antibodies - using a new polymerase
 PT chain reaction technique
 PS Example 1; Page 36; 67pp; English.
 CC Primer A (Q24648) was used with Primer D (Q24651) in a secondary PCR
 CC reaction to generate fragment AD (Q24654). The secondary PCR
 CC used as template fragments AB and CD (see Q24652 and Q24653)
 CC annealed together. The two fragments constitute the whole length of
 CC the HUMDXCH.23 insert but with point mutations to convert Phe 27
 CC and Thr 30 of CAMPATH-1H back to Ser residues present in the NEW
 CC FRH1 and the CAMPATH-1H CDRH1 replaced by the CDRH1 sequence of
 CC DX48.
 SQ Sequence 265 BP; 34 A; 36 C; 44 G; 31 T;

Query Match 81.0%; Score 17; DB 4; Length 265;
 Best Local Similarity 90.5%; Pred. No. 9,99e-01;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 130 acttatggtatgggtgtgggc 150
 |||| ||||||||||||| ||
 Qy 1 ACTTCTGGTATGGGTGTGAGC 21

RESULT 10

ID T09300 standard; DNA; 360 BP.
 AC T09300;
 DT 25-JUL-1996 (first entry)
 DE Murine anti-Protein C MAb HPC-4 VH gamma mature protein coding region.

KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
 KW zymogen; cleavage; mouse; humanised antibody; variable region;
 KW light chain; inhibition; anticoagulant; coagulation; tumour; ss.
 OS Mus musculus.
 PN W09534652-A1.
 PD 21-DEC-1995.
 PF 09-JUN-1995; 007372.
 PR 10-JUN-1994; US-259321.
 PA (OKLA-) OKLAHOMA MED RES FOUND.
 PI Esmon CT, Rezaie A;
 DR WPI; 96-049681/05.
 DR P-PSDB; R88109.
 PT Calcium-binding monoclonal antibody immunoreactive with Protein C -
 PT inhibits Protein C anticoagulant activation by
 PT thrombin-thrombomodulin, e.g. for treating tumours
 PS Claim 4; Page 30; 41pp; English.
 CC This is the nucleotide sequence encoding the mature protein from the
 CC murine anti-protein C monoclonal antibody HPC-4 heavy chain variable
 CC region (VH gamma). HPC-4 recognises the activation peptide region
 CC (888106) of the heavy chain of protein C, a vitamin K-dependent plasma
 CC protein zymogen. Protein C is activated to activated protein C (APC)
 CC by cleavage between the Arg-Leu amino acid contained within the
 CC activation peptide sequence. HPC-4 prevents protein C activation to
 CC APC by binding to this region. The DNA sequences encoding the variable
 CC regions of the heavy and light chains of the antibody (T09299-302) were
 CC used to construct humanised antibodies using the PCR primers T09303-9.
 CC The humanised antibodies are useful as inhibitors of coagulation and can
 CC be used for the treatment of tumours by inhibiting the anticoagulant
 CC activity of APC by preventing conversion of protein C to APC.
 SQ Sequence 360 BP; 82 A; 91 C; 95 G; 92 T;

Query Match 81.0%; Score 17; DB 19; Length 360;
 Best Local Similarity 100.0%; Pred. No. 9.99e-01;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 91 actctgtgtatgggtgt 107
 QY 1 ACTTCTGGTATGGGTGT 17
 RESULT 11
 ID T09299 standard; DNA; 417 BP.
 AC T09299;
 DT 25-JUL-1996 (first entry)
 DE Murine anti-Protein C MAb HPC-4 VH gamma coding region.
 KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
 KW zymogen; cleavage; mouse; humanised antibody; variable region;
 KW light chain; inhibition; anticoagulant; coagulation; tumour; ss.
 OS Mus musculus.
 EH Key Location/Qualifiers
 FT sig_peptide 1..57
 FT /tag= a
 FT mat_peptide 58..417
 FT /tag= b
 PN W09534652-A1.
 PD 21-DEC-1995.
 PF 09-JUN-1995; 007372.
 PR 10-JUN-1994; US-259321.
 PA (OKLA-) OKLAHOMA MED RES FOUND.
 PI Esmon CT, Rezaie A;
 DR WPI; 96-049681/05.
 DR P-PSDB; R88109.
 PT Calcium-binding monoclonal antibody immunoreactive with Protein C -
 PT inhibits Protein C anticoagulant activation by

PT thrombin-thrombomodulin, e.g. for treating tumours
 PS Claim 4; Page 29-30; 41pp; English.
 CC This is the nucleotide sequence encoding the heavy chain variable region
 CC from the murine anti-protein C monoclonal antibody HPC-4 which recognises
 CC the activation peptide region (888106) of the heavy chain of protein C,
 CC a vitamin K-dependent plasma protein zymogen. Protein C is converted to
 CC activated protein C (APC) by cleavage between the Arg-Leu amino acid
 CC contained within the activation peptide sequence. HPC-4 prevents protein
 CC C activation to APC by binding to this region. The DNA sequences encoding
 CC the variable regions of the heavy and light chains of the antibody
 CC (T09299-302) were used to construct humanised antibodies using the PCR
 CC primers T09303-9. The humanised antibodies are useful as inhibitors of
 CC coagulation and can be used for the treatment of tumours by inhibiting
 CC the anticoagulant activity of APC by preventing conversion of protein C
 CC to APC.
 SQ Sequence 417 BP; 89 A; 108 C; 106 G; 114 T;

Query Match 81.0%; Score 17; DB 19; Length 417;
 Best Local Similarity 100.0%; Pred. No. 9.99e-01;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 148 actctgtgtatgggtgt 164
 QY 1 ACTTCTGGTATGGGTGT 17

RESULT 12
 ID Q64166 standard; cDNA to mRNA; 429 BP.
 AC Q64166;
 DT 29-DEC-1994 (first entry)
 DE Sequence of mouse VH showing the sequences of recombinant
 DE anti-FHV-1 antibody CDRs 1, 2 and 3.
 KW Feline herpes virus; FHV-1; monoclonal antibody; CDR;
 KW complementarity determining region; ss.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT CDS 1..429
 FT /tag= a
 FT misc_feature 19
 FT /tag= b
 FT /label= MHL341
 FT misc_feature 385..429
 FT /tag= c
 FT /label= MJH3
 PN W09412661-A.
 PD 09-JUN-1994.
 PF 25-NOV-1993; J01724.
 PR 28-NOV-1992; JP-341255.
 PA (KAGA) CEMO SERO THERAPEUTIC RES INST.
 PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;
 DR WPI; 94-200288/24.
 DR P-PSDB; R54092.
 PT Feline monoclonal antibody and recombinant antibodies specific
 PT for FHV-1 - for detection, treatment and prevention of FHV-1
 PT infection.
 PS Disclosure; Page 17-18; 53pp; Japanese.
 CC The inventors claim a monoclonal antibody against feline herpes
 CC virus (FHV-1). They also claim a recombinant antibody against FHV-1
 CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
 CC used in the detection, treatment and prevention of FHV-1. The
 CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
 CC antibody are given in R54092. The sequences of the CDRs in the VL of
 CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR
 CC sequences are claimed.

SQ Sequence 429 BP; 84 A; 116 C; 109 G; 120 T;
Query Match 76.2%; Score 16; DB 11; Length 429;
Best Local Similarity 100.0%; Pred. No. 3.45e+00;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 148 actctgtgtggtg 163
|||||
QY 1 ACTTCTGATGGG 16

RESULT 13
ID Q78948;
AC Q78948;
DT 01-AUG-1995 (first entry)
DE Human immunoglobulin Vh gene #10.
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 71..495
FT /tag= a
FT /product= human immunoglobulin variable heavy chain
FT intron 114..199
FT /tag= b
FT misc_signal 322..324
FT /tag= c
FT /transl_except= unused termination codon
FT misc_signal 373..375
FT /tag= d
FT /transl_except= unused termination codon
FT misc_signal 496..498
FT /tag= e
FT /note= "miscellaneous signal, does not conform to
FT termination or splice site sequence"
PN W09426895-A.
PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PR 10-MAY-1993; W0-J00603.
PA (NIBS) JAPAN TOBACCO INC.
PI Honjo T, Matsuda F;
DR WPI; 95-006791/01.
DR P-PSDB; R66304.
PT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts
PS Claim 19; Page 43-44; 130pp; Japanese.
CC A series of genes (Q78939-79002) encoding human immunoglobulin variable
CC heavy chains. The genes were isolated and cloned from a series of cosmid
CC constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131, by PCR
CC amplification using primers Q78917-38. The genes are subdivided into 5
CC families of Vh genes. The fragments cover a region of 800 kb. The DNA
CC fragments were isolated from high molecular weight DNA from human
CC placenta. The DNA was partially digested with TaqI restriction enzyme.
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
CC were collected. The fragments were ligated with ClaI-digested cosmid
CC vector pJB81. The ligation products were in vitro packed and infected
CC into E.coli 490A. The fragments were then subcloned by colony
CC hybridisation. The Vh genes and the DNA fragments encoding them are
CC useful in producing human immunoglobulin in mammalian hosts.
SQ Sequence 630 BP; 141 A; 179 C; 148 G; 162 T;

Query Match 76.2%; Score 16; DB 13; Length 630;
Best Local Similarity 94.4%; Pred. No. 3.45e+00;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 301 actctggaatggtgtg 318
|||||
QY 1 ACTTCTGATGGG 18

RESULT 14
ID Q37056 standard; DNA; 812 BP.
AC Q37056;
DT 12-JUL-1993 (first entry)
DE Rat immunoglobulin H chain promoter and variable region coding sequence.
KW Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
KW humanised; chimeric; antibody; expression vector; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 300..806
FT /tag= a
FT exon 300..345
FT /tag= b
FT /number= Exon 1
FT intron 346..429
FT /tag= c
FT /number= Intron 1
FT exon 430..806
FT /tag= d
FT /number= Exon 2
FT sig_peptide 300..441
FT /tag= e
FT mat_peptide 442..806
FT /tag= f
FT TATA_signal 256..262
FT /tag= g
PN EP-533199-A.
PD 24-MAR-1993.
PF 18-SEP-1992; 116026.
PR 18-SEP-1991; JP-238375.
PA (KYOWA) KYOWA HAKKO KOGYO CO LTD.
PI Hanai N, Hasegawa M, Kuwana Y, Miyaji H, Shitara K;
DR WPI; 93-095510/12.
DR P-PSDB; R33255.
PT Humanised chimeric antibody prodn. against ganglioside GD3 - for
PT treating cancers, such as melanoma, neuroblastoma, etc.
PS Disclosure; Page 27-28; 63pp; English.
CC This sequence contains the promoter and variable regions of the rat
CC immunoglobulin heavy (H) chain. This sequence was used in the
CC construction of humanised chimeric antibody expression vectors. In
CC these humanised antibodies none of the amino acids of the non-human
CC animal Ab variable region have been changed.
SQ Sequence 812 BP; 201 A; 205 C; 186 G; 220 T;

Query Match 71.4%; Score 15; DB 6; Length 812;
Best Local Similarity 85.7%; Pred. No. 1.16e+01;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 531 acttatgtatgtgtgtggc 551
|||||
QY 1 ACTTCTGATGGG 21

RESULT 15
ID Q04729 standard; DNA; 2352 BP.
AC Q04729;
DT 12-OCT-1990 (first entry)
DE Xylene oxygenase gene.

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13

KW Xylene oxygenase; ds.
FH Key Location/Qualifier
FT CDS 27..1136
FT /*tag= a
FT CDS 1286..2338
FT /*tag= b
PN J0211977-A.
PD 7-MAY-1990.
PF 28-OCT-1988; 272328.
PR 28-OCT-1988; JP-272328.
PA (MTU) Mitsubishi Kasei Corp, (MITS) Mitubishi.
DR WPI; 90-182380/24.
DR N-PSDB; R05384 & R05385.
PT Xylene oxygenase gene - used to create the blue colour of flowering plants.
PS Claim 2; Page 581; 15pp; Japanese.
CC Useful in creating the blue colour from flowering plants.
SQ Sequence 2352 BP; 545 A; 518 C; 629 G; 660 T;

Query Match 71.4%; Score 15; DB 1; Length 2352;
Best Local Similarity 89.5%; Pred. No. 1.16e+01;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1506 cttctgctatgggtctgaag 1524
Qy 2 CTTCTGCTATGGGTCTGAG 20

Search completed: Wed Mar 19 08:23:59 1997
Job time : 15 secs.

Mar 19 08:27

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3

c 43 16 33.3 610 86 R52751 yg99q06.r1 Homo sapie 7.57e-02
 44 16 33.3 2881 137 HWSWS1883 human chromosome 7 ST 7.57e-02
 45 16 33.3 2881 174 HWSWS1883 human chromosome 7 ST 7.57e-02

ALIGNMENTS

RESULT 1
 ID HS724291 standard; RNA; EST; 427 BP.

AC N62724;
 DT 02-MAR-1996 (Rel. 47, Created)
 DT 02-MAR-1996 (Rel. 47, Last updated, Version 1)
 DE yz76f06.s1 Homo sapiens cDNA clone 288995 3'.

KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homidae.

RN [1]

RP 1-427

RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,

RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,

RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,

RA Trevasis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;

RT *The WashU-Merck EST Project*;

RL Unpublished.

CC Contact: Wilson RK WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC est@wustl.edu Source: IMAGE Consortium, LNL This clone is

CC available royalty-free through LNL; contact the IMAGE Consortium

CC (info@image.lnl.gov) for further information. NCBI gi: 1210553

FH Key Location/Qualifiers

FH source

FT 1..427

FT /organism="Homo sapiens"

FT /clone="288995"

FT /note="human"

FT <1..>427

SQ Sequence 427 BP; 129 A; 76 C; 112 G; 110 T; 0 other;

Query Match 41.7%; Score 20; DB 164; Length 427;

Best Local Similarity 79.4%; Pred. No. 4.78e-07;

Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 353 ggatgggtatgtgctgttcttcataacagtaa 386

||||| ||| ||||| ||||| |||||

Cp 39 GGATGGGTTATACCGCTTGTCTCATCATCCAGTAA 6

RESULT 2

LOCUS N62724

DEFINITION yz76f06.s1 Homo sapiens cDNA clone 288995 3'.

ACCESSION N62724

NID 91210553

KEYWORDS EST.

SOURCE human clone=288995 primer=ml3 -40 forward library=Soares multiple

sclerosis 2NHMSF vector=pT73D (Pharmacia) with a modified

polylinker V TYPE: phagemid host=DH10B (ampicillin resistant)

Reit1=Not I Rsite2=Eco RI 46 year old male. 1st strand cDNA was

primed with a Not I - oligo(dT) primer

[5'-TGTACCAATCTGAAGTGGAGCGCCGCAATTTTTTTTTTTTTT-3'],

double-stranded cDNA was size selected, ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I and Eco

RI sites of a modified pT7 vector (Pharmacia). Library went

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through one round of normalization to a Cot = 5. Library
 constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4
 multiple sclerosis lesions from one patient was kindly provided by
 Dr. Kevin G. Becker (NINDS/NIH).

ORGANISM

Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 427)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevasis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.

TITLE

JOURNAL

COMMENT

The WashU-Merck EST Project
 Unpublished (1995)
 Contact: Wilson RK
 WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

FEATURES

source

1..427

/organism="Homo sapiens"

/clone="288995"

/note="human"

<1..>427

mRNA 129 a 76 c 112 g 110 t

BASE COUNT

ORIGIN

Query Match 41.7%; Score 20; DB 65; Length 427;
 Best Local Similarity 79.4%; Pred. No. 4.78e-07;
 Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 353 ggatgggtatgtgctgttcttcataacagtaa 386

||||| ||| ||||| ||||| |||||

Cp 39 GGATGGGTTATACCGCTTGTCTCATCATCCAGTAA 6

RESULT 3

LOCUS

DEFINITION

H64550 429 bp mRNA EST 11-DEC-1995
 yu63d03.s1 Homo sapiens cDNA clone 238469 3' similar to contains

Alu repetitive element; contains THR repetitive element ;

ACCESSION

NID

KEYWORDS

SOURCE

human clone=238469 primer=Promega -21ml3 library=Weizmann Olfactory
 Epithelium vector=pBluescript SK- host=SOIR cells (kanamycin
 resistant) Reit1=EcoRI Rsite2=XhoI From 35 year old female. The
 cDNA was oligo (dT) primed with an XhoI restriction enzyme
 recognition site and an 18 base poly dT sequence. For the 5' end,
 the synthesized cDNA termini were treated with T4 DNA polymerase
 and EcoRI adaptors were ligated to the blunt ends.

ORGANISM

Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;

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mRNA <1..>444
 BASE COUNT 101 a 108 c 129 g 105 t 1 others
 ORIGIN

Query Match 37.5%; Score 18; DB 66; Length 444;
 Best Local Similarity 75.0%; Pred. No. 2.37e-04;
 Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 315 tgggtcagaccggtgctccatccctgtacctgtg 350
 ||||| |||| |||| |||| |||| |||| |||| ||||
 Cp 36 TGGGTATACCGCTTGTTCATCATCCACGTAATGTC 1

RESULT 6
 LOCUS MUSGS00994 477 bp mRNA EST 09-DEC-1995
 DEFINITION Mouse 3'-directed cDNA, MUSGS00994, clone md0295.
 ACCESSION D18296
 NID g1089445
 KEYWORDS EST(expressed sequence tag); Gene signature (GS); development;
 transcribed sequence.
 SOURCE Mus musculus (strain C57BL/6Jsub_species domesticus,) decidua
 tissue (day 6.5-8.5 of gestation) cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Eukaryota; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sclerognathi; Myomorpha; Muridae;
 Murinae; Mus.

REFERENCE 1 (bases 1 to 477)
 AUTHORS Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara, K.
 TITLE Analysis of gene expression in mouse embryogenesis by 3'-directed
 cDNA sequencing
 JOURNAL Unpublished (1993)
 COMMENT Submitted (10-Sep-1993) to DDBJ by:
 Shoko Kawamoto
 Institute for Cellular and Molecular Biology
 Osaka University
 3-1, Yamadaoka
 Suita, Osaka, 565
 Japan
 Phone: 06-879-7992
 Fax : 06-877-1922
 Email: shoko@imcb.osaka-u.ac.jp.
 Location/Qualifiers
 1..477
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /sub_species="domesticus"
 /sequenced_mol="cDNA to mRNA"
 /tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
 137 a 89 c 95 g 133 t 23 others

BASE COUNT 137 a 89 c 95 g 133 t 23 others
 ORIGIN

Query Match 37.5%; Score 18; DB 52; Length 477;
 Best Local Similarity 90.9%; Pred. No. 2.37e-04;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 256 tgggatgatgacaagagctgta 277
 ||||| |||| |||| |||| |||| |||| |||| ||||
 Qy 10 TCGGATGATGACAAAGCGCTATA 31

RESULT 7
 LOCUS M88987 389 bp mRNA EST 16-SEP-1992
 DEFINITION CEL12G12 Caenorhabditis elegans cDNA clone cm12g12 5'.
 ACCESSION M88987

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NID g275488
 EST.
 KEYWORDS Nematodes clone=cm12g12 library=Chris Martin sorted cDNA library
 SOURCE strain=Bristol N2 vector=lambdaphage SHLX2 host=MC1061 Mixed stage
 hermaphrodite cDNA library. Partially normalized by successively
 picking groups of clones that didn't hybridize to previously picked
 clones. Vector: lambdaphage SHLX2 (lupshlitz, D.H. et al., Gene
 88:25-36 (1990)) Host: MC1061.

ORGANISM Caenorhabditis elegans
 Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;
 Rhabditina; Rhabditoidea; Rhabditidae.

REFERENCE 1 (bases 1 to 389)
 AUTHORS Waterston, R., Martin, C., Craxton, M., Huynh, C., Coulson, A.,
 Hillier, L., Durbin, R.K., Green, P., Shownkeen, R., Halloran, N.,
 Hawkins, T., Wilson, R., Berks, M., Du, Z., Thomas, K., Thierry-Mieg, J.
 and Sulston, J.
 TITLE A survey of expressed genes in Caenorhabditis elegans
 JOURNAL Nature Genet. 1, 114-123 (1992)
 COMMENT

Contact: Waterston R.H. (USA) and Sulston J.E. (UK)
 (USA) Dept. of Genetics or (UK)
 (USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of
 Molecular Biology
 Box 8232, 4566 Scott Ave., St. Louis, MI 63110, USA, or, Hills
 Road, Cambridge CB2 2QH, UK
 Tel: (USA) (314) 3627072 or (UK) (0223) 248011
 Fax: (USA) (314) 3624137 or (UK) (0223) 402008
 Email: rwnematode.wustl.edu or jes@mc-lmb.cam.ac.uk.
 Location/Qualifiers
 1..389
 /organism="Caenorhabditis elegans"
 /clone="cm12g12"
 /strain="Bristol N2"
 /note="Nematodes"

BASE COUNT 121 a 63 c 86 g 114 t 5 others
 ORIGIN

Query Match 35.4%; Score 17; DB 51; Length 389;
 Best Local Similarity 94.7%; Pred. No. 4.51e-03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 111 cacattactgtgtgatg 129
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 1 CACATTACTGGGATGATG 19

RESULT 8
 LOCUS H20550 434 bp mRNA EST 03-JUL-1995
 DEFINITION Ym47e06.s1 Homo sapiens cDNA clone 51324 3' similar to gb:M29874
 CYTOCHROME P450 IIB6 (HUMAN);.
 ACCESSION H20550
 NID g889245
 KEYWORDS EST.
 SOURCE human clone=51324 library=Soares infant brain lNIB vector=lafmid BA
 host=DHI0B (ampicillin resistant) primer=Promega -21m13 Rsite=Not
 I Rsite2=Hind III Whole brain from a 73 days post natal female. 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 AACCTGGAAGATTCCGGCCGACGAATTTTTTTTTTTT 3']; double-stranded
 cDNA was ligated to Hind III adaptors (Pharmacia), digested with
 Not I and directionally cloned into the Not I and Hind III sites of
 the Lafmid BA vector. Library went through one round of
 normalization. Library constructed by Bento Soares and M.Fatima
 Bonaldo.

ORGANISM Homo sapiens


```
1..504
/organism="Arabidopsis thaliana"
/clone="168P21T7"
/strain="var columbia"
```

Db 265 attactgagatggagtctgtcctctgtcaccacaggctggagtc 309
 ||||| ||||| | | | | | | | |
Qv 4 ATTTACTGGGATGATGCAAGCGCTATAACCATCCCTCAAGACC 48

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```
OC Cyclorrhapha; Schizophora; Drosophiloidea; Drosophilidae.
RN [1]
RP 1-182
RA European Drosophila Mapping Consortium;
RT ;
RL Submitted (08-APR-1994) to the EMBL/GenBank/DBJ databases.
RL Michael Ashburner, Department of Genetics, Downing St., Cambridge
RL CB2 3EH, England
RN [2]
RC Updated comments
RA European Drosophila Mapping Consortium;
RT ;
RL Submitted (15-APR-1996) to the EMBL/GenBank/DBJ databases.
RL Michael Ashburner, Department of Genetics, Downing St., Cambridge
RL CB2 3EH, England
CC STS_name = Dm9G3S
CC clone_name = 9c3
CC STS_from_promoter = SP6
CC vector_class = cosmid, Lorient 6
CC origin_of_clone = Oregon-R
CC in_situ_site_primary = 260
CC in_situ_site_heterochromatin = BH
CC STS_dbSTS_AC = 4932
CC BLAST_program = BLASTN
CC database_searched = EMBL
CC database_version = 45.0 and updates till date_of_search
CC date_of_search = 08-01-1996
CC BLAST_program = BLASTX
CC database_searched = SWISSPROT
CC database_version = 32.0
CC date_of_search = 15-12-1995
FH Key Location/Qualifiers
FH source 1..182
FT /organism="Drosophila melanogaster"
FT /strain="Oregon-R"
FT /clones="9c3"
SQ Sequence 182 BP; 49 A; 35 C; 51 G; 47 T; 0 other;

Query Match 33.3%; Score 16; DB 173; Length 182;
Best Local Similarity 71.1%; Pred. No. 7.57e-02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 145 ggatggcgaatagatctccattatctcgagtgaatgt 182
||||| ||||| | ||||| |||||
Cp 39 GCATGGCTATACCGCTTGTCATCATCCAGTAATGT 2
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Search completed: Wed Mar 19 08:29:11 1997
Job time : 77 secs.

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.
		Match						
1	48	100.0	423	14	Q83492		Chimeric antibody 3B9	2.80e-19
2	48	100.0	483	14	Q83491		Mouse Mab 3B9 heavy c	2.80e-19
3	42	87.5	366	11	Q68709		Humanised MAb H-chain	2.82e-15
4	42	87.5	738	12	T070612		IL-6 binding inhibito	2.92e-15
5	40	83.3	360	19	Q93000		Murine anti-Protein C	5.84e-14
6	40	83.3	417	19	T09299		Murine anti-Protein C	5.84e-14
7	40	83.3	429	11	Q64166		Sequence of mouse VH	5.84e-14
8	36	75.0	423	7	Q45599		Sequence encoding the	2.33e-11

DR WPI; 95-123387/16.
 DR P-PSDB; R70191.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Fig.3; 97pp; English.
 CC A human/mouse chimeric antibody heavy chain variable region was
 CC constructed (given in R70191) that contained the mouse anti-human
 CC IL-4 MAb 3B9 variable region including 3 CDRs (R70198-200) and a
 CC human antibody signal peptide (R70193). The construct was used
 CC for humanized antibody production.
 SQ Sequence 423 BP; 87 A; 115 C; 110 G; 111 T;

Query Match 100.0%; Score 48; DB 14; Length 423;
 Best Local Similarity 100.0%; Pred. No. 2.80e-19;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 214 cacatttactggatgacgaagcgtataaaccatccctgaagc 261
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 QY 1 CACATTACTGGGATGATGACAGCGCTATAACCCATCCCTGAAGAGC 48

RESULT 2

ID Q83491 standard; cDNA; 483 BP.
 AC Q83491;
 DT 20-SEP-1995 (first entry)
 DE Mouse MAb 3B9 heavy chain.
 KW Chimeric antibody; humanized antibody; antibody engineering;
 KW monoclonal antibody; MAb; Interleukin-4; IL-4; allergy; ds.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT CDS 64..483
 FT /*tag= a 64..120
 FT /*tag= b 121..483
 FT mat_peptide 121..483
 FT /*tag= c
 PN W09507301-A.
 PD 16-MAR-1995.
 PE 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR P-PSDB; R70190.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Fig.2; 97pp; English.
 CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 CC chains were cloned into pCEM7/+ and transformed into E. coli
 CC DH5-alpha. The clones were sequenced (Q83490-91), and used for
 CC antibody engineering.
 SQ Sequence 483 BP; 108 A; 130 C; 124 G; 121 T;

Query Match 100.0%; Score 48; DB 14; Length 483;
 Best Local Similarity 100.0%; Pred. No. 2.80e-19;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 274 cacatttactggatgacgaagcgtataaaccatccctgaagc 321

QY 1 CACATTACTGGGATGATGACAGCGCTATAACCCATCCCTGAAGAGC 48
 ||||||||||||||||||||||||||||||||||||||||||||
 RESULT 3
 ID Q8709 standard; cDNA to mRNA; 366 BP.
 AC Q8709;
 DT 08-FEB-1995 (first entry)
 DE Humanised MAb H-chain coding sequence.
 KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
 KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIN; ds.
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 PN J06141885-A.
 PD 24-MAY-1994.
 PF 05-NOV-1992; 322476.
 PR 05-NOV-1992; JP-322476.
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 DR WPI; 94-205040/25.
 DR P-PSDB; R54101.
 PT Recombinant anti-HIV monoclonal antibody - capable of
 PT neutralising strains which can not be neutralised by anti-IIIB
 PT and IIIN antibodies
 PS Disclosure; Page 13; 23pp; Japanese.
 CC The sequences given in Q8709-10 encode the heavy and light chains
 CC respectively of the humanised monoclonal antibody (MAb) of the
 CC invention. The antibody has the ability to neutralise human
 CC immunodeficiency virus. The antibody is classified as IgG kappa and
 CC has the sequence RIGPCR or RVGPR in the principal neutralising
 CC domain. The antibody may be used to neutralise the clinically
 CC separate strains which cannot be neutralised by the neutralising
 CC antibodies against IIIB and IIIN strains.
 SQ Sequence 366 BP; 85 A; 98 C; 84 G; 99 T;

Query Match 87.5%; Score 42; DB 11; Length 366;
 Best Local Similarity 93.8%; Pred. No. 2.82e-15;
 Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 154 cacatttactggatgacgaagcgtataaaccatccctgaagc 201
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 QY 1 CACATTACTGGGATGATGACAGCGCTATAACCCATCCCTGAAGAGC 48

RESULT 4

ID Q70612 standard; DNA; 738 BP.
 AC Q70612;
 DT 28-APR-1995 (first entry)
 DE IL-6 binding inhibitor DNA.
 KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
 KW septic shock; multiple myeloma; ss.
 OS Homo sapiens.
 PN EP-617126-A.
 PD 28-SEP-1994.
 PR 16-FEB-1994; 102346.
 PR 17-FEB-1993; JP-028173.
 PA (AJIN) AJINOMOTO KK.
 PI Hamuro J, Nakazawa H, Shimamura T;
 DR WPI; 94-295777/37.
 DR P-PSDB; R58612.
 PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to
 PT its receptor - useful for treating auto-immune disease induced
 PT or aggravated by IL-6
 PS Claim 9; Page 19; 26pp; English.
 CC Q70612 codes for human interleukin-6 binding inhibitor, the

FN /label= MJH3
 PD W09412661-A.
 PF 09-JUN-1994.
 PR 28-NOV-1992; JP-341255.
 PA (KAGA) CEMO SERO THERAPEUTIC RES INST.
 PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;
 DR WPI: 94-200288/24.
 DR P-PSDB; R54092.
 PT Feline monoclonal antibody and recombinant antibodies specific
 PT for FHV-1 - for detection, treatment and prevention of FHV-1
 PT infection.
 PS Disclosure; Page 17-18; 53pp; Japanese.
 CC The inventors claim a monoclonal antibody against feline herpes
 CC virus (FHV-1). They also claim a recombinant antibody against FHV-1
 CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
 CC used in the detection, treatment and prevention of FHV-1. The
 CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
 CC antibody are given in R54092. The sequences of the CDRs in the VL of
 CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR
 CC sequences are claimed.
 SQ Sequence 429 BP; 84 A; 116 C; 109 G; 120 T;

Query Match 83.3%; Score 40; DB 11; Length 429;
 Best Local Similarity 91.7%; Pred. No. 5.84e-14;
 Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 211 cacatttggtgatgtatgaagcgctataaccacccctctgaagc 258
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 1 CACATTACTGGATGATGACAGCGCTATACCCATCCCTGAAGAGC 48

RESULT 8

ID Q45597 standard; DNA; 423 BP.
 AC Q45597;
 DT 04-DEC-1993 (first entry)
 DE Sequence encoding the VH of antibody B17X2
 KW Variable heavy antibody chain; human subgroup 4 germline; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 7..423
 FT /*tag= a
 PN W09312231-A.
 PD 24-JUN-1993.
 PF 13-DEC-1991; AU0583.
 PR 13-DEC-1991; WO-AU0583.
 PA (DOWC) DOW CHEM AUSTRALIA LTD.
 PI Johnson KS, Mezes PS, Richard RA;
 DR WPI: 93-214173/26.
 DR P-PSDB; R38315.
 PT New composite antibody binding to tumour associated TAG-72
 PT antigen - includes light chain variable region from human
 PT subgroup 4 germline gene, useful, opt. as conjugate, for
 PT diagnosis or treatment of cancer
 PS Disclosure; Figure 4; 150pp; English.
 CC Cell line B17X2 expresses an antibody utilising a variable light
 CC chain encoded by a gene derived from Hum4 VL and a variable heavy
 CC chain which makes a stable VL and VH combination.
 SQ Sequence 423 BP; 98 A; 120 C; 102 G; 97 T;

Query Match 75.0%; Score 36; DB 7; Length 423;
 Best Local Similarity 89.1%; Pred. No. 2.33e-11;
 Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 219 cattattggatgataagcgctacagccatctctgaagc 264
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 3 CATTACTGGATGATGACAGCGCTATACCCATCCCTGAAGAGC 48

RESULT 9

ID Q78943 standard; DNA; 613 BP.
 AC Q78943;
 DT 07-AUG-1995 (first entry)
 DE Human immunoglobulin variable heavy chain #5.
 KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 71..513
 FT /*tag= a
 FT /product= human immunoglobulin variable heavy chain
 FT intron 117..202
 FT /*tag= b
 FT misc signal 514..516
 FT /*tag= c
 FT /note= "miscellaneous signal, does not conform to
 FT terminator or splice site sequence"
 PN W09426895-A.
 PD 24-NOV-1994.
 PF 10-MAY-1993; J00603.
 PR 10-MAY-1993; WO-J00603.
 PA (NLSB) JAPAN TOBACCO INC.
 PI Honjo T, Matsuda F;
 DR WPI: 95-006791/01.
 DR P-PSDB; R66299.
 PT DNA fragment comprising human immunoglobulin Vh genes - for the
 PT production of human immunoglobulin in mammalian hosts
 PS Disclosure; Page 36-37; 130pp; Japanese.
 CC A series of genes (Q78939-79002) encoding human immunoglobulin variable
 CC heavy chains. The genes were isolated and cloned from a series of cosmid
 CC constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M118 and M131, by PCR
 CC amplification using primers Q78917-38. The genes are subdivided into 5
 CC families of Vh genes. The fragments cover a region of 800 kb. The DNA
 CC fragments were isolated from high molecular weight DNA from human
 CC placenta. The DNA was partially digested with TaqI restriction enzyme.
 CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
 CC were collected. The fragments were ligated with ClaI-digested cosmid
 CC vector pJB81. The ligation products were in vitro packed and infected
 CC into E.coli 490A. The fragments were then subcloned by colony
 CC hybridisation. The Vh genes and the DNA fragments encoding them are
 CC useful in producing human immunoglobulin in mammalian hosts.
 SQ Sequence 613 BP; 139 A; 194 C; 139 G; 141 T;

Query Match 70.8%; Score 34; DB 13; Length 613;
 Best Local Similarity 87.0%; Pred. No. 4.46e-10;
 Matches 40; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 369 cattattggatgataagcgctacagccatctctgaagc 414
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 3 CATTACTGGATGATGACAGCGCTATACCCATCCCTGAAGAGC 48

RESULT 10

ID Q75889 standard; cDNA; 418 BP.
 AC Q75889;
 DT 21-AUG-1995 (first entry)
 DE Mouse heavy chain variable region in plasmid pUC-SK2-Vh.
 KW Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;

CC antigenicity due to the use of human derived sequences and low
 CC antigenicity mouse derived sequences.
 SQ Sequence 96 BP; 18 A; 24 C; 25 G; 29 T;

Query Match 58.3%; Score 28; DB 13; Length 96;
 Best Local Similarity 81.8%; Pred. No. 2.52e-06;
 Matches 36; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 41 ttcaaggcaggttagtactatcatcattccaccacaatgtg 84
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Cp 44 TTCAGGATGGCTTAGCCCTTCATCATCCAGTAAATGTG 1

RESULT 13

ID Q75917 standard; DNA; 418 BP.
 AC Q75917;
 DT 23-AUG-1995 (first entry)
 DE Anti-human IL-6 chimaeric Ab H chain V region in HEL-RVH-SK2b.
 KW Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;
 KW interleukin; antibody; hybridoma; CDR; framework; constant region;
 KW heavy chain; disorder; antigenicity; ds.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT CDS 1..417
 FT /*tag= a
 FT /note= "Anti-human IL-6 H chain V region"
 FT sig_peptide 1..57
 FT /*tag= b
 FT mat_peptide 58..417
 FT /*tag= c
 PN W09428159-A.
 PD 08-DEC-1994.
 PF 30-MAY-1994; J00859.
 PR 31-MAY-1993; JP-129787.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PA (CHUS) CHUGAI PHARM CO LTD.
 PI Hirata Y, Sato K, Tsuchiya M;
 DR WPI; 95-022828/03.
 DR P-PSDB; R67659.
 PT Antibody against IL-6 - useful for the therapy and treatment of IL-6 related disorders.

PS Claim 21; Page 62-63; 82pp; Japanese.
 CC The sequence of a recombinant gene encoding the heavy chain variable region of a chimaeric antibody against human interleukin-6 (IL-6). The sequence is found on the plasmid HEL-RVH-SK2a. This vector and vectors CC Q75914, -5 and -6 express constructs encoding fragments of a chimaeric CC antibody to the human IL-6 comprising (a) a light chain with (i) a CC variable region containing 3 complementarity determining regions (CDR) CC (R77201-3) inserted into several framework regions (FR) (R77204-7) and CC (ii) a human light chain constant region and (b) a heavy chain with (i) a CC variable region containing 3 CDR (R77212-4) inserted into an FR CC (R77215-8) and (ii) a human light chain constant region. The FR of the CC light chain may be mouse derived (Q75888) or from the human antibody REL. CC The heavy chain FR may also be mouse derived (Q75889) or from the human CC antibody DAM. The antibodies can be used in the treatment of IL-6 CC related disorders. The antibodies are useful as they have low CC antigenicity due to the use of human derived sequences and low CC antigenicity mouse derived sequences.

SQ Sequence 418 BP; 95 A; 116 C; 109 G; 98 T;

Query Match 58.3%; Score 28; DB 13; Length 418;
 Best Local Similarity 81.8%; Pred. No. 2.52e-06;
 Matches 36; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 211 cacatttggtgaatgatgaatgactataaccctgcctgaa 254
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 Qy 1 CACATTACTGGGATGATGACAGCGCTATATACCCATCCCTGAA 44

RESULT 14

ID Q75916 standard; DNA; 418 BP.
 AC Q75916;
 DT 23-AUG-1995 (first entry)
 DE Anti-human IL-6 chimaeric Ab H chain V region in HEL-RVH-SK2a.
 KW Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;
 KW interleukin; antibody; hybridoma; CDR; framework; constant region;
 KW heavy chain; disorder; antigenicity; ds.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT CDS 1..417
 FT /*tag= a
 FT /note= "Anti-human IL-6 H chain V region"
 FT sig_peptide 1..57
 FT /*tag= b
 FT mat_peptide 58..417
 FT /*tag= c
 PN W09428159-A.
 PD 08-DEC-1994.
 PF 30-MAY-1994; J00859.
 PR 31-MAY-1993; JP-129787.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PA (CHUS) CHUGAI PHARM CO LTD.
 PI Hirata Y, Sato K, Tsuchiya M;
 DR WPI; 95-022828/03.
 DR P-PSDB; R67658.
 PT Antibody against IL-6 - useful for the therapy and treatment of IL-6 related disorders.

PS Claim 21; Page 60-61; 82pp; Japanese.
 CC The sequence of a recombinant gene encoding the heavy chain variable region of a chimaeric antibody against human interleukin-6 (IL-6). The sequence is found on the plasmid HEL-RVH-SK2a. This vector and vectors CC Q75914, -5 and -7 express constructs encoding fragments of a chimaeric CC antibody to the human IL-6 comprising (a) a light chain with (i) a CC variable region containing 3 complementarity determining regions (CDR) CC (R77201-3) inserted into several framework regions (FR) (R77204-7) and CC (ii) a human light chain constant region and (b) a heavy chain with (i) a CC variable region containing 3 CDR (R77212-4) inserted into an FR CC (R77215-8) and (ii) a human light chain constant region. The FR of the CC light chain may be mouse derived (Q75888) or from the human antibody REL. CC The heavy chain FR may also be mouse derived (Q75889) or from the human CC antibody DAM. The antibodies can be used in the treatment of IL-6 CC related disorders. The antibodies are useful as they have low CC antigenicity due to the use of human derived sequences and low CC antigenicity mouse derived sequences.

SQ Sequence 418 BP; 94 A; 116 C; 110 G; 98 T;

Query Match 58.3%; Score 28; DB 13; Length 418;
 Best Local Similarity 81.8%; Pred. No. 2.52e-06;
 Matches 36; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 211 cacatttggtgaatgatgaatgactataaccctgcctgaa 254
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 1 CACATTACTGGGATGATGACAGCGCTATATACCCATCCCTGAA 44

RESULT 15

ID Q51746 standard; cDNA; 91 BP.
 AC Q51746;

Db . 13 vhsyyvvhvvshhsvhhhvhsvvvhhhvvhvvhvhyv 58
:: :: :: :: :: :: :: :: :: :: :: ::
Cp 48 GCTCTTCAGGATGGGTATAGCGCTGTCA TCATCCCAATAATG 3

Search completed: Wed Mar 19 08:27:33 1997
Job time : 21 secs.

SUMMARIES

8	48	100.0	360	91	MMU22994	Mus musculus	CB17 SCI	1.72e-25
9	48	100.0	360	65	MMU22979	Mus musculus	CB17 SCI	1.72e-25
10	48	100.0	360	12	MMU22979	Mus musculus	CB17 SCI	1.72e-25

[illegible]

18	48	100.0	438	70	S75897	Ig VH-IgG heavy chain	1.72e-23
19	46	95.8	234	66	MUSIGHAHL	Mouse Ig heavy-chain	1.29e-23
20	46	95.8	286	65	MM023021	Mus musculus C57BL/6	1.29e-23
21	45	95.8	318	65	MM022990	Mus musculus CB17 SCI	1.29e-23
22	46	95.8	318	12	MM022990	Mus musculus CB17 SCI	1.29e-23

Accession	Species	Accession	Species	Accession	Species
24	46	95.8	MMU22986	Mus musculus	CB17 SCI 1.29e-23
25	46	95.8	MMU22986	Mus musculus	CB17 SCI 1.29e-23

Run	Iteration	Mean	Stdev	Min	Max	Mean	Stdev	Min	Max
27	46	95.8	330 65	MMU22975	Mus musculus	CB17	SCI	1.29e-23	
28	46	95.8	330 91	MMU22975	Mus musculus	CB17	SCI	1.29e-23	
29	46	95.8	330 12	MMU22975	Mus musculus	CB17	SCI	1.29e-23	

[illegible]

Accession	Species	Accession	Species	Accession	Species
33	<i>Mus musculus</i>	33	<i>Mus musculus</i>	33	<i>Mus musculus</i>
34	<i>Mus musculus</i>	34	<i>Mus musculus</i>	34	<i>Mus musculus</i>
35	<i>Mus musculus</i>	35	<i>Mus musculus</i>	35	<i>Mus musculus</i>
36	<i>Mus musculus</i>	36	<i>Mus musculus</i>	36	<i>Mus musculus</i>

37	46	95.8	360	65	MM223013	Mus musculus CB17 SCI	1.29e-23
38	46	95.8	360	12	MM22981	Mus musculus CB17 SCI	1.29e-23
39	46	95.8	360	91	MM222981	Mus musculus CB17 SCI	1.29e-23
40	46	95.8	360	91	MM222992	Mus musculus CB17 SCI	1.29e-23
41	46	95.8	360	65	MM222992	Mus musculus CB17 SCI	1.29e-23
42	46	95.8	361	65	MM223004	Mus musculus CB17 SCI	1.29e-23
43	44	91.7	359	65	MM223004	Mus musculus (clone 5)	9.40e-22
44	44	91.7	338	65	MM223000	Mus musculus CB17 SCI	9.40e-22
45	44	91.7	360	12	MM22984	Mus musculus CB17 SCI	9.40e-22

ALIGNMENTS

LOCUS	MMU23019	286 bp	DNA	ROD	06-MAY-1995
DEFINITION	Mus musculus C57BL/6 immunoglobulin heavy chain V region mRNA, clone CBI7H-1, partial cds.				

ACCESSION	U23019	
NID	q780640	
KEYWORDS	.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Young, D.C. and Kearney, J.F.

Sequence analysis and antigen binding characteristics of

immunoglobulins from SCID Ig⁺ mice

JOURNAL

Int. Immunol. 7 (1995) In press

REFERENCE

2 (bases 1 to 286)

AUTHORS

Young, D.C.

Direct Submission

Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

Location/Qualifiers

1..286

/clone="CB17H-1"

/strain="CS7BL/6"

/organism="Mus musculus"

/sub_species="domesticus"

/germline

/tissue_type="liver"

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/notes="7183 Vh gene family"

/codon_start=2

/product="immunoglobulin heavy chain"

/db_xref="PID:g780641"

/translation="QVTLKESGPGILQSSQTLSTCSFGSFLSTSGMGVSWIROPSSG

KGLEWLAHYWDDDKRYNPSIKSLRITSKDTSRNQVFIKITSVDATATY"

BASE COUNT 67 a 71 c 70 g 72 t

ORIGIN

Query Match 100.0%; Score 48; DB 65; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.72e-25;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 155 cacattactgggatgacagcgctataacccatccctgaagc 202

|||||

QY 1 CACATTTACTGGGATGATGACAAAGCGCTATAACCCATCCCTGAGAGC 48

RESULT 2

LOCUS MM023024 286 bp DNA ROD 06-MAY-1995

DEFINITION Mus musculus C57BL/6 immunoglobulin heavy chain V region mRNA,

clone CB17H-8, partial cds.

ACCESSION U23024

NID g780650

KEYWORDS

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 286)

Young, D.C. and Kearney, J.F.

Sequence analysis and antigen binding characteristics of

immunoglobulins from SCID Ig⁺ mice

Int. Immunol. 7 (1995) In press

REFERENCE

2 (bases 1 to 286)

Young, D.C.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

Location/Qualifiers

source 1..286

/clone="CB17H-8"

/strain="CS7BL/6"

/organism="Mus musculus"

/sub_species="domesticus"

/germline

/tissue_type="liver"

<1..>286

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/codon_start=2

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/db_xref="PID:g780651"

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KGLEWLAHYWDDDKRYNPSIKSLRITSKDTSRNQVFIKITSVDATATY"

BASE COUNT 68 a 77 c 69 g 72 t

ORIGIN

Query Match 100.0%; Score 48; DB 65; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.72e-25;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 155 cacattactgggatgacagcgctataacccatccctgaagc 202

|||||

QY 1 CACATTTACTGGGATGATGACAAAGCGCTATAACCCATCCCTGAGAGC 48

RESULT 3

LOCUS MUSB 306 bp mRNA ROD 14-MAR-1994

DEFINITION Mus musculus immunoglobulin heavy chain (Igh) mRNA, VDJ4 region,

partial cds.

ACCESSION L22743

NID g348959

KEYWORDS Ig heavy chain; diversity region; immunoglobulin; joining region;

variable region.

SOURCE Mus musculus (strain BALB/cByJ) female adult spleen cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE

1 (bases 1 to 306)

Sheehan, K.M., Mainville, C.A., Willert, S. and Brodeur, P.H.

The utilization of individual VH exons in the primary repertoire of

adult BALB/c mice

J. Immunol. 151 (10), 5364-5375 (1993)

JOURNAL

MEDLINE 94044761

Location/Qualifiers

source 1..306

/organism="Mus musculus"

/strain="BALB/cByJ"

/cell_type="B-lymphocyte"

/dev_stage="adult"

/sequenced_mol="cDNA to mRNA"

/sex="female"

/tissue_type="spleen"

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/gene="Igh"

/map="chromosome 12"

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/map="chromosome 12"

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/product="immunoglobulin heavy chain"
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/translation="LTCFSGFSLSSTGSGXSVIRQPSCKGLEHLAHYWDGKRYNP
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SIKSRITKSDTSKNQVFIKITSVDTAATYTCARAWILRDYMDYWGQGTSTVYS

BASE COUNT 72 a 80 c 75 g 79 t

ORIGIN

Query Match 100.0%; Score 48; DB 66; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 97 cacattactgggatgatgacagcgctataaccatccctgaagac 144
|||||
1 CACATTTACTGGGATGATGACAGCGCTATACCCATCCTCGAAGAC 48

RESULT 4

LOCUS MUSIGHAE0 328 bp mRNA ROD 14-NOV-1991
DEFINITION Mouse Ig heavy-chain mRNA V region, partial cds. L2-5D2HV.

ACCESSION M36234

NID g194851

KEYWORDS V-region; immunoglobulin heavy chain; processed gene.

SOURCE Mouse (strain BALB/c), cDNA to mRNA, from hybridoma L2-5D2.

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 328)

AUTHORS Kavalier,J., Caton,A.J., Staudt,L.M., Schwartz,D. and Gerhard,W.

TITLE A set of closely related antibodies dominates the primary antibody

response to the antigenic site CB of the A/PR/8/34 influenza virus

hemagglutinin

J. Immunol. 145, 2312-2321 (1990)

MEDLINE 90375932

COMMENT Draft entry and computer-readable sequence for [J. Immunol. (1990)

In press] kindly submitted

by J.Kavaler, 06-JUL-1990.

FEATURES

source Location/Qualifiers

1..328

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/sub_species="domesticus"

/cell_line="L2-5D2"

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/issue_type="hybridoma"

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/map="chromosome 12"

/codon_start=2

/product="immunoglobulin heavy chain V-region"

/db_xref="PID:g194852"

/translation="PGILQPSQTLSITCSFGSLSSTGSGXSVIRQPSCKGLEHLAH
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YWGQGTSTV

BASE COUNT 76 a 85 c 82 g 83 t 2 others

ORIGIN

Query Match 100.0%; Score 48; DB 66; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 131 cacattactgggatgatgacagcgctataaccatccctgaagac 178
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Qy 1 CACATTTACTGGGATGATGACAGCGCTATACCCATCCTCGAAGAC 48

RESULT 5

LOCUS MMHCVR4 348 bp RNA ROD 23-FEB-1994

DEFINITION M.musculus (A.SM) mRNA for ASWP1 antibody heavy chain variable

region.

ACCESSION X75098

NID g414167

KEYWORDS antibody; variable region; VH region.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 348)

AUTHORS Monestier,M.

TITLE Direct Submission

JOURNAL Submitted (09-SEP-1993) to the EMBL/GenBank/DBJ databases. M.

Monestier, Center for Molecular Medicine and Immunology, one Bruce

Street, Newark, NJ 07103-2763, USA

REFERENCE 2 (bases 1 to 348)

AUTHORS Monestier,M., Losman,M.J., Novick,K.E. and Aris,J.P.

TITLE Molecular analysis of mercury-induced antinuclear antibodies in

H-2S mice

JOURNAL J. Immunol. 152 (2), 667-675 (1994)

MEDLINE 94110621

FEATURES

source Location/Qualifiers

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/organism="Mus musculus"

/strain="A.SM"

/cell_type="hybridoma"

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/gene="VH ASWP1"

/codon_start=1

/product="ASWP1 heavy chain variable region"

<1..>348

/gene="VH ASWP1"

/codon_start=1

/product="ASWP1 heavy chain variable region"

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GFDYWGQGTTLTVS"

BASE COUNT 81 a 95 c 85 g 85 t 2 others

ORIGIN

Query Match 100.0%; Score 48; DB 63; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacattactgggatgatgacagcgctataaccatccctgaagac 201
|||||

1 CACATTTACTGGGATGATGACAGCGCTATACCCATCCTCGAAGAC 48

RESULT 6

LOCUS MMU23007 359 bp mRNA ROD 26-APR-1995

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,

clone 45-4h, partial cds.

ACCESSION UZ3007
NID g780616
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 359)
Young, D.C. and Kearney, J.F.
Sequence analysis and antigen binding characteristics of
immunoglobulins from SCID Ig+ mice

JOURNAL
Int. Immunol. 7 (1995) In press

REFERENCE
2 (bases 1 to 359)
Young, D.C.

AUTHORS
Direct Submission

TITLE
Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

JOURNAL
Houston, TX 77030, USA

FEATURES
Location/Qualifiers
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/organism="Mus musculus"
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/tissue_type="spleen"
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BASE COUNT 83 a 97 c 87 g 92 t
ORIGIN

Query Match 100.0%; Score 48; DB 65; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 153 cacattactgggatgacgaagcgctataaccatccctgaagc 200
|||||
Qy 1 CACATTACTGGGATGATGACGAAGCGCTATACCCATCCCTGAAGC 48

RESULT 7
LOCUS MMHVR3 360 bp RNA ROD 23-FEB-1994
DEFINITION M.musculus (A.SW) mRNA for ASWB1 antibody heavy chain variable
region.
ACCESSION X75097
NID g414165
KEYWORDS antibody; variable region; VH region.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 360)
Monestier, M.

TITLE Direct Submission
JOURNAL Submitted (09-SEP-1993) to the EMBL/GenBank/DBJ databases. M.
Monestier, Center for Molecular Medicine and Immunology, one Bruce
Street, Newark, NJ 07103-2763, USA

REFERENCE
2 (bases 1 to 360)
Monestier, M., Losman, M.J., Novick, K.E. and Aris, J.P.
Molecular analysis of mercury-induced antinuclear antibodies in
H-2S mice

AUTHORS
J. Immunol. 152 (2), 667-675 (1994)

TITLE
MEDLINE 94110621

JOURNAL
FEATURES Location/Qualifiers
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BASE COUNT 82 a 95 c 89 g 94 t
ORIGIN

Query Match 100.0%; Score 48; DB 63; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacattactgggatgacgaagcgctataaccatccctgaagc 201
|||||
Qy 1 CACATTACTGGGATGATGACGAAGCGCTATACCCATCCCTGAAGC 48

RESULT 8
LOCUS MMU22994 360 bp mRNA ROD 09-APR-1996
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-27h, partial cds.

ACCESSION U22994
NID g780590
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.

REFERENCE
1 (bases 1 to 360)
Young, D. and Kearney, J.F.
Sequence analysis and antigen binding characteristics of Ig SCID
Ig+ mice

JOURNAL
Int. Immunol. 7 (5), 807-819 (1995)

MEDLINE 96053543

REFERENCE
2 (bases 1 to 360)
Young, D.C.

AUTHORS
Direct Submission

TITLE
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

Mar 19 16:07

US-08-612-929-23.rge

9

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COMMENT  NCBI gi: 780590
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            /tissue_type="spleen"
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            GSSYFDYWGQGTTLTVSS"
BASE COUNT      84 a   95 c   87 g   94 t
ORIGIN

Query Match      100.0%; Score 48; DB 91; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacatttactgggatgatgacagcgctataaccatccctgaagc 201
|||||
Qy 1 CACATTTTACTGGGATGATGACAGCGCTATACCCATCCCTGAGAGC 48

RESULT 9
LOCUS      MMU22979      360 bp      mRNA      ROD      26-APR-1995
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
            clone 45-12h, partial cds.
ACCESSION  U22979
NID        g780560
KEYWORDS   .
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Eumetazoa; Bilateria; Chordata; Chordata;
            Metazoa; Eumetazoa; Bilateria; Chordata; Chordata;
            Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
            Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
            Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 360)
AUTHORS   Young,D.C. and Kearney,J.F.
TITLE     Sequence analysis and antigen binding characteristics of
            immunoglobulins from SCID Ig+ mice
JOURNAL   Int. Immunol. 7 (1995) In press
REFERENCE  2 (bases 1 to 360)
AUTHORS   Young,D.C.
TITLE     Direct Submission
JOURNAL   Submitted (17-MAR-1995) David C. Young, University of Texas Health
            Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
            Houston, TX 77030, USA
FEATURES
  source      Location/Qualifiers
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            /strain="CB17 SCID"
            /organism="Mus musculus"
            /sub_species="domesticus"
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Mar 19 16:07

US-08-612-929-23.rge

10

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GSSYFDYWGQGTTLTVSS"
BASE COUNT      84 a   98 c   87 g   91 t
ORIGIN

Query Match      100.0%; Score 48; DB 65; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacatttactgggatgatgacagcgctataaccatccctgaagc 201
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Qy 1 CACATTTTACTGGGATGATGACAGCGCTATACCCATCCCTGAGAGC 48

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ID      MM22979      standard; RNA; ROD; 360 BP.
AC      U22979;
DT      29-APR-1995 (Rel. 43, Created)
DE      09-APR-1996 (Rel. 47, Last updated, Version 2)
DE      Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DE      clone 45-12h, partial cds.
KW      .
OS      Mus musculus (mouse)
OC      Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC      Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN      [1]
RP      1-360
RA      Young D., Kearney J.F.;
RT      *Sequence analysis and antigen binding characteristics of Ig SCID
RT      Ig+ mice";
RL      Int. Immunol. 7:807-819 (1995).
RN      [2]
RP      1-360
RA      Young D.C.;
RT      .
RL      Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.
RL      David C. Young, University of Texas Health Science Center, Houston,
RL      Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
CC      NCBI gi: 780560
FH      Key      Location/Qualifiers
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FT      S
SQ      Sequence 360 BP; 84 A; 98 C; 87 G; 91 T; 0 other;
Query Match      100.0%; Score 48; DB 12; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
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Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacatttactggatgacagcgctataaaccatccctgaagac 201
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Qy 1 CACATTACTGGGATGATGACAAAGCGCTATAACCCATCCCTGAAGAC 48

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AC U22994;
DT 29-APR-1995 (Rel. 43, Created)
DT 09-APR-1996 (Rel. 47, Last updated, Version 2)
DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DE clone 45-27h, partial cds.
KW .
OS Mus musculus (mouse)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-360
RA Young D., Kearney J.F.;
RT *Sequence analysis and antigen binding characteristics of Ig SCID
RT Ig⁺ mice";
RL Int. Immunol. 7:807-819(1995).
RN [2]
RP 1-360
RA Young D.C.;

Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.
RL David C. Young, University of Texas Health Science Center, Houston,
RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
CC NCBI gi: 780590
FH Key Location/Qualifiers
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SYFDYWGQGTLLTVSS"
SQ Sequence 360 BP; 84 A; 95 C; 87 G; 94 T; 0 other;

Query Match 100.0%; Score 48; DB 12; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacatttactggatgacagcgctataaaccatccctgaagac 201
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Qy 1 CACATTACTGGGATGATGACAAAGCGCTATAACCCATCCCTGAAGAC 48

RESULT 12
ID MM22977 standard; RNA; ROD; 360 BP.
AC U22977;

DT 29-APR-1995 (Rel. 43, Created)
DT 09-APR-1996 (Rel. 47, Last updated, Version 2)
DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DE clone 45-11h, partial cds.
KW .

OS Mus musculus (mouse)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-360
RA Young D., Kearney J.F.;
RT *Sequence analysis and antigen binding characteristics of Ig SCID
RT Ig⁺ mice";
RL Int. Immunol. 7:807-819(1995).
RN [2]
RP 1-360
RA Young D.C.;

Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.
RL David C. Young, University of Texas Health Science Center, Houston,
RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
CC NCBI gi: 780556
FH Key Location/Qualifiers
FH

source 1..360
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S
SYFDYWGQGTLLTVSS"
SQ Sequence 360 BP; 84 A; 97 C; 87 G; 92 T; 0 other;

Query Match 100.0%; Score 48; DB 12; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacatttactggatgacagcgctataaaccatccctgaagac 201
|||||
Qy 1 CACATTACTGGGATGATGACAAAGCGCTATAACCCATCCCTGAAGAC 48

RESULT 13
LOCUS MMU22994 360 bp mRNA ROD 26-APR-1995
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-27h, partial cds.
ACCESSION U22994
NID g780590
KEYWORDS .
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;


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/product="immunoglobulin he

Mar 19 16:07

US-08-612-929-23.rge

15

/db xref="PID:g780557"
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GSSYFDYWGQGTTLTVSS"

BASE COUNT 84 a 97 c 87 g 92 t
ORIGIN

Query Match 100.0%; Score 48; DB 91; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 cacatttactgggatgacaaagcgctataaccatccctgaagc 201
|||||
Qy 1 CACATTACTGGGATGATGACAAAGCGCTATTAACCCATCCCTGAAGC 48
GSSYFDYWGQGTTLTVSS

RESULT 16
LOCUS MMU22979 360 bp mRNA ROD 09-APR-1996
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-12h, partial cds.

ACCESSION U22979
NID g780560

KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.

REFERENCE 1 (bases 1 to 360)
AUTHORS Young, D. and Kearney, J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
Ig⁺ mice
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)

MEDLINE 96053543
REFERENCE 2 (bases 1 to 360)

AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

COMMENT NCBI gi: 780560
FEATURES Location/Qualifiers
source
1..360

/organism="Mus musculus"
/strain="CB17 SCID"
/sub_species="domesticus"
/clone="45-12h"
/cell_type="lymphocyte"
/tissue_type="spleen"

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/db_xref="PID:g780561"
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GSSYFDYWGQGTTLTVSS"

BASE COUNT 84 a 98 c 87 g 91 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mar 19 16:07

US-08-612-929-23.rge

16

Db 154 cacatttactgggatgacaaagcgctataaccatccctgaagc 201
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Qy 1 CACATTACTGGGATGATGACAAAGCGCTATTAACCCATCCCTGAAGC 48

RESULT 17
LOCUS MMIGMSMJ 366 bp RNA ROD 03-APR-1995
DEFINITION Mouse mRNA for variable region of IgM heavy immunoglobulin chain.
ACCESSION X53097
NID g52368
KEYWORDS autoantibody; Ig heavy chain; variable region.
SOURCE house mouse.

ORGANISM Mus musculus
Eukaryotae; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 366)
AUTHORS Carmack, C.E.

TITLE Direct Submission
JOURNAL Submitted (16-MAY-1990) to the EMBL/GenBank/DBJ databases. Carmack
C.E., Medical Biology Institute, 11077 North Torrey Pines Road, La
Jolla California 92037 USA

REFERENCE 2 (bases 21 to 366)
AUTHORS Hayakawa, K., Carmack, C.E., Hyman, R. and Hardy, R.R.

TITLE Natural autoantibodies to thymocytes: origin, VH genes, fine
specificities, and the role of Thy-1 glycoprotein
JOURNAL J. Exp. Med. 172 (3), 869-878 (1990)

MEDLINE 90354788

FEATURES Location/Qualifiers

source

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/organism="Mus musculus"
/strain="SM/J"
/tissue_type="spleen"
/cell_type="B-lymphocyte"
/cell_line="1-6C10 hybridoma (with SP2/0)"
/chromosome="12"
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/notes="IgM heavy chain variable region (122 AA)"

V_region

sig_peptide

1..21
/notes="leader (7 AA)"

CDS

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misc_feature

109..132
/notes="CDR1 (8 AA)"

misc_feature

133..174
/notes="framework 2 (14 AA)"

misc_feature

175..222
/notes="CDR2 (16 AA)"

misc_feature

223..318
/notes="framework 3 (32 AA)"

D_segment

319..336
/notes="CDR3 or D segment (6 AA)"

J_segment

337..366
/notes="joining (2) region (10 AA)"

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ORIGIN

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Mar 19 16:07

US-08-612-929-23.rgc

17

Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 175 cacattactgggatgatgacaaagcgctataaacccatccctgaagagc 222
|||||
Qy 1 CACATTTACTGGGATGATGACAAAGCGCTATACCCATCCCTCGAGAGC 48

RESULT 18
LOCUS S75897 438 bp mRNA ROD 14-JUN-1995
DEFINITION Ig VH=IgG heavy chain variable region [mice, Ric45.14.U1 hybridoma,
secondary variant DMK, mRNA Partial, 438 nt].
ACCESSION S75897
NID g861529
KEYWORDS
SOURCE mice Ric45.14.U1 hybridoma secondary variant DMK.
ORGANISM Mus sp.
Unclassified.
REFERENCE 1 (bases 1 to 438)
AUTHORS Kobrin,B.J., Schiff,C., Zivion,D., Scharff,M.D. and Spira,G.
TITLE In vitro activation of a nonproductive immunoglobulin allele by a
single base pair insertion
JOURNAL Hybridoma 13 (4), 257-261 (1994)
MEDLINE 95104873
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 161740] from the original journal article.
This sequence comes from Fig. 2.
COMMENT Insertion of a single A converts nonproductive allele to productive
one.

FEATURES
source Location/Qualifiers
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/note="mice"
307..438
/partial
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/note="Method: conceptual translation supplied by author.
This sequence comes from Fig. 3."
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/product="IgG heavy chain variable region"
/db_xref="PID:g861530"
/translation="KNFYGSADFYGQGTTLTVSAKTPPSVYPLAPGSAAGTNSMVT"

BASE COUNT 100 a 131 c 99 g 108 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.72e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 163 cacattactgggatgatgacaaagcgctataaacccatccctgaagagc 210
|||||
Qy 1 CACATTTACTGGGATGATGACAAAGCGCTATACCCATCCCTCGAGAGC 48

Search completed: Wed Mar 19 16:08:57 1997
Job time : 104 secs.

(ML)

[illegible]

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MPsrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

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Run on: Wed Mar 19 08:31:27 1997; MasPar time 62.46 Seconds
233.015 Million cell updates/sec
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Tabular output not generated.

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Title:
Description:
Perfect Score:
N.A. Sequence:
Comp:

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Scoring table: TABLE default
Gap 10

Nmatch STD :ibase 0: Query 0

Searched: 630489 seqs. 220513910 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

EST-STPS

1:EST1	2:EST2	3:EST4	5:EST5	6:EST6	7:EST7	8:EST8
9:EST9	10:EST10	11:EST11	12:EST12	13:EST13	14:EST14	
15:EST15	16:EST16	17:EST17	18:EST18	19:EST19	20:EST20	
21:EST21	22:EST22	23:EST23	24:EST24	25:EST25	26:EST26	
27:EST27	28:EST28	29:EST29	30:EST30	31:EST31	32:EST32	
33:EST33	34:EST34	35:EST35	36:EST36	37:EST37	38:EST38	
39:EST39	40:EST40	41:EST41	42:EST42	43:EST43	44:EST44	
45:EST45	46:EST46	47:EST47	48:EST48	49:EST49	50:EST50	
51:EST51	52:EST52	53:EST53	54:EST54	55:EST55	56:EST56	
57:EST57	58:EST58	59:EST59	60:EST60	61:EST61	62:EST62	
63:EST63	64:EST64	65:EST65	66:EST66	67:EST67	68:EST68	
69:EST69	70:EST70	71:EST71	72:EST72	73:EST73	74:EST74	
75:EST75	76:EST76	77:EST77	78:EST78	79:EST79	80:EST80	
81:EST81	82:EST82	83:EST83	84:EST84	85:EST85	86:EST86	
87:EST87	88:EST88	89:EST89	90:EST90	91:EST91	92:EST92	
93:EST93	94:EST94	95:EST95	96:EST96	97:EST97	98:EST98	
99:EST99						

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7
136:STS8 137:STS9 138:STS10 139:enEST1 140:enEST1
141:enEST2 142:enEST3 143:enEST4 144:enEST5 145:enEST6
146:enEST7 147:enEST8 148:enEST9 149:enEST10 150:enEST11
151:enEST12 152:enEST13 153:enEST14 154:enEST15
155:enEST16 156:enSTS 157:enEST1 158:enEST2 159:enEST3
160:enEST4 161:enEST5 162:enEST6 163:enEST7 164:enEST8
165:enEST9 166:enEST10 167:enEST11 168:enEST12
169:enEST13 170:enEST14 171:enEST15 172:enEST16
173:enSTS1 174:enSTS2

Statistics: Mean 7.079; Variance 1.441; scale 4.911

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description	Pred. No.	
							Length
1	18	54.5	136	166	HS941327	z42h04.r1 Soares par	3.36e-05
2	18	54.5	136	153	W19941	z42h04.r1 Soares par	3.36e-05
3	18	54.5	491	147	W04200	z457g09.r1 Soares fet	3.36e-05
4	18	54.5	491	168	HSW04200	z457g09.r1 Soares fet	3.36e-05
c 5	17	51.5	332	135	HSW2482C1	H. sapiens (D195225)	6.87e-04
c 6	17	51.5	395	7	H03526	yj37c07.r1 Homo sapie	6.87e-04
c 7	16	48.5	280	16	H33284	EST109132 Rattus sp.	1.25e-02
c 8	16	48.5	361	169	M27122	ma05h12.r1 Soares mou	1.25e-02
c 9	16	48.5	361	148	W12272	ma05h12.r1 Soares mou	1.25e-02
c 10	16	48.5	487	47	H120242	Human fetal brain cDN	1.25e-02
c 11	16	48.5	578	1	ATTS10923	A. thaliana transcrib	1.25e-02
c 12	15	45.5	207	49	H5W333C03B	Human placenta cDNA 5	2.02e-01
c 13	15	45.5	213	173	BT641	cow STS BMS1242.	2.02e-01
c 14	15	45.5	213	135	G18641	cow STS BMS1242.	2.02e-01
c 15	15	45.5	218	123	T82160	y495f01.r1 Homo sapie	2.02e-01
c 16	15	45.5	248	67	N67197	y248a06.s1 Homo sapie	2.02e-01
c 17	15	45.5	248	159	HS197306	y48a06.s1 Homo sapie	2.02e-01
c 18	15	45.5	260	172	T62922	TgESTzy19f01.r1 Toxop	2.02e-01
c 19	15	45.5	260	140	N61292	TgESTzy19f01.r1 Toxop	2.02e-01
c 20	15	45.5	281	160	HS270310	E0004F Homo sapiens c	2.02e-01
c 21	15	45.5	281	142	N83270	E0004F Homo sapiens c	2.02e-01
c 22	15	45.5	293	1	ATTS1048	A. thaliana transcrib	2.02e-01
c 23	15	45.5	326	72	R02441	ye82e05.r1 Homo sapie	2.02e-01
c 24	15	45.5	335	58	N93763	yf46e09.r1 Homo sapie	2.02e-01
c 25	15	45.5	352	87	S33386	yf70a05.r1 Homo sapie	2.02e-01
c 26	15	45.5	353	102	R1CS10879A	Rice cDNA, partial se	2.02e-01
c 27	15	45.5	353	172	TG2511	TgESTzy1ld04.r1 Toxop	2.02e-01
c 28	15	45.5	353	65	N60251	TgESTzy1ld04.r1 Toxop	2.02e-01
c 29	15	45.5	353	140	N60251	TgESTzy1ld04.r1 Toxop	2.02e-01
c 30	15	45.5	364	174	HS3436XF5	H. sapiens (DMS2954) D	2.02e-01
c 31	15	45.5	368	135	HS263W65	H. sapiens (D5S436) D	2.02e-01
c 32	15	45.5	375	118	T63447	yc07f01.r1 Homo sapie	2.02e-01
c 33	15	45.5	386	105	T08689	EST045681 Homo sapiens	2.02e-01
c 34	15	45.5	389	159	HS162324	zB55dl1.s1 Homo sapie	2.02e-01
c 35	15	45.5	411	81	R35425	yq65f11.r1 Homo sapie	2.02e-01
c 36	15	45.5	434	92	R71985	yj84h03.r1 Homo sapie	2.02e-01
c 37	15	45.5	440	89	R61773	yn09f12.r1 Homo sapie	2.02e-01
c 38	15	45.5	441	88	R59187	yq97b08.s1 Homo sapie	2.02e-01
c 39	15	45.5	451	172	SP007	EST178 Strongylocentr	2.02e-01
c 40	15	45.5	451	19	H41947	yo60b07.r1 Homo sapie	2.02e-01
c 41	15	45.5	459	8	H07088	z181g12.r1 Homo sapie	2.02e-01
c 42	15	45.5	471	47	HUM146G05B	Human fetal brain cDN	2.02e-01


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c 43 15 45.5 498 76 R17844 yg09h03.r1 Homo sapie 2.02e-01
c 44 15 45.5 686 154 W23231 81A2 Human retina CDN 2.02e-01
c 45 15 45.5 981 169 MM1627 ma74d12.r1 Soares mou 2.02e-01

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ALIGNMENTS

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RESULT 1
ID HS941327 standard; RNA; EST; 136 BP.
AC W19941;
DT 05-MAY-1996 (Rel. 47, Created)
DT 05-MAY-1996 (Rel. 47, Last updated, Version 1)
DE z642h04.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
DE 306295 5' similar to SW:PPCT BOVIN P02720
DE PHOSPHATIDYLCHOLINE-TRANSFER PROTEIN. [1] ;.
KW EST.
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RN [1]
RP 1-136
RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
RA Trevasakis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;
RT "The WashU-Merck EST Project";
RL Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu This clone is available royalty-free through
CC LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Trace considered overall poor quality Possible
CC reversed clone: similarity on wrong strand Seq primer: mob.REGA+ET
CC High quality sequence stop: 1. NCBI gi: 1296114
FH Key Location/Qualifiers
FH source 1..136
FH /organism="Homo sapiens"
FH /note="Vector: pT7T3D (Pharmacia) with a modified
FH polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
FH was primed with a Not I - oligo(dT) primer [5'-
FH TCTTACCAATCTGAAGTGGGAGCGCGCCACCAATTTTTTTTTTTTTTTTTT
FH T-3'] , double-stranded cDNA was size selected, ligated to
FH Eco RI adapters (Pharmacia), digested with Not I and clone
FH
FH into the Not I and Eco RI sites of a modified pT7T3 vector
FH (Pharmacia) . Library went through one round of
FH normalization to a Cot = 5. Library constructed by Bento
FH Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
FH adenomas was kindly provided by Dr. Stephen Marx, National
FH Institute of Diabetes and Digestive and Kidney Diseases,
FH NIH."
FH /clone="306295"
FH /clone_lib="Soares parathyroid tumor NbHPA"
FH /dev_stage="adult"
FH /lab_host="DH10B (ampicillin resistant)"
FH mRNA <1..>136
SQ Sequence 136 BP; 44 A; 28 C; 33 G; 28 T; 3 other;

Query Match 54.5%; Score 18; DB 166; Length 136;
Best Local Similarity 95.0%; Pred. No. 3.36e-05;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 48 gagagactgggtctactgg 67
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Qy 2 GAGACTGTGTCTACTGG 21

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RESULT 2
LOCUS W19941 136 bp mRNA EST 03-MAY-1996
DEFINITION z642h04.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
306295 5' similar to SW:PPCT BOVIN P02720
PHOSPHATIDYLCHOLINE-TRANSFER PROTEIN. [1] ;.
ACCESSION W19941
NID g1296114
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 136)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: mob.REGA+ET
High quality sequence stop: 1.
NCBI gi: 1296114
FEATURES
source
Location/Qualifiers
1..136
/organism="Homo sapiens"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer
[5'-
TCTTACCAATCTGAAGTGGGAGCGCGCCACCAATTTTTTTTTTTTTTTTTT
T-3'] , double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."
/clone="306295"
/clone_lib="Soares parathyroid tumor NbHPA"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
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BASE COUNT

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Mar 19 08:30

US-08-612-929-25.rst

5

ORIGIN

Query Match 54.5%; Score 18; DB 153; Length 136;
Best Local Similarity 95.0%; Pred. No. 3.36e-05;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 48 gagagactgtgtctactgg 67
|||||
Qy 2 GAGAGACTGTGTCTACTGG 21

RESULT 3

LOCUS W04200 491 bp mRNA EST 22-APR-1996
DEFINITION za57q09.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
296704 5' similar to SW:PPCT_BOVIN P02720
PHOSPHATIDYLCHOLINE-TRANSFER PROTEIN. [1] ;.

ACCESSION W04200

NID g1276109

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Eukaryotes; Chordata; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 491)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

Unpublished (1995)

JOURNAL

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ETPRimer
High quality sequence stop: 449.

NCBI gi: 1276109

Location/Qualifiers

FEATURES

source

1..491
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/note="Organ: Liver and Spleen; Vector: pTT3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACTGGAAGATTAAATTAAGATCTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pTT3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
/clone="296704"

/clone_lib="Soares fetal liver spleen INFLS"

/sex="male"

/dev stage="20 week-post conception fetus"

/lab_host="DHI0B (ampicillin resistant)"

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BASE COUNT

131 a 113 c 142 g 102 t 3 others

Mar 19 08:30

US-08-612-929-25.rst

6

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Query Match 54.5%; Score 18; DB 147; Length 491;
Best Local Similarity 95.0%; Pred. No. 3.36e-05;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2 gagagactgtgtctactgg 21
|||||
Qy 2 GAGAGACTGTGTCTACTGG 21

RESULT 4

ID HSW04200 standard; RNA; EST; 491 BP.
AC W04200;
DT 30-APR-1996 (Rel. 47, Created)
DT 30-APR-1996 (Rel. 47, Last updated, Version 1)
DE za57q09.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
296704 5' similar to SW:PPCT_BOVIN P02720
DE PHOSPHATIDYLCHOLINE-TRANSFER PROTEIN. [1] ;.

KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.

RN [1]

RP 1-491

RA Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P., Wilson, R.;
RA "The WashU-Merck EST Project";
RT Unpublished.

CC Contact: Wilson RK WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC est@watson.wustl.edu This clone is available royalty-free through

CC LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for

CC further information. Seq primer: ETPRimer High quality sequence

CC stop: 449. NCBI gi: 1276109

FH Key

Location/Qualifiers

FT source

1..491

/organism="Homo sapiens"

/note="Organ: Liver and Spleen; Vector: pTT3D (Pharmacia)

with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dT) primer

[5' AACTGGAAGATTAAATTAAGATCTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Pac I and cloned into the Pac I

and Eco RI sites of the modified pTT3 vector. Library wen

t through one round of normalization. Library constructed by

Bento Soares and M.Fatima Bonaldo."

/clone="296704"

/clone_lib="Soares fetal liver spleen INFLS"

/sex="male"

/dev stage="20 week-post conception fetus"

/lab_host="DHI0B (ampicillin resistant)"

<1..>491

FT mRNA

SQ Sequence 491 BP; 131 A; 113 C; 142 G; 102 T; 3 other;

Query Match 54.5%; Score 18; DB 168; Length 491;

Best Local Similarity 95.0%; Pred. No. 3.36e-05;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2 gagagactgtgtctactgg 21
 ||||| ||||| ||||| ||||| |||||
 Oy 2 GAGAGACTGTGTCTACTGG 21

RESULT 5
 LOCUS HS2482C1 332 bp DNA STS 28-NOV-1994
 DEFINITION H. sapiens (D19S225) DNA segment containing (CA) repeat; clone
 AFW2482cl; single read.
 ACCESSION Z17126
 NID g23751
 KEYWORDS CA repeat; dinucleotide repeat; CT repeat; microsatellite DNA;
 microsatellite marker; repeat polymorphism.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Eumetazoa; Bilateria; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Mollusca; Cephalopoda; Mammalia; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 332)
 Weissenbach, J.
 Direct Submission
 Submitted (05-OCT-1992) to the EMBL/GenBank/DBJ databases.
 Genethon, B.P. 60, 91002 Evry Cedex France. E-mail:
 Jean.Weissenbach@genethon.fr
 2 (bases 1 to 332)
 Weissenbach, J., Gyapay, G., Dib, C., Vignal, A., Morissette, J.,
 Millasseau, P., Vaysseix, G. and Lathrop, M.
 A second-generation linkage map of the human genome [see comments]
 Nature 359 (6398), 794-801 (1992)
 93063290
 3 (bases 1 to 332)
 Gyapay, G., Morissette, J., Vignal, A., Dib, C., Fizames, C.,
 Millasseau, P., Marc, S., Bernardi, G., Lathrop, M. and Weissenbach, J.
 The 1993-94 Genethon human genetic linkage map [see comments]
 Nature Genet. 7 (2 Spec No), 246-339 (1994)
 95004593
 clonng vector is M13mpl8;
 full automatic.
 FEATURES
 source
 Location/Qualifiers
 1..332
 /organism="Homo sapiens"
 /cell_line="CEPH 134702"
 /clone_lib="genomic DNA"
 /chromosome="19"
 BASE COUNT 97 a 89 c 49 g 97 t
 ORIGIN
 Query Match 51.5%; Score 17; DB 135; Length 332;
 Best Local Similarity 87.0%; Pred. No. 6.87e-04;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 232 catctaaagcaccagtcgaacaca 254
 ||||| ||||| ||||| ||||| |||||
 Cp 31 CATCGAGTACAGTACAGTACACA 9

RESULT 6
 LOCUS H03526 395 bp mRNA EST 20-JUN-1995
 DEFINITION yj37c07.r1 Homo sapiens cDNA clone 150924 5'.
 ACCESSION H03526
 NID g866459
 KEYWORDS EST.

SOURCE human clone=150924 library=Soares placenta Nb2HP vector=p7T73D
 (Pharmacia) with a modified polylinker host=DH10B (ampicillin
 resistant) primer=M13Rp1 Rsite1-Not I Rsite2-Eco RI Female Placenta
 obtained at birth (full term). 1st strand cDNA was primed with a
 Not I - oligo(dT) primer [5'
 AACTGGAGAAATTCCGCCGCGAGGAATTTTTTTTTTTTTTTT 3'], double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the modified p7T73
 vector. Library went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo.
 ORGANISM Homo sapiens
 Eukaryota; Eumetazoa; Bilateria; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Deuterostomia; Chordata; Tetrapoda; Amniota; Mammalia; Theria;
 Sarcopterygii; Chonata; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 395)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlffing, T., Soares, M., Tan, F.,
 Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 High quality sequence stops: 314
 Source: IMAGE Consortium, LINL
 This clone is available royalty-free through LINL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 FEATURES
 source
 Location/Qualifiers
 1..395
 /organism="Homo sapiens"
 /clone="150924"
 /note="human"
 BASE COUNT 81 a 95 c 79 g 139 t 1 others
 ORIGIN
 Query Match 51.5%; Score 17; DB 7; Length 395;
 Best Local Similarity 90.5%; Pred. No. 6.87e-04;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 254 aagaccagttcaacacagtc 274
 ||||| ||||| ||||| ||||| |||||
 Cp 26 AAGTACCAGTAGACACAGTC 6

RESULT 7
 LOCUS H33284 280 bp mRNA EST 08-SEP-1995
 DEFINITION EST109132 Rattus sp. cDNA 5' end.
 ACCESSION H33284
 NID g978701
 KEYWORDS EST.
 SOURCE rat primer=M13 Reverse library=rat PC-12 cells, NGF-treated (9
 days) vector=pBluescript SK- Rsite1-EcoRI Rsite2-XhoI poly(A) + RNA
 was purified from 9-day NGF treated PC12 cells. cDNA was
 constructed using an oligo-dT primer and directionally cloned using
 the Lambda ZAP II Vector Kit by Stratagene.
 ORGANISM Rattus sp.

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Murinae; Murinae; Rattus.

REFERENCE

AUTHORS Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A., Fuldner, R.A., Marmaras, S., Glodek, A., Cocayne, J.D., Adams, M.D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.

TITLE Comparative expressed sequence tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment

JOURNAL Proc. Natl. Acad. Sci. USA 92, 8303-8307 (1995)

COMMENT

Contact: Lee NH
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: nhlee@tigr.org
For clone availability please contact the TIGR Database (tdbinfo@db.tigr.org)

FEATURES

source location/Qualifiers
1..280
/organism="Rattus sp."

/note="rat"

<1..>280

BASE COUNT

ORIGIN 75 a 68 c 62 g 73 t 2 others

Query Match 48.5%; Score 16; DB 16; Length 280;
Best Local Similarity 90.0%; Pred. No. 1.25e-02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 80 agtaccagtcacaccacgctc 99

|||||

Cp 25 AGTACCAGTCAGACACACTC 6

RESULT

ID M2722 standard; RNA; EST; 361 BP.

AC M2722;

DT 29-APR-1996 (Rel. 47, Created)

DT 29-APR-1996 (Rel. 47, Last updated, Version 1)

DE ma05hl2.rl Soares mouse p3NMF19.5 Mus musculus cDNA 5'.

KW EST.

OS Mus musculus (mouse)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

RN [1]

RP 1-361

RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,

RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,

RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,

RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,

RA Waterston R.;

RT "The WashU-HMI Mouse EST Project";

RL Unpublished.

CC Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project

CC Washington University School of Medicine 4444 Forest Park Parkway,

CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810

CC Email: mouseest@watson.wustl.edu This clone is available

CC royalty-free through LNL; contact the IMAGE Consortium

CC (info@image.llnl.gov) for further information. Putative full length

CC read Seq primer: mob.REGA+ET. NCBI gi: 1282961

FH Key

Location/Qualifiers

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FH source

FT 1..361

/organism="Mus musculus"

/note="Vector: pT7T3D (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TCTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo."

/clone_lib="Soares mouse p3NMF19.5"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

<1..>361

FT mRNA

SQ Sequence 361 BP; 89 A; 77 C; 104 G; 91 T; 0 other;

Query Match 48.5%; Score 16; DB 16; Length 361;

Best Local Similarity 90.0%; Pred. No. 1.25e-02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 225 cgaagtacctgcagaacaca 244

|||||

Cp 28 CGAAGTACCAGTAGAACACA 9

RESULT

LOCUS M2722 361 bp mRNA EST 26-APR-1996

DEFINITION ma05hl2.rl Soares mouse p3NMF19.5 Mus musculus cDNA 5'.

ACCESSION M2722

NID g1282961

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;

Murinae; Mus.

REFERENCE 1 (bases 1 to 361)

AUTHORS Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,

Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,

Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,

Theising B., Wylie T., Lennon G., Soares B., Wilson R. and

Waterston R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Putative full length read

Seq primer: mob.REGA+ET.

NCBI gi: 1282961

FEATURES

source

1..361

/organism="Mus musculus"

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/notes=Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGGATTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo.*

/clone_lib="Soares mouse p3NMF19.5"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

<1..>361

BASE COUNT 89 a 77 c 104 g 91 t

ORIGIN

Query Match 48.5%; Score 16; DB 148; Length 361;

Best Local Similarity 90.0%; Pred. No. 1.25e-02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 225 cgaagctactgcagaacaca 244

||||||| | |||||

Cp 28 CGAGTACCACTAGACACA 9

RESULT 10

LOCUS HUM094E12A 487 bp mRNA EST 18-DEC-1995

DEFINITION Human fetal brain cDNA 3'-end GEN=094E12.

ACCESSION D80657

NID g1178534

KEYWORDS EST (expressed sequence tag); Human fetal brain.

SOURCE Homo sapiens Fetus brain cDNA to mRNA, clone_lib:human fetal brain.

ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 487)

Fujiwara, T.

Direct Submission

TITLE Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu

JOURNAL Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical

Co., Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,

Japan

2 (bases 1 to 487)

Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuqa, Y., Nagata, M.,

Okuno, S., Ozaki, K., Shimizu, F., Shinada, Y., Shinomiya, H.,

Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,

Maekawa, H., Shin, S. and Nakamura, Y.

Large-scale sequencing project at Otsuka GEN Research Institute

Unpublished (1995)

COMMENT Submitted (7-Nov-1995) to DDBJ by:

Tsutomu Fujiwara

Otsuka GEN Research Institute

Otsuka Pharmaceutical Co., Ltd

463-10 Kagasuno Kawauchi-cho

Tokushima, Tokushima

771-01

Japan

Phone: 0886-65-2888

Fax : 0886-37-1035.

Location/Qualifiers

1..487

/clone_lib="human fetal brain"

/dev_stage="Fetus"

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/organism="Homo sapiens"

/sequenced_mol="cDNA to mRNA"

/tissue_type="brain"

BASE COUNT 130 a 104 c 100 g 137 t 16 others

ORIGIN

Query Match 48.5%; Score 16; DB 47; Length 487;

Best Local Similarity 63.6%; Pred. No. 1.25e-02;

Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 305 taammvtaaaataacvgtctcts 326

|| ::||| || ||:|||||

Cp 23 TACCACTAGAACACAGTCTCTC 2

RESULT 11

LOCUS ATTS1023 578 bp RNA EST 13-AUG-1993

DEFINITION A. thaliana transcribed sequence; clone GBGe85.

ACCESSION Z25510

NID g396646

KEYWORDS expressed sequence tag; partial cDNA sequence.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryotae; mitochondrial eukaryotes; Chlorophyta/Embryophyta

group; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;

Magnoliopsida; Dilleniidae; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 578)

AUTHORS Quigley, and Mache R. and Mache, R.

Direct Submission

TITLE Submitted (10-AUG-1993) to the EMBL/GenBank/DBJ databases. CNRS,

JOURNAL GDR-1003 ACS, INRA, laboratoire de Biologie Moleculaire, BP 27,

31326 Castanet-Tolosan cedex, France.

E-mail: gdr-svpetoulouse.inra.fr. On behalf of: CNRS URA 1178,

Laboratoire de Biologie Moleculaire vegetale, B.P. 53X, 38041

Grenoble Cedex, France. E-mail: FQUIGLEY@grenet.fr

2 (bases 1 to 578)

CNRS.

The Arabidopsis thaliana transcribed genome: the GDR cDNA program

Unpublished

TITLE Cloning vector: Lambda ZAPII.;

JOURNAL full automatic.

COMMENT Location/Qualifiers

1..578

source

/organism="Arabidopsis thaliana"

/clones="GBGe85"

/tissue_type="Flower buds of A.thaliana ecotype columbia

C24"

/clone_lib="Grenoble-B"

BASE COUNT 143 a 116 c 126 g 193 t

ORIGIN

Query Match 48.5%; Score 16; DB 1; Length 578;

Best Local Similarity 86.4%; Pred. No. 1.25e-02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 148 gtgttctaccggtgctcggtg 169

||||||| ||| ||||| ||

QY 10 GTCTTCTACTGGTACTTCGATG 31

RESULT 12

LOCUS HUM533E03B 207 bp mRNA EST 13-DEC-1995

DEFINITION Human placenta cDNA 5'-end GEN=533E03.

ACCESSION D79180

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```
NID      g1181053
KEYWORDS EST(expressed sequence tag); Human placenta.
SOURCE   Homo sapiens placenta cDNA to mRNA, clone_lib:human placenta
          polyA+.
ORGANISM  Homo sapiens
          Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
          Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 207)
          Fujiwara,T.
          Direct Submission
          Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu
          Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
          Co.,Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
          Japan
REFERENCE 2 (bases 1 to 207)
          Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuwa,Y., Nagata,M.,
          Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,
          Takaichi,A., Takeda,S., Watanabe,F., Takahashi,E., Hirai,Y.,
          Maekawa,H., Shin,S. and Nakamura,Y.
          Large-scale sequencing project at Otsuka GEN Research Institute
          Unpublished (1995)
JOURNAL   Submitted (7-Nov-1995) to DDBJ by:
          Tsutomu Fujiwara
          Otsuka GEN Research Institute
          Otsuka Pharmaceutical CO.,Ltd
          463-10 Kagasuno Kawauchi-cho
          Tokushima, Tokushima
          771-01
          Japan
          Phone:0886-65-2888
          Fax :0886-37-1035.
FEATURES
          source
            1..207
            /clone_lib="human placenta polyA+"
            /organism="Homo sapiens"
            /sequenced_mol="cDNA to mRNA"
            /tissue_type="placenta"
BASE COUNT 52 a 41 c 42 g 72 t
ORIGIN
Query Match 45.5%; Score 15; DB 49; Length 207;
Best Local Similarity 89.5%; Pred. No. 2.02e-01;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 54 agtacaagttagaccacagt 72
      ||||| ||||| |||||
Cp 25 AGTACCAGTAGACACACT 7

RESULT 13
ID      BT641      standard; DNA; STS; 213 BP.
AC      G18641;
DT      13-MAR-1996 (Rel. 47, Created)
DT      13-MAR-1996 (Rel. 47, Last updated, Version 1)
DE      cow STS BMS1242.
KW      primer; sequence tagged site; STS sequence.
OS      Bos taurus (cattle)
OC      Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC      Theria; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae.
RN      [1]
RP      1-213
RA      Stone R.T., Pulido J.C., Duyk G.M., Kappes S.M., Keele J.W.,
RA      Beattie C.W.;
RT      *A small-insert bovine genomic library highly enriched for
```

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```
RT      microsatellite repeat sequences*;
RL      Mamm. Genome 6:714-724(1995).
CC      Contact: Roger Stone U.S. Meat Animal Research Center U.S. Dept. of
CC      Agriculture - Agricultural Research Service P.O. Box 166, Clay
CC      Center, NE 68933 Tel: (402) 762-4166 Fax: (402) 762-4173 Primer A:
CC      AGTGTGATCAACACGGCAG Primer B: AGTGACTGTCAGTGTTC STS size: 107.
CC      NCBI gi: 1223098
FH      Key      Location/Qualifiers
FH      source      1..213
FH      /organism="Bos taurus"
FH      /note="cow"
FT      STS      84..190
FT      primer_bind      84..103
FT      primer_bind      complement(171..190)
SQ      Sequence 213 BP; 41 A; 41 C; 64 G; 67 T; 0 other;

Query Match 45.5%; Score 15; DB 173; Length 213;
Best Local Similarity 94.1%; Pred. No. 2.02e-01;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 196 gtagaacacattctctc 212
      ||||| ||||| |||||
Cp 18 GTAGACACAGTCTCTC 2

RESULT 14
LOCUS      G18641      213 bp      DNA      STS      12-MAR-1996
DEFINITION cow STS BMS1242.
ACCESSION      G18641
NID      g1223098
KEYWORDS      STS sequence; primer; sequence tagged site.
SOURCE      cow.
ORGANISM      Bos taurus
REFERENCE      1 (bases 1 to 213)
AUTHORS      Stone,R.T., Pulido,J.C., Duyk,G.M., Kappes,S.M., Keele,J.W. and
            Beattie,C.W.
TITLE      A small-insert bovine genomic library highly enriched for
            microsatellite repeat sequences
JOURNAL      Mamm. Genome 6 (10), 714-724 (1995)
MEDLINE      96116960
COMMENT      Contact: Roger Stone
            U.S. Meat Animal Research Center
            U.S. Dept. of Agriculture - Agricultural Research Service
            P.O. Box 166, Clay Center, NE 68933
            Tel: (402) 762-4166
            Fax: (402) 762-4173

Primer A: AGTGTGATCAACACGGCAG
Primer B: AGTGACTGTCAGTGTTC
STS size: 107.
FEATURES
          source
            1..213
            /organism="Bos taurus"
            /note="cow"
            84..190
            primer_bind      84..103
            primer_bind      complement(171..190)
BASE COUNT 41 a 41 c 64 g 67 t
ORIGIN
Query Match 45.5%; Score 15; DB 135; Length 213;
```


16

Db 74 tgctactggtttctatg 94
|| ||||| |||| ||||
Qy 11 TGTTACTGGTACTTCGATG 31

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1

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Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:30:52 1997; MasPar time 11.30 Seconds
254.786 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-25
Description: (1-33) from US08612929.seq
Perfect Score: 33
N.A. Sequence: 1 AGAGAGACTGTTCTACTGGTACTTCGATGTC 33
Comp: TCTCTGACACAGATGACCATGAAGCTACAG

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.740; Variance 3.559; scale 1.613

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	Pred. No.
1	33	100.0	423 14 Q83492
2	33	100.0	483 14 Q83491
3	25	75.8	91 9 Q51746
4	21	63.6	91 9 Q51746
5	21	63.6	120 14 Q83500
6	21	63.6	423 14 Q83493
7	20	60.6	417 9 Q51555
8	20	60.6	417 12 Q73023

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2

9	20	60.6	417 12 Q73025	CY1748RHC VH region.	1.20e-01
10	20	60.6	417 12 Q73024	CY1748RHB VH region.	1.20e-01
11	20	60.6	417 9 Q51551	PB1.3/Humanised heavy	1.20e-01
12	19	57.6	30 13 Q78738	Murine anti-human ath	4.02e-01
13	19	57.6	39 7 Q51787	Mixed oligonucleotide	4.02e-01
14	19	57.6	318 1 Q04593	Sequence encoding reg	4.02e-01
15	19	57.6	364 22 T12813	Murine antibody ZCE-0	4.02e-01
16	19	57.6	364 22 T12831	Human antibody hZCE g	4.02e-01
17	19	57.6	366 1 N90814	DNA encoding heavy ch	4.02e-01
18	19	57.6	390 13 Q78730	Murine anti-human ath	4.02e-01
19	19	57.6	453 4 N30166	Sequence encoding the	4.02e-01
20	19	57.6	462 21 T31541	3H1 heavy chain varia	4.02e-01
21	19	57.6	462 22 T34542	Monoclonal anti-idiot	4.02e-01
22	18	54.5	36 2 Q11195	Ballast Constituent c	1.31e+00
23	18	54.5	444 16 Q99035	Murine antibody Fv bi	1.31e+00
24	18	54.5	444 4 Q27133	Heavy chain variable	1.31e+00
25	18	54.5	458 1 N91146	2H7 VH sequence.	1.31e+00
26	18	54.5	459 2 N70971	2H7 VH sequence which	1.31e+00
27	18	54.5	717 13 Q76275	ScFv anti-HCG.	1.31e+00
28	18	54.5	734 12 Q67359	Anti-HCG scFv.	1.31e+00
29	17	51.5	30 7 Q45602	Mixed oligonucleotide	4.20e+00
c	30	17	51.5	HUH-G6.	4.20e+00
c	31	17	51.5	HUH-G16.	4.20e+00
32	17	51.5	354 4 Q26757	431/26 VH hum.	4.20e+00
33	17	51.5	354 13 Q75544	Humanised antibody he	4.20e+00
34	17	51.5	357 2 N60249	Immunoglobulin heavy	4.20e+00
35	17	51.5	366 16 Q90418	DNA encoding immunogl	4.20e+00
36	17	51.5	420 2 N60253	Mouse Ig heavy chain	4.20e+00
37	17	51.5	425 7 Q44060	H65 heavy chain varia	4.20e+00
38	17	51.5	437 1 N90934	Y22 heavy chain of an	4.20e+00
39	17	51.5	438 16 Q90427	DNA encoding anti-idi	4.20e+00
40	17	51.5	711 9 Q55180	Sequence encoding the	4.20e+00
41	17	51.5	723 7 Q42284	V-J(kappa)/(Gly)4Ser	4.20e+00
42	17	51.5	748 17 T05782	ScFv(FWP51) cDNA.	4.20e+00
43	17	51.5	913 12 Q81076	Bispecific CD3-L6FvIg	4.20e+00
44	17	51.5	2012 4 Q28263	Fv(FRP51)-ETA fusion	4.20e+00
45	17	51.5	3314 10 Q58896	Humanised anti-CEA sF	4.20e+00

ALIGNMENTS

RESULT 1
ID Q83492 standard; cDNA; 423 BP.
AC Q83492;
DT 20-SEP-1995 (first entry)
DE Chimeric antibody 3B9 heavy chain.
KW Chimeric antibody; antibody engineering; monoclonal antibody;
KW MAb; interleukin-4; IL-4; allergy; ds.
OS Homo sapiens; Mus sp.
FH Key Location/Qualifiers
FT CDS 1..423
FT /tag= a
FT sig_peptide 1..57
FT /tag= b
FT mat_peptide 58..423
FT /tag= c
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Cross MS, Holmes SD, Sylvester DR;

Query Match	63.6%;	Score 21;	DB 9;	Length 91;	
Best Local Similarity	0.0%;	Pred. No. 3.54e-02;			
Matches	0;	Conservative	26;	Mismatches	5;
				Indels	0;
				Gaps	0;

Db	18	vvhvvshhshvhhvhhvshvvvvvhhvhhv 48
		##### : ##### : #####
Qy	1	AGAGAGACTGTTCTTACTGCTACTTGCATG 31

RESULT	5	
ID	Q83500	standard; DNA; 120 BP.
AC	Q83500;	
DT	20-SEP-1995	(first entry)
DE	Heavy chain variable region fragment.	
KW	Humanized antibody; antibody engineering; monoclonal antibody;	
KW	MAb; interleukin-4; IL-4; allergy; heavy chain; ss.	
OS	Synthetic.	
PN	W09507301-A.	
PF	16-MAR-1995.	
PD	07-SEP-1994;	U10308.
PR	07-SEP-1993;	US-117366.
PR	14-OCT-1993;	US-136783.
PA	(SMIK) SMITHKLINE BEECHAM CORP.	
PA	(SMIK) SMITHKLINE BEECHAM PLC.	
PI	Gross MS, Holmes SD, Sylvester DR;	
DR	WPI; 95-123387/16.	
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived	
PT	from high affinity mAbs - useful in treatment of IL-4-mediated	
PT	and IgE-mediated allergic conditions	
PS	Example 3; Page 62; 9pp; English.	
CC	A humanized antibody was designed to contain mouse CDRs (from	
CC	anti-IL-4 MAb 3B9 MAb) within a human antibody framework. A	
CC	synthetic heavy chain was made using the oligonucleotides given	
CC	in Q83498-502 and amplified by PCR using the primers given in	
CC	Q83503-04. The construct was ligated into vector pCD, along	
CC	with a signal sequence (Q83494) and an IgG1 human constant	
CC	framework. The CDR gene regions of a pre-existing light chain	
CC	segment were replaced with synthetic IL-4 CDR genes constructed	
CC	from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),	
CC	and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into	
CC	the vector. The anti-IL4 engineered antibody was expressed in	
CC	COS and CHO cells.	
SQ	Sequence	120 BP; 20 A; 39 C; 29 G; 32 T;

Query Match	63.6%;	Score 21;	DB 14;	Length 120;	
Best Local Similarity	86.2%;	Pred. No. 3.54e-02;			
Matches	25;	Conservative	0;	Mismatches	4;
				Indels	0;
				Gaps	0;

Query Match 63.6%; Score 21; DB 14; Length 120;
Best Local Similarity 86.2%; Pred. No. 3.54e-02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

[illegible]

MA 190829 US-08-612-929-25 JRG

FT	/*tag= a	
FT	sig_peptide	1..57
FT	/*tag= b	
FT	mat_peptide	58..423
FT	/*tag= c	
PN	W09507301-A.	
PD	16-MAR-1995.	
PF	07-SEP-1994; U10308.	
PR	07-SEP-1993; US-117366.	
PR	14-OCT-1993; US-136783.	
PA	(SMIK) SMITHKLINE BEECHAM CORP.	
PA	(SMIK) SMITHKLINE BEECHAM PLC.	
PI	Gross MS, Holmes SD, Sylvestre DR;	
DR	WPI; 95-123387/16.	
DR	P-PSDB; R70192.	
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived	
PT	from high affinity mAbs - useful in treatment of IL-4-mediated	
PT	and IgE-mediated allergic conditions	
PS	Disclosure; Fig.4; 97pp; English.	
CC	A humanized antibody heavy chain variable region and signal	
CC	sequence is given in R70192. The signal sequence is also	
CC	provided in R70193. The CDR sequences of the construct are	
CC	identical to the native CDRs of mouse anti-human IL-4 Mab	
CC	3B9 (R70198-200).	
SQ	Sequence	423 BP; 84 A; 131 C; 102 G; 106 T;
Query Match		63.6%; Score 21; DB 14; Length 423;
Best Local Similarity		86.2%; Pred. No. 3,54e-02;
Matches	25; Conservative	0; Mismatches 4; Indels 0; Gaps 0;

Db 361 gaaacggttttctactggtacttcgacgt 389
 || | | | | | | | | | | | | | |
Ov 4 GAGACTGTGTTCTACTGGTACTTCGATGT 32

RESULT	7	
ID	Q51555 standard; DNA; 417 BP.	
AC	Q51555;	
DT	25-MAY-1994 (first entry)	
DE	PB1.3/Humanised heavy chain-C signal peptide and variable region DNA.	
KE	Human; immunoglobulin; constant; region; humanised; p-selectin; light;	
KW	blocking; antibody; heavy; chain; variable; murine; thrombotic disease;	
KW	monoclonal; PB1.3; CDR; complementarity determining region; leukocyte;	
KW	expression vector; coexpression; pHCW-1748RIA-gammaCI-dhfr; epitope;	
KW	pHCW-1748RIA-KB-neo; PB1.3/Humanised version A; vascular endothelium;	
KW	pHCW-1747CH-gammaCI-neo; pHCW-1747-CL-KR-neo; PB1.3 chimera;	
KW	acute lung injury; ischaemia reperfusion injury; inflammation; ss.	
OS	Chimera Mus musculus.	
OS	Chimera Homo sapiens.	
PN	W09321956-A.	
PD	11-NOV-1993.	
PF	04-MAY-1993; U04274.	
PR	05-MAY-1992; US-880196.	
PA	(CYTE-) CYTEL CORP.	
PI	Chestnut RM, Paulson JC, Polley MJ;	
DR	WPI; 93-368423/46.	
DR	P-PSDB; R43693.	
PT	Anti-P-selectin antibody for ischaemia acute lung injury treatment -	
PT	useful to treat inflammation and pathological conditions of	
PT	intercellular adhesion by competitive inhibition assays	
PS	Example 10; Fig 17; 82pp; English.	
CC	The sequences given in Q51551-55 encode the heavy and light chains of	
CC	the PB3.1/humanised P-selectin blocking antibody of the invention.	
CC	The sequences given in Q51549-50 which encode the heavy and light	

QY 12 GTTCTACTGGTACTCGATGTC 33

RESULT 10

ID Q73024 standard; cDNA; 417 BP.
AC Q73024;
DT 12-JUN-1995 (first entry)
DE CY1748RHB VH region.
KW P-selectin; CY1748RHB; light chain; heavy chain; variable region;
KW VL; VH; complementarity determining region; CDR;
KW antibody engineering; humanized antibody; leukocyte adhesion;
KW transplant rejection; autoimmune disease; therapeutic; diagnostic;
KW monoclonal antibody; Mab; COS; es.
OS Homo sapiens. Location/Qualifiers
FH Key 1..417
FT CDS /*tag= a
FT sig_peptide 1..57
FT /*tag= b
FT mat_peptide 58..417
FT /*tag= c
PN W09425067-A.
PD 10-NOV-1994.
PF 04-MAY-1994; U04935.
PR 04-MAY-1993; W0-004272.
PR 05-MAY-1993; US-057292.
PR 25-FEB-1994; US-202047.
PA (CYTE-) CYTEL CORP.
PI Bayer R, Bendig MM, Chesnut RW, Jones ST, Krieglner M;
PI Nunn M, Paulson JC, Perez C, Polley MJ, Saldanha JW;
PI WP1; 94-357916/44.
DR P-PSDB; R62679.
PT Blocking antibodies against P-selectin - used to treat
PT inflammation and inhibit leukocyte adhesion to platelets and/or
PT activated vascular endothelium
PS Disclosure; Fig. 12; 138pp; English.
CC Human Mab DEN VL and human Mab 21/28'CL VH regions were selected
CC as fragments to join the corresponding CDRs of mouse anti-P-selectin
CC Mab PBL.3 (ATCC HB 11041) for construction of humanized antibodies.
CC 3 Versions of the VH region (CY1748RHA, CY1748RHB, CY1748RHC) were
CC designed (given in R62678-80, respectively) and 4 versions of the VL
CC region (CY1748RLA, CY1748RLB, CY1748RLC, CY1748RLD) (R62674-77).
CC Humanized antibodies were expressed in COS cells. The preferred
CC construct was formed from CY1748RHB and CY1748RLD.
SQ Sequence 417 BP; 94 A; 102 C; 118 G; 103 T;

Query Match 60.6%; Score 20; DB 12; Length 417;
Best Local Similarity 95.5%; Pred. No. 1.20e-01;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 363 gttcgaactggtactcgatgc 384

||||| ||||| ||||| ||||| |||||

QY 12 GTTCTACTGGTACTCGATGTC 33

RESULT 11

ID Q51551 standard; DNA; 417 BP.
AC Q51551;
DT 25-MAY-1994 (first entry)
DE PBL.3/Humanised heavy chain signal peptide and variable region DNA.
KW Human; immunoglobulin; constant; region; humanised; P-selectin; light;
KW blocking; antibody; heavy; chain; variable; murine; thrombotic disease;
KW monoclonal; PBL.3; CDR; complementarity determining region; leukocyte;
KW expression vector; coexpression; pHCW-1748RHA-gamma1C1-dhfr; epitope;

KW pHCW-1748RLA-KR-neo; PBL.3/Humanised version A; vascular endothelium;
KW pHCW-1747CH-gamma1C1-neo; pHCW-1747-CL-KR-neo; PBL.3 chimera;
KW acute lung injury; ischaemia reperfusion injury; inflammation; ss.

OS Chimera Mus musculus.

OS Chimera Homo sapiens.

PN W09321956-A.

PD 11-NOV-1993.

PF 04-MAY-1993; U04274.

PR 05-MAY-1992; US-880196.

PA (CYTE-) CYTEL CORP.

PI Chestnut RW, Paulson JC, Polley MJ;

DR WP1; 93-368423/46.

DR P-PSDB; R43689.

PT Anti-P-selectin antibody for ischaemia acute lung injury treatment -

PT useful to treat inflammation and pathological conditions of

PT intercellular adhesion by competitive inhibition assays

PS Example 10; Fig 13; 82pp; English.

CC The sequences given in Q51551-55 encode the heavy and light chains of

CC the PB3.1/humanised P-selectin blocking antibody of the invention.

CC The sequences given in Q51549-50 which encode the heavy and light

CC chain variable region sequences of the murine monoclonal antibody

CC PBL.3 and the sequences given in Q51547-48 which encode human

CC immunoglobulin constant regions were used in the production of this

CC antibody. The CDRs from PBL.3 heavy and light chains were substituted

CC for the CDRs of human heavy and light chains. The humanised variable

CC regions were inserted into expression vectors. By coexpression of

CC appropriate combinations of heavy and light chains, several humanised

CC antibodies can be expressed. Coexpression of pHCW-1748RHA-gamma1C1-

CC dhfr and pHCW-1748RLA-KR-neo gives rise to the PBL.3/Humanised

CC version A. Coexpression of pHCW-1747CH-gamma1C1-neo and pHCW-1747-

CC CI-KR-neo gives rise to the PBL.3 chimera. These humanised antibodies

CC selectively bind epitopes on P-selectin and block adhesion of

CC leukocytes to the vascular endothelium. They may be used to treat

CC inflammatory and thrombotic diseases and other pathological conditions

CC involving P-selectin and antibodies to it, esp. acute lung injury and

CC ischaemia reperfusion injury.

SQ Sequence 417 BP; 94 A; 101 C; 119 G; 103 T;

Query Match 60.6%; Score 20; DB 9; Length 417;
Best Local Similarity 95.5%; Pred. No. 1.20e-01;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 363 gttcgaactggtactcgatgc 384

||||| ||||| ||||| ||||| |||||

QY 12 GTTCTACTGGTACTCGATGTC 33

RESULT 12

ID Q78738 standard; DNA; 30 BP.
AC Q78738;
DT 18-JUL-1995 (first entry)
DE Murine anti-human atherosclerotic plaque Mab 22D3 VH CDR3 DNA.
KW Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;
KW murine monoclonal antibody; heavy chain variable region; CDR3;
KW complementarity determining region; imaging; plaque ablation; ds.

OS Mus musculus.

FH Key Location/Qualifiers

FT misc RNA 1..30

FT /*tag= a

FT /product= CDR3

PN W09425053-A.

PD 10-NOV-1994.

PF 26-APR-1994; U04641.

PR 26-APR-1993; US-053451.

PPA	(SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
PPR	Galenoff E, Chen FW, Ditlow CC;
PPD	WPI; 94-357904/44.
PPC	p-PSDB; R62884.
DR	
PPPT	New antigen comprising hydroxy:steroid and quat. ammonium salt -
PPPT	and related antibodies, useful e.g. for imaging, ablating or
PPPT	treating atherosclerotic plaque, and detecting plaque specific
PPPT	antibodies
PPS	Claim 210; Page 148; 288pp; English.
PPC	Mice were immunised with an extract of human atherosclerotic plaque,
CC	then spleen cells were fused with SP2/01-Ag-14 myeloma cells.
CC	Hybridomas were screened by ELISA for reactivity with the immunogen
CC	and clone 2ZD3 was isolated. The 2ZD3 antibody reacts specifically
CC	with atherosclerotic tissue; it recognises a non-protein antigen
CC	containing cholesterol (or similar steroid that is a substrate for
CC	cholesterol oxidase) and a quaternary ammonium salt (pref. a
CC	phosphatidylcholine or related compound that is a substrate for
CC	phospholipase C). The CDR sequences for the heavy and light chains
CC	of 2ZD3 were determined; isolated nucleic acid molecules comprising
CC	sequences coding for the CDRs are claimed, including chimeric (CDR-
CC	grafted) murine-human antibody coding sequences.
SO	Sequence 30 BP: 6 A: 5 G: 7 C: 12 T:

Query Match	57.6%;	Score 19;	DB 13;	Length 30;
Best Local Similarity	100.0%;	Pred. No. 4.02e-01;		
Matches	19;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Db 12 ctactggtacttcgatgctc 30
11 |||||
Ov 15 CTACTGGTACTTCGATGTC 33

RESULT	13
ID	Q51787 standard; DNA; 39 BP.
AC	Q51787;
DT	20-DEC-1993 (first entry)
DE	Mixed oligonucleotide #19 encodes ballast constituent.
KW	Fusion protein; ballast constituent; pro-insulin production; recombinant protein production; HMG CoA reductase; human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase; mixed oligonucleotide; ss.

OS	synthetic.	Key	Location/Qualifiers
FT		repeat_unit	4..6
FT		/*tag=	a
FT		/rpt_type=	tandem
FT		/note=	'can be repeated y times, where y is 4-11,
FT		provided that y*z is 6-12"	
FT		repeat region	4..36
FT		/*tag=	b
FT		/note=	'(DCD)11"
FT		repeat_unit	36..38
FT		/*tag=	c
FT		/rpt_type=	tandem
FT		/note=	'can be repeated z times, where z is 1-4,
FT		provided that y*z is 6-12; N stands for	
FT		identical or different nucleotides,	
FT		excluding stop codons"	
PN		US5227293-A.	
PD		13-JUL-1993.	
PF		29-AUG-1989;	399874.
PR		29-AUG-1989;	US-399874.
PR		23-APR-1992;	US-838221.
PA		(GENO) GEN HOSPITAL CORP.	

PA (FARH) HOECHST AG.
 PI Habermann P, Seed B, Stengelin S, Uhlmann E, Ulmer W;
 PR WPI; 93-235119/29.
 PT Fusion proteins for prodn. of e.g. pro-insulin - comprise gene
 PT for desired protein and oligo-nucleotide(s) encoding ballast
 PT protein
 PT Claim 9; Column 30; 22pp; English.
 PS This preferred mixed oligonucleotide encodes a ballast constituent
 CC and is inserted between a regulatory region and the structural gene
 CC encoding a desired protein, esp. pro-insulin. The short ballast
 CC component improves protease resistance of the fusion protein while
 CC still allowing the desired protein to adopt its correct conformation
 CC prior to cleavage of the ballast constituent.
 SO Sequence 39 BP; 1 A; 11 C; 1 G; 1 T;

Query Match	57.6%	Score 19;	DB 7;	Length 39;
Best Local Similarity	28.0%;	Pred. No. 4.02e-01;		
Matches	7: Conservative	15: Mismatches	3: Indels	0: Gaps
				0:

Db 2 t g d c d d d c d d c d d d c d d c d d c 26
 || : : | : | : : : | : | : : : |
Ov 9 T G T G T C T A C T G G T A C T T C G A T G C 33

RESULT	14
ID	Q04593 standard; DNA; 318 BP.
AC	Q04593;
DT	28-SEP-1990 (first entry)
DE	Sequence encoding region of human carcinoembryonic heavy chain antigen (CEA).
KW	Carcinoembryonic antigen; CEA; Chelate-specific antigen; CEA;
KW	tumor; cancer; serum sickness.

OS	Homo sapiens.
PN	EP-369586-A.
PD	23-MAY-1990.
PF	8-MAR-1989; 302313.
PR	17-NOV-1988; US-274105; EP-302313.
PA	(HYBR-) Hybritech Inc.
PI	J Johnson MJ, Phelps JL;
PI	WPI; 90-157695/21.
DR	P-ESDB; R04937.
PT	Bifunctional chimeric antibodies -
PT	having variable regions which recognise different antigens and
PT	metal chelates and human constant regions.
PS	Claim 2; Page 24; 40pp; English.
CC	Gene encodes portion of CEA heavy chain antigen, useful in
CC	generating chimeric monoclonal antibody binding to CEA at a tumour
CC	site and a metal chelate bonded to say a toxin or other drug.
SO	Sequence 318 BP; 74 A; 86 C; 83 G; 75 T;

Query Match	57.6%;	Score 19;	DB 1;	Length 318;
Best Local Similarity	100.0%;	Pred. No. 4.02e-01;		
Matches	19;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;

Db 264 ctactggtacttcgatgtc 282
|||
Ov 15 CTACTGGTACTTCGATGTC 33

RESULT 15
ID T12813 standard; cDNA; 364 BP.
AC T12813;
DT 10-OCT-1996 (first entry)
DE Murine antibody ZCE-025 heavy chain variable region cDNA.

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13

KW Heavy chain; variable region; murine; tumour antigen; antibody;
KW ZCE-025; construction; CDR switched variable light chain region;
KW kappa-body fragment; in vitro; diagnosis; therapy;
KW naked antibody; radioimmunotherapy; radioimmunodiagnosics;
KW radioimmunometric assays; ELISA; immunohistochemical;
KW complementarity determining region; ss.

OS Mus musculus.

FH Key Location/Qualifiers
FT mat_peptide 1..363

FT /*tag= a

PN M09606625-A1.

PD 07-MAR-1996.

PF 25-AUG-1995; U10791.

PR 26-AUG-1994; US-296625.

PA (ELIL) LILLY & CO ELL.

PI ILL CR, Ludwig JR, Rathnachalam R;

DR WPI; 96-160137/16.

DR P-PSDB; R88846.

PT Recombinant antibody comprising CDR-switched light chain variable
PT region - having VL domain framework and VH domain CDRs, useful in
PT radioimmunotherapy, ELISA assays, etc.

PS Example 1; Page 61; 162pp; English.

CC The present sequence encodes the heavy chain variable (HL) region
CC of the murine anti-ZCE-025 tumour antigen antibody (Ab), ZCE-025,
CC which was used in the construction of a CDR switched light chain
CC variable (VL) region (CSVL) Ab, or kappa-body fragment. A CSVL
CC comprises at least 1 VL region with 3 CDR, where 1 or more of the

CC CDR is derived from the corresponding CDR of a VH region of 1
CC (donor) Ab, and 4 framework (FW) regions where 1 or more of the
CC regions is derived from the corresponding FW region(s) from the VL
CC region of the same or different (acceptor) Ab.

CC The CSVL Ab, or kappa-body fragment can be used in in vitro and
CC in vivo diagnostic and therapeutic applications, including naked Ab
CC therapy, radioimmunotherapy (i.e. when fused to a chelating peptide
CC incorporating Yttrium-90 as the therapeutic radioion), in vivo
CC radioimmunodiagnosics, in vitro radioimmunometric assays, ELISA
CC and immunohistochemical applications.

SQ Sequence 364 BP; 85 A; 91 C; 101 G; 87 T;

Query Match 57.6%; Score 19; DB 22; Length 364;

Best Local Similarity 100.0%; Pred. No. 4.02e-01;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 312 ctactggtacttcgatgtc 330

|||||

Qy 15 CTACTGCTACTTCGATGTC 33

Search completed: Wed Mar 19 08:31:07 1997

Job time : 15 secs.

Mar 19:08:28

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3

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Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE
AUTHORS      Caton,A.J., Swartzentruber,J.R., Kuhl,A.L., Carding,S.R. and
              Stark,S.E.
TITLE         Activation and negative selection of functionally distinct subsets
              of antibody-secreting cells by influenza hemagglutinin as a viral
              and a neo-self antigen
JOURNAL       J. Exp. Med. 183 (1), 13-26 (1996)
MEDLINE       96136744
REFERENCE     2 (bases 1 to 324)
AUTHORS      Swartzentruber,J.R.
DIRECT SUBMISSION
TITLE         Submitted (10-OCT-1995) Jennifer R. Swartzentruber, The Wistar
              Institute, 3601 Spruce St., Philadelphia, PA 19104, USA
JOURNAL
FEATURES     source
              1..324
              /organism="Mus musculus"
              /isolate="h920-293"
              /strain="BALB/c"
              /cell_type="B-lymphocyte"
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              /product="rearranged immunoglobulin heavy chain variable
              region"
              /db_xref="PID:g1127629"
              /translation="LVKPGASVKLSCKASGYTFTSYINWIKORPGQGLEWIGRIAPG
              SGSTYYNEMFKGKATLTVDTSSTAYIQISSLSSDSAVYFCAREDFSYWYEDVWGAG
              TTVTVS"
BASE COUNT   77 a 84 c 85 g 78 t
ORIGIN
Query Match   69.7%; Score 23; DB 65; Length 324;
Best Local Similarity 84.8%; Pred. No. 9.34e-04;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 262 agagagattctctactgtactgtactgtc 294
||||| | | | | | | | | | | | | | | | | | | | | |
Qy 1 AGAGAGACTGCTGTTCTACTGTTCTGTTCTGATGTC 33
RESULT
ID MM37857 standard; RNA; ROD; 324 BP.
AC U37857;
DT 23-DEC-1995 (Rel. 46, Created)
DT 20-MAR-1996 (Rel. 47, Last updated, Version 2)
DE Mus musculus rearranged immunoglobulin heavy chain variable region
DE mRNA, partial cds.
KW Mus musculus (mouse)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-324
RA Caton A.J., Swartzentruber J.R., Kuhl A.L., Carding S.R.,
RA Stark S.E.;
RT "Activation and negative selection of functionally distinct
RT subsets of antibody-secreting cells by influenza hemagglutinin as
RT a viral and a neo-self antigen";
RL J. Exp. Med. 183:13-26(1996).
RN [2]
RP 1-324
RA Swartzentruber J.R.;
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US-08-612-929-25.fgc

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; Submitted (10-OCT-1995) to the EMBL/GenBank/DBJ databases.
RL Jennifer R. Swartzentruber, The Wistar Institute, 3601 Spruce St.,
RL Philadelphia, PA 19104, USA
CC NCBI gi: 1127628 Location/Qualifiers
FH Key
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FT region"
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FT VTVS"
SQ Sequence 324 BP; 77 A; 84 C; 85 G; 78 T; 0 other;
Query Match 69.7%; Score 23; DB 12; Length 324;
Best Local Similarity 84.8%; Pred. No. 9.34e-04;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 262 agagagattctctactgtactgtactgtc 294
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RESULT
LOCUS MUS1HCB 414 bp mRNA ROD 05-MAY-1995
DEFINITION Mus musculus immunoglobulin heavy chain mRNA, 5' end of cds.
ACCESSION L41877
NID g798802
KEYWORDS immunoglobulin heavy chain.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 414)
AUTHORS Asakura,K., Miller,D.J., Pogulis,R.J., Pease,L.R. and Rodriguez,M.
TITLE Oligodendrocyte-specific O1, O4, and HNK-1 monoclonal antibodies
are encoded by germline immunoglobulin genes
JOURNAL DNA (1995) In press
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Best Local Similarity 84.8%; Pred. No. 9.34e-04;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 349 agagggccaggttctactgtactgtatgc 381
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QY 1 AGAGAGACTGCTTCTACTGCTACTTCGATGC 33

RESULT 4
LOCUS S67978 53 bp mRNA ROD 15-MAR-1994
DEFINITION Ig VH81X=Ig heavy chain VDJ region [mice, BALB/c, liver, mRNA
Partial, 53 nt].
ACCESSION S67978
NID 9460843
KEYWORDS
SOURCE mice liver BALB/c.
ORGANISM Mus sp.
Unclassified.
REFERENCE 1 (bases 1 to 53)
AUTHORS Chukwuocha,R.U. and Feeney,A.J.
TITLE Role of homology-directed recombination: predominantly productive
rearrangements of VH81X in newborns but not in adults
JOURNAL Mol. Immunol. 30 (16), 1473-1479 (1993)
MEDLINE 94049838
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 142175] from the original journal article.
This sequence comes from Fig. 3.
FEATURES
source Location/Qualifiers
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/note="mice"
CDS
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/notes="Description: Ig heavy chain VDJ region"
/codon start=1
/translation="ARPSMVTHTVPSTGTSMS"
BASE COUNT 12 a 16 c 11 g 14 t
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Best Local Similarity 100.0%; Pred. No. 2.52e-02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 33 ttctactgtactgtatgc 53
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QY 13 TTCTACTGCTACTTCGATGC 33

RESULT 5
LOCUS MUSIGHAVRN 339 bp mRNA ROD 27-APR-1995
DEFINITION Mouse mRNA for IgH variable region.
ACCESSION D25498
NID 9624903
KEYWORDS IgH variable region.
SOURCE Mus musculus (strain BALB/c) cell-line hybridoma 1F7 (library:
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lambda HL) cDNA to mRNA, clone 1F7802.
Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 339)
AUTHORS Chin,I.-S., Lin,C.-P. and Tseng,T.-C.
TITLE Molecular cloning and expression of Anti-aflatoxin B1 monoclonal
antibody fragment in E.coli
JOURNAL Unpublished (1993)
COMMENT Submitted (24-Nov-1993) to DDBJ by:
Tsung-Che Tseng
Phone: 7899590 x424
Email: BOCHAW@TNAS886.BITNET
Fax: 7827954.
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/cell_line="hybridoma 1F7"
/sequenced_mol="cDNA to mRNA"
/clone_lib="lambda HL"
BASE COUNT 90 a 78 c 91 g 80 t
ORIGIN
Query Match 63.6%; Score 21; DB 66; Length 339;
Best Local Similarity 81.8%; Pred. No. 2.52e-02;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 274 agagtgtacgggctactgtactgtatgc 306
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QY 1 AGAGAGACTGCTTCTACTGCTACTTCGATGC 33

RESULT 6
LOCUS MMIG03 532 bp DNA ROD 29-JAN-1994
DEFINITION Part of mouse gene for immunoglobulin heavy chain J segments.
ACCESSION V00759
NID g51578
KEYWORDS germ line; immunoglobulin.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 532)
AUTHORS Early,P., Huang,H., Davis,M., Calame,K. and Hood,L.
TITLE An immunoglobulin heavy chain variable region gene is generated
from three segments of DNA: VH, D and JH
JOURNAL Cell 19 (4), 981-992 (1980)
MEDLINE 80199926
COMMENT KST MMU.IGHC.GL.2.
FEATURES
source Location/Qualifiers
1..532
/organism="Mus musculus"
163..213
/note="reading frame (JOINING SEGMENT H107)"
482..526
/note="reading frame (JOINING SEGMENT H315)"
BASE COUNT 126 a 118 c 148 g 140 t
ORIGIN
Query Match 63.6%; Score 21; DB 64; Length 532;
Best Local Similarity 95.7%; Pred. No. 2.52e-02;
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Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 158 tgtgctactgtacttcgatgtc 180
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Qy 11 TGTCTACTGCTACTTCGATGTC 33

RESULT 7
ID MMIG03
AC V00759;
DT 09-JUN-1982 (Rel. 01, Created)
DT 07-MAY-1996 (Rel. 47, Last updated, Version 7)
DE Part of mouse gene for immunoglobulin heavy chain J segments.
KW germ line; immunoglobulin.
OS Mus musculus (mouse)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-532
RX MEDLINE; 80199926.
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated
RT from three segments of DNA: VH, D and JH";
RL Cell 19:981-992(1980).
DR IMG7/LIGM; V00759; Release 3.0.
CC KST MMU.IGHC.GL.2
FH Key Location/Qualifiers

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FT /translation="*YFDYMGQGTTLTVSS"
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Query Match 63.6%; Score 21; DB 12; Length 532;
Best Local Similarity 95.7%; Pred. No. 2.52e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 158 tgtgctactgtacttcgatgtc 180
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Qy 11 TGTCTACTGCTACTTCGATGTC 33

RESULT 8
LOCUS MMC57IG 1338 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (C57BL/10) DNA for Igh-J locus.
ACCESSION X63167
NID g50243
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1338)
AUTHORS Solin,M.

TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Solin, Dept. of Bacteriology and Immunology, University of Finland,
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND

REFERENCE 2 (bases 1 to 1338)
AUTHORS Solin,M.L. and Kaartinen,M.
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes
immunoglobulin heavy chain joining (JH) segments

JOURNAL Immunogenetics 36 (5), 306-313 (1992)
MEDLINE 92355114

FEATURES Location/Qualifiers
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/chromosome="12"

misc_feature 11..61
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misc_feature 330..374
/note="JH2"

misc_feature 710..757
/note="JH3"

misc_feature 1278..1328
/note="JH4"

BASE COUNT 308 a 293 c 356 g 371 t 10 others
ORIGIN

Query Match 63.6%; Score 21; DB 63; Length 1338;
Best Local Similarity 95.7%; Pred. No. 2.52e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 6 tgtgctactgtacttcgatgtc 28
|||||

Qy 11 TGTCTACTGCTACTTCGATGTC 33

RESULT 9
LOCUS MMSJLIG 1338 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (SJL) DNA for Igh-J locus.
ACCESSION X63175
NID g54100
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1338)
AUTHORS Solin,M.

TITLE Direct Submission

JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Solin, Dept. of Bacteriology and Immunology, University of Finland,
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND

REFERENCE 2 (bases 1 to 1338)

AUTHORS Solin,M.L. and Kaartinen,M.

TITLE Allelic polymorphism of mouse Igh-J locus, which encodes

immunoglobulin heavy chain joining (JH) segments

JOURNAL Immunogenetics 36 (5), 306-313 (1992)
MEDLINE 92355114

FEATURES Location/Qualifiers
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Best Local Similarity 95.7%; Pred. No. 2.52e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 6 tgtgtactgttacttcgatgctc 28
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Qy 11 TGTCTACTGCTACTTCGATGTC 33
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LOCUS MMC581G 1338 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (C58) DNA for Igh-J locus.
ACCESSION X63168
NID g50244
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1338)
AUTHORS Solin, M.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND
REFERENCE 2 (bases 1 to 1338)
AUTHORS Solin, M.L. and Kaartinen, M.
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes
immunoglobulin heavy chain joining (JH) segments
JOURNAL Immunogenetics 36 (5), 306-313 (1992)
MEDLINE 92355114
FEATURES
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misc_feature 1278..1328
/notes="JH4"
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Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 11 TGTCTACTGCTACTTCGATGTC 33
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LOCUS MMRFIG 1339 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (RF) DNA for Igh-J locus.
ACCESSION X63173
NID g53978
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1339)
AUTHORS Solin, M.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND
REFERENCE 2 (bases 1 to 1339)
AUTHORS Solin, M.L. and Kaartinen, M.
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes
immunoglobulin heavy chain joining (JH) segments
JOURNAL Immunogenetics 36 (5), 306-313 (1992)
MEDLINE 92355114
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Location/Qualifiers
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Best Local Similarity 95.7%; Pred. No. 2.52e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 11 TGTCTACTGCTACTTCGATGTC 33
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Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 5 tgtgtactgttacttcgatgctc 27
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Qy 11 TGTCTACTGCTACTTCGATGTC 33
|||||
RESULT 11
LOCUS MMRFIG 1339 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (RF) DNA for Igh-J locus.
ACCESSION X63173
NID g53978
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1339)
AUTHORS Solin, M.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND
REFERENCE 2 (bases 1 to 1339)
AUTHORS Solin, M.L. and Kaartinen, M.
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes
immunoglobulin heavy chain joining (JH) segments
JOURNAL Immunogenetics 36 (5), 306-313 (1992)
MEDLINE 92355114
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misc_feature 1279..1329
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Query Match 63.6%; Score 21; DB 64; Length 1339;
Best Local Similarity 95.7%; Pred. No. 2.52e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 6 tgtgtactgttacttcgatgctc 28
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Qy 11 TGTCTACTGCTACTTCGATGTC 33
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RESULT 12
LOCUS MMBALB1G 1339 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (Balb/c) DNA for Igh-J locus.
ACCESSION X63166 S41804
NID g50121
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 2 (bases 1 to 1339)
AUTHORS Solin, M.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Solin, Dept. of Bacteriology and Immunology, University of Finland,
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND
MEDLINE 92355114
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misc_feature 710..757
misc_feature 1279..1329
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BASE COUNT 313 a 292 c 359 g 375 t
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Best Local Similarity 95.7%; Pred. No. 2.52e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 6 tgtgtactgtacttcgatgctc 28
||| ||||||||||||||||||
Qy 11 TGTCTACTGGTACTTCGATGTC 33

RESULT 13
LOCUS MMCE1G 1339 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (CE) DNA for Igh-J locus.
ACCESSION X63170
NID g50380
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;

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Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1339)
AUTHORS Solin, M.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Solin, Dept. of Bacteriology and Immunology, University of Finland,
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND

REFERENCE 2 (bases 1 to 1339)
AUTHORS Solin, M.L. and Kaartinen, M.
TITLE Allelic polymorphism of mouse Igh-J locus, which encodes
immunoglobulin heavy chain joining (JH) segments
JOURNAL Immunogenetics 36 (5), 306-313 (1992)
MEDLINE 92355114
FEATURES Location/Qualifiers
source 1..1339
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misc_feature 330..374
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/note="JH1"
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BASE COUNT 312 a 293 c 359 g 374 t 1 others
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Query Match 63.6%; Score 21; DB 63; Length 1339;
Best Local Similarity 95.7%; Pred. No. 2.52e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 6 tgtgtactgtacttcgatgctc 28
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Qy 11 TGTCTACTGGTACTTCGATGTC 33

RESULT 14
LOCUS MMCBA1G 1339 bp DNA ROD 09-DEC-1992
DEFINITION M.musculus (CBA) DNA for Igh-J locus.
ACCESSION X63169
NID g50309
KEYWORDS immunoglobulin heavy chain J locus.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1339)
AUTHORS Solin, M.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.
Solin, Dept. of Bacteriology and Immunology, University of Finland,
Haartmaninkatu 3, SF-00290 Helsinki, FINLAND
MEDLINE 92355114
FEATURES Location/Qualifiers
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/strain="CE"
/tissue_type="liver"
/chromosome="12"
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misc_feature 330..374
misc_feature 710..757
misc_feature 1279..1329
/note="JH1"
/note="JH2"
/note="JH3"
/note="JH4"

Mar 19 08:28

US-08-612-929-25.rge

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JOURNAL Immunogenetics 36 (5), 306-313 (1992)

MEDLINE 92355114

FEATURES

source

Location/Qualifiers

1..1339

/organism="Mus musculus"

/germline

/strain="CBA"

/tissue_type="liver"

/chromosome="12"

11..61

/note="JH1"

330..374

/note="JH2"

710..757

/note="JH3"

1279..1329

/note="JH4"

BASE COUNT 313 a 291 c 358 g 371 t 6 others

ORIGIN

Query Match 63.6%; Score 21; DB 63; Length 1339;

Best Local Similarity 95.7%; Pred. No. 2.52e-02;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 6 tgtgtactgtacttcgatgtc 28

|||||

Qy 11 TGTCTACTGGTACTTCGATGTC 33

RESULT 15

LOCUS

MMDBA21G 1339 bp DNA ROD 09-DEC-1992

DEFINITION M.musculus (DBA2) DNA for Igh-J locus.

ACCESSION X63171

NID g50670

KEYWORDS immunoglobulin heavy chain J locus.

SOURCE house mouse.

ORGANISM

Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1339)

AUTHORS Solin,M.

TITLE Direct Submission

JOURNAL Submitted (11-NOV-1991) to the EMBL/GenBank/DBJ databases. M.

Solin, Dept. of Bacteriology and Immunology, University of Finland,

Haartmaninkatu 3, SF-00290 Helsinki, FINLAND

REFERENCE 2 (bases 1 to 1339)

AUTHORS Solin,M.L. and Kaartinen,M.

TITLE Allelic polymorphism of mouse Igh-J locus, which encodes

immunoglobulin heavy chain joining (JH) segments

JOURNAL Immunogenetics 36 (5), 306-313 (1992)

MEDLINE 92355114

FEATURES

source

Location/Qualifiers

1..1339

/organism="Mus musculus"

/germline

/strain="DBA/2"

/tissue_type="liver"

/chromosome="12"

11..61

/note="JH1"

330..374

misc_feature

misc_feature

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US-08-612-929-25.rge

14

/note="JH2"

710..757

/note="JH3"

1279..1329

/note="JH4"

BASE COUNT 313 a 291 c 359 g 374 t 2 others

ORIGIN

Query Match 63.6%; Score 21; DB 63; Length 1339;

Best Local Similarity 95.7%; Pred. No. 2.52e-02;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 6 tgtgtactgtacttcgatgtc 28

|||||

Qy 11 TGTCTACTGGTACTTCGATGTC 33

Search completed: Wed Mar 19 08:30:34 1997

Job time : 63 secs.

cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGACGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomi; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 408)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE
JOURNAL
COMMENT

The WashU-Merck EST Project
Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence stops: 281

Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

Location/Qualifiers

source

1..408

/organism="Homo sapiens"

/clone="234692"

/note="human"

<1..>408

BASE COUNT

116 a 50 c 85 g 154 t 3 others

ORIGIN

Query Match 59.3%; Score 16; DB 30; Length 408;
Best Local Similarity 94.4%; Pred. No. 2.98e-03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 155 ggaggtatctctcattatt 172

|||||

Cp 23 GGAGATCCTCATTACTT 6

RESULT 4

LOCUS T98290 482 bp mRNA EST 31-MAR-1995
DEFINITION ye59q06.s1 Homo sapiens cDNA clone 122074 3' similar to contains
Alu repetitive element.

ACCESSION
NID
KEYWORDS
SOURCET98290
q748027
EST.

human clone=122074 library=Soares fetal liver spleen INFLS
vector=pTT3D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=-21ml3 Rsite1=Pac I Rsite2=Eco RI
Liver and spleen from a 20 week-post conception male fetus. 1st
strand cDNA was primed with a Pac I - oligo(dT) primer [5'
AACTGACGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pTT3

vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 482)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE
JOURNAL
COMMENT

The WashU-Merck EST Project
Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence stops: 288

Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

Location/Qualifiers

source

1..482

/organism="Homo sapiens"

/clone="122074"

/note="human"

BASE COUNT 119 a 89 c 142 g 123 t 9 others

ORIGIN

Query Match 59.3%; Score 16; DB 128; Length 482;
Best Local Similarity 90.0%; Pred. No. 2.98e-03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 166 caacacagtaatgagatcc 185

|||||

Qy 1 CAGCAAGTAATGAGGATCC 20

RESULT 5

LOCUS R21547 522 bp mRNA EST 18-APR-1995

DEFINITION yhi9h02.s1 Homo sapiens cDNA clone 130227 3'.

ACCESSION R21547

NID q776328

KEYWORDS EST.

SOURCE

human clone=130227 library=Soares placenta Nb2HP vector=pTT3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=-21ml3 Rsite1=Not I Rsite2=Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5'
AACTGGAAGATTCGGCGCGAGGAATTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pTT3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 522)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

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Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

High quality sequence stops: 433
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES Location/Qualifiers
source
1..522
/organism="Homo sapiens"
/clone="130227"
/note="human"

BASE COUNT 136 a 122 c 117 g 143 t 4 others
ORIGIN

Query Match 59.3%; Score 16; DB 78; Length 522;
Best Local Similarity 82.6%; Pred. No. 2.98e-03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 469 cctccaggtcagctactacttt 491

Cp 27 CCTCGGAGGATCCTCATTACTTT 5

RESULT 6

LOCUS R69241 179 bp mRNA EST 01-JUN-1995
DEFINITION Y144C03.s1 Homo sapiens cDNA clone 142084 5' similar to gb:U01120
GLUCOSE-6-PHOSPHATASE (HUMAN); contains Alu repetitive element;.
R69241
ACCESSION
NID g842758
KEYWORDS EST.

SOURCE human clone=142084 library=Soares placenta Nb2HP vector=pT7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13R1 Rsite1=Not I Rsite2=Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5'
AATCGAGATTCGGCGCGGAGGATTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 179)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

Mar 19 08:33

US-08-612-929-27.rst

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COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read.

FEATURES Location/Qualifiers
source
1..179
/organism="Homo sapiens"
/clone="142084"
/note="human"

BASE COUNT 34 a 40 c 41 g 64 t
ORIGIN

Query Match 55.6%; Score 15; DB 91; Length 179;
Best Local Similarity 80.0%; Pred. No. 5.84e-02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 45 cctcagtgatcctcataactctgc 69

Cp 27 CCTCGGAGGATCCTCATTACTTGC 3

RESULT 7

LOCUS N49151 215 bp mRNA EST 14-FEB-1996
DEFINITION Y94b12.r1 Homo sapiens cDNA clone 280223 5'.
ACCESSION N49151
NID g1190317
KEYWORDS EST.

SOURCE human clone=280223 primer=T7 library=Soares multiple sclerosis
2NBHSP vector=pT7T3D (Pharmacia) with a modified polylinker
V_TYPE: phagemid host=DH10B (ampicillin resistant) Rsite1=Not I
Rsite2=Eco RI 46 year old male. 1st strand cDNA was primed with a
Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTCGCGCGGCGCATTTTTTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pT7T vector (Pharmacia). Library went
through one round of normalization to a Cot = 5. Library
constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4
multiple sclerosis lesions from one patient was kindly provided by
Dr. Kevin G. Becker (NINDS/NIH).

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 215)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 193

Source: IMAGE Consortium, L1NL

This clone is available royalty-free through L1NL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

1..215
/organism="Homo sapiens"
/clone="280223"
/note="human"

<1..>215

BASE COUNT 43 a 43 c 46 g 80 t 3 others
ORIGIN

Query Match 55.6%; Score 15; DB 61; Length 215;
Best Local Similarity 85.7%; Pred. No. 5.84e-02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 151 agtatcctcattgcttgcgtg 171

|| ||||| ||||| |||||

Cp 21 AGGATCCTCATTTACTTTGCTG 1

RESULT 8

LOCUS N48736 236 bp mRNA EST 14-FEB-1996

DEFINITION yy55dl1.r1 Homo sapiens cDNA clone 277461 5'.

ACCESSION N48736

NID g1189902

KEYWORDS EST.

SOURCE human clone=277461 primer=T7 library=Soares multiple sclerosis

2NBHSP vector-pTT3D (Pharmacia) with a modified polylinker

V TYPE: phagemid host=DH10B (ampicillin resistant) Reitel=Not I

Rsite2=Eco RI 46 year old male. 1st strand cDNA was primed with a

Not I - oligo(dT) primer

[5'-GTGTACCAATCTGAAGTGGGCGCGCATTTTTTTTTTTTTTTT-3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters

(Pharmacia), digested with Not I and cloned into the Not I and Eco

RI sites of a modified pTT vector (Pharmacia). Library went

through one round of normalization to a Cot = 5. Library

constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4

multiple sclerosis lesions from one patient was kindly provided by

Dr. Kevin G. Becker (NINDS/NIH).

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 236)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

TITLE The WashU-Merck EST Project

Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 193

Source: IMAGE Consortium, L1NL

This clone is available royalty-free through L1NL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

1..236
/organism="Homo sapiens"
/clone="277461"
/note="human"

<1..>236

BASE COUNT 51 a 44 c 50 g 87 t 4 others
ORIGIN

Query Match 55.6%; Score 15; DB 61; Length 236;
Best Local Similarity 85.7%; Pred. No. 5.84e-02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 168 agtatcctcattgcttgcgtg 188

|| ||||| ||||| |||||

Cp 21 AGGATCCTCATTTACTTTGCTG 1

RESULT 9

LOCUS W12396 329 bp mRNA EST 26-APR-1996

DEFINITION ma67ql1.r1 Soares mouse p3NMF19.5 Mus musculus cDNA 5'.

ACCESSION W12396

NID g1286526

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Eukaryota; Eumetazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae;

Murinae; Mus.

1 (bases 1 to 329)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

TITLE The WashU-HMI Mouse EST Project

Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through L1NL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Putative full length read

Seq primer: ETPrimer

High quality sequence stop: 321.

NCBI gi: 1286526

Location/Qualifiers

1..329

/organism="Mus musculus"

/note="Vector: pT73D (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

Mar 19 08:33

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was primed with a Not I - oligo(dT) primer [5'
TCTTACCAATCTGAAGTCGAGCGCGCGCATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo.*
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
<1..>329
79 a 87 c 68 g 95 t
BASE COUNT
ORIGIN

Query Match 55.6%; Score 15; DB 149; Length 329;
Best Local Similarity 85.7%; Pred. No. 5.84e-02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 181 gcagagcattgaggtctcc 201

Qy 3 GCAGAGTAATGAGGATCTCC 23

RESULT 10

ID MM3966 standard; RNA; EST; 329 BP.

AC W12396;

DT 29-APR-1996 (Rel. 47, Created)

DT 29-APR-1996 (Rel. 47, Last updated, Version 1)

DE ms67g11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA 5'.

KW EST.

OS Mus musculus (mouse)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

RN [1]

RP 1-329

RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,

RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,

RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,

RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,

RA Waterston R.;

RT "The WashU-HHMI Mouse EST Project";

RL Unpublished.

CC Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
CC Washington University School of Medicinep 4444 Forest Park Parkway,
CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC Email: mouseest@wustl.edu This clone is available
CC royalty-free through INL; contact the IMAGE Consortium
CC (info@image.llnl.gov) for further information. Putative full length
CC read Seq primer: ESTPrimer High quality sequence stop: 321. NCBI gi:
CC 1286526

FH Key Location/Qualifiers

FH source

1..329

/organism="Mus musculus"

/notes="Vector: pT7T3D (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTTCACCAATCTGAAGTCGAGCGCGCGCATTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

FT

Mar 19 08:33

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12

FT Soares and M.Fatima Bonaldo.*
FT /clone_lib="Soares mouse p3NMF19.5"
FT /dev_stage="19 weeks"
FT /lab_host="DH10B (ampicillin resistant)"
FT mRNA
FT <1..>329
SQ Sequence 329 BP; 79 A; 87 C; 68 G; 95 T; 0 other;
Query Match 55.6%; Score 15; DB 170; Length 329;
Best Local Similarity 85.7%; Pred. No. 5.84e-02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 181 gcagagcattgaggtctcc 201
Qy 3 GCAGAGTAATGAGGATCTCC 23

RESULT 11
LOCUS RICC10026A 336 bp mRNA EST 25-MAY-1995
DEFINITION Rice cDNA, partial sequence (C10026_1A).
ACCESSION D21897
NID g426041

KEYWORDS EST(expressed sequence tag).
SOURCE Oryza sativa (strain Nipponbare,) Callus Callus cDNA to mRNA.
ORGANISM Oryza sativa

Eukaryota; mitochondrial eukaryotes; Chlorophyta/Embryophyta
group; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Commelinidae; Poales; Poaceae; Oryza.

REFERENCE 1 (bases 1 to 336)

AUTHORS Minobe, Y. and Sasaki, T.

TITLE Rice cDNA from callus

JOURNAL Unpublished (1993)

COMMENT Submitted (2-NOV-1993) to DDBJ by:

Yuzo Minobe

Dept. Rice Genome Research Program

National Institute of Agrobiological Resources

Kannondai 2-1-2

Tsukuba, Ibaraki

Japan

Phone: 0298-38-7441

Fax: 0298-38-7468

PROJECT = 'RGP'.

Location/Qualifiers

1..336

/organism="Oryza sativa"

/strain="Nipponbare"

/dev_stage="Callus"

/sequenced_mol="cDNA to mRNA"

/tissue_type="Callus"

BASE COUNT 101 a 68 c 80 g 86 t 1 others

ORIGIN

Query Match 55.6%; Score 15; DB 101; Length 336;
Best Local Similarity 85.7%; Pred. No. 5.84e-02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 53 aaggaatgaggtctccag 73

Qy 6 AAGTAATGAGGATCTCCGAG 26

RESULT 12

LOCUS H69879 349 bp mRNA EST 24-OCT-1995

DEFINITION yr88r01.s1 Homo sapiens cDNA clone 212401 3'.

ACCESSION H69879

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US-08-612-929-27.rst

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NID q1040085

KEYWORDS EST.

SOURCE human clones-212401 primer=Promega -21m13 library=Soares fetal liver spleen INFLS vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver cDNA was primed with a Pac I - oligo(dT) primer [5'

AAC TCGAAGATTTATTTAATGATCTTTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 349)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 323

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers

FEATURES

source

1..349
/organism="Homo sapiens"
/clone="212401"
/note="human"

mRNA

BASE COUNT 99 a 62 c 91 g 96 t 1 others

ORIGIN

Query Match 55.6%; Score 15; DB 27; Length 349;
Best Local Similarity 85.7%; Pred. No. 5.84e-07;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 175 aggaagtattgaagatcctc 195

II IIIII IIII IIIIIII

QY 2 ACCAAAGTATGAGGATCTCTC 22

RESULT 13

LOCUS R82708 358 bp mRNA EST 14-JUN-1995

DEFINITION yj20e08.r1 Homo sapiens cDNA clone 149318 5' similar to contains

MER22 repetitive element ;.

ACCESSION R82708

NID g862099

KEYWORDS EST.

SOURCE human clone=149318 library=Soares placenta Nb2HP vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin

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14

resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'

AAC TCGAAGATTTCCGCCGCCGAGGATTTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 358)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 284

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers

FEATURES

source

1..358
/organism="Homo sapiens"
/clone="149318"
/note="human"

BASE COUNT 68 a 123 c 65 g 101 t 1 others

ORIGIN

Query Match 55.6%; Score 15; DB 95; Length 358;
Best Local Similarity 80.0%; Pred. No. 5.84e-02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 229 agcaaaqtcataaataatgctccag 253

II IIIII IIII IIII IIII

QY 2 ACCAAAGTATGAGGATCTCTCCGAG 26

RESULT 14

LOCUS T26512 361 bp mRNA EST 15-APR-1996

DEFINITION AB284F11R Homo sapiens cDNA clone LLAB284F11 5'.

ACCESSION T26512

NID g773829

KEYWORDS EST.

SOURCE human clone=LLAB284F11 primer=M13 Reverse library=Infant brain, LML array of Dr. M. Soares INIB vector=Infmid BA Reitel-HindIII Rsite2=NotI Normalized infant brain cDNA library made by Dr. M. Soares (Columbia University), oligo-dT primed and directionally cloned between HindIII (5') and NotI (3') sites.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Mar 19 08:33

US-08-612-929-27.fst

15

Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 361)

Authors: Ghiso, N.S., Eveleth, G.G., Lieuallen, K. and Lennon, G.G.

Title: Chromosomal assignment of 20 cDNAs using flow-sorted spot-blot stamps

Journal: Genomics 28 (3), 570-572 (1995)

Medline: 96039272

Comment:

Contact: Greg G. Lennon
Human Genome Center, L-452
Lawrence Livermore National Laboratory
Livermore CA 94550
Tel: 510 422 8361
Fax: 510 422 2282
Email: info@image.llnl.gov.

NCBI gi: 773829

Location/Qualifiers

1..361

/organism="Homo sapiens"

/clone="LLAB284F11"

/note="human"

<1..>361

BASE COUNT 101 a 124 c 39 g 94 t 3 others

ORIGIN

Query Match 55.6%; Score 15; DB 143; Length 361;

Best Local Similarity 89.5%; Pred. No. 5.84e-02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 286 gatcctcattactattctg 304

|||||

Cp 19 GATCCTCATTACTTTGCTG 1

RESULT 15

ID HS1288 standard; RNA; EST; 361 BP.

AC T26512;

DT 23-APR-1995 (Rel. 43, Created)

DT 18-APR-1996 (Rel. 47, Last updated, Version 3)

DE AB284F11R Homo sapiens cDNA clone LLAB284F11 5'.

KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

RN [1]

RP 1-361

RA Ghiso N.S., Eveleth G.G., Lieuallen K., Lennon G.G.;

RT "Chromosomal assignment of 20 cDNAs using flow-sorted spot-blot

stamps";

RL Genomics 28:570-572 (1995).

CC Contact: Greg G. Lennon Human Genome Center, L-452 Lawrence

CC Livermore National Laboratory Livermore CA 94550 Tel: 510 422 8361

CC Fax: 510 422 2282 Email: info@image.llnl.gov. NCBI gi: 773829

FH Key Location/Qualifiers

FH

source 1..361

/organism="Homo sapiens"

/clone="LLAB284F11"

/note="human"

<1..>361

FT mRNA

FT Sequence 361 BP; 101 A; 124 C; 39 G; 94 T; 3 other;

Mar 19 08:33

US-08-612-929-27.fst

16

Query Match 55.6%; Score 15; DB 162; Length 361;
Best Local Similarity 89.5%; Pred. No. 5.84e-02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 286 gatcctcattactattctg 304

|||||

Cp 19 GATCCTCATTACTTTGCTG 1

Search completed: Wed Mar 19 08:35:56 1997

Job time : 67 secs.

CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A
CC synthetic heavy chain was made using the oligonucleotides given
CC in Q83498-502 and amplified by PCR using the primers given in
CC Q83503-04. The construct was ligated into vector pCD, along
CC with a signal sequence (Q83494) and an IgG1 human constant
CC region. The CDR gene regions of a pre-existing light chain
CC framework were replaced with synthetic IL-4 CDR genes constructed
CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),
CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into
CC the vector. The anti-IL4 engineered antibody was expressed in
CC COS and CHO cells.
SQ Sequence 51 BP; 14 A; 11 C; 16 G; 10 T;

Query Match 100.0%; Score 27; DB 14; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.07e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 cagcaagtaagatcctcctcgagg 37
|||||
Qy 1 CAGCAAGTAAGTACGATCCTCGAGG 27

RESULT 2

ID Q83512 standard; DNA; 53 BP.
AC Q83512;
DT 20-SEP-1995 (first entry)
DE IL-4 CDR3 gene fragment.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;
KW complementarity determining region; ss.
OS Synthetic.
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross M5, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Example 3; Page 28; 97pp; English.

CC A humanized antibody was designed to contain mouse CDRs (from
CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A
CC synthetic heavy chain was made using the oligonucleotides given
CC in Q83498-502 and amplified by PCR using the primers given in
CC Q83503-04. The construct was ligated into vector pCD, along
CC with a signal sequence (Q83494) and an IgG1 human constant
CC region. The CDR gene regions of a pre-existing light chain
CC framework were replaced with synthetic IL-4 CDR genes constructed
CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),
CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into
CC the vector. The anti-IL4 engineered antibody was expressed in
CC COS and CHO cells.
SQ Sequence 53 BP; 9 A; 17 C; 12 G; 15 T;

Query Match 100.0%; Score 27; DB 14; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.07e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 cctcggaggatcctcattctgtg 45
|||||

Cp 27 CCTCGAGGATCCTCATTCTGTC 1

RESULT 3

ID Q73986 standard; cDNA; 393 BP.
AC Q73986;
DT 20-SEP-1995 (first entry)
DE Humanized antibody 3B9 light chain.
KW Humanized antibody; antibody engineering; monoclonal antibody;
KW Mab; interleukin-4; IL-4; allergy; ds.
OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 1..393

FT /tag= a
FT sig_peptide 1..60
FT /tag= b
FT mat_peptide 61..393
FT /tag= c

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross M5, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.

DR P-PSDB; R75355.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.5; 97pp; English.

CC A humanized antibody light chain variable region and signal
CC sequence is given in R75355. The signal sequence is also
CC provided in R70194. The sequences of the first 2 CDRs
CC are identical to mouse anti-human IL-4 Mab 3B9 light chain
CC CDRs (given in R70195-96), but the third (R70201) differs
CC by a single amino acid from the native mouse CDR (R70197).
SQ Sequence 393 BP; 97 A; 96 C; 108 G; 92 T;

Query Match 100.0%; Score 27; DB 14; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.07e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 334 cagcaagtaagatcctcctcgagg 360
|||||

Qy 1 CAGCAAGTAAGTACGATCCTCGAGG 27

RESULT 4

ID Q83520 standard; cDNA; 393 BP.

AC Q83520;

DT 20-SEP-1995 (first entry)

DE Humanized antibody 3B9 light chain.

KW Humanized antibody; antibody engineering; monoclonal antibody;
KW Mab; interleukin-4; IL-4; allergy; ds.

OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 1..393

FT /tag= a

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR P-PSDB; R70202.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions
 PS Disclosure; Page 71-72; 97pp; English.
 CC A humanized antibody light chain variable region and signal CC sequence is given in R75355. The signal sequence is also CC provided in R70194. The sequences of the 3 CDRs CC are identical to mouse anti-human IL-4 MAb 3B9 light chain CC CDRs (given in R70195-97).
 SQ Sequence 393 BP; 97 A; 98 C; 105 G; 93 T;

Query Match 92.6%; Score 25; DB 14; Length 393;
 Best Local Similarity 100.0%; Pred. No. 3.58e-05;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 334 cagcaagaatgagatcctccga 358
 |||||
 Qy 1 CAGCAAGTATGAGATCCTCCGA 25

RESULT 5
 ID Q83490 standard; cDNA; 396 BP.
 AC Q83490;
 DT 20-SEP-1995 (first entry)
 DE Mouse MAb 3B9 light chain.
 KW Chimeric antibody; humanized antibody; antibody engineering;
 KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT CDS 1..396
 FT /tag= a
 FT sig_peptide 1..60
 FT /tag= b
 FT mat_peptide 61..396
 FT /tag= c
 PN W09507301-A.
 PD 16-MAR-1995.
 PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR P-PSDB; R70189.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions
 PS Disclosure; Fig.1; 97pp; English.
 CC Spleen cells from mice immunized with human IL-4 were used to prepare CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy CC chains were cloned into pGEM7f+ and transformed into E. coli CC DH5-alpha. The clones were sequenced (Q83490-91), and used for CC antibody engineering.
 SQ Sequence 396 BP; 99 A; 103 C; 103 G; 91 T;

Query Match 92.6%; Score 25; DB 14; Length 396;

Best Local Similarity 100.0%; Pred. No. 3.58e-05;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 337 cagcaagaatgagatcctccga 361
 |||||
 Qy 1 CAGCAAGTATGAGATCCTCCGA 25

RESULT 6
 ID Q55014 standard; DNA; 99 BP.
 AC Q55014;
 DT 06-JUL-1994 (first entry)
 DE Humanised Ab 60.3 VL oligonucleotide.
 KW Monoclonal antibody; MAb; heavy chain; light chain;
 KW constant region; variable region; amplification; primer;
 KW polymerase chain reaction; PCR; chimera; Ig;
 KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.
 OS Synthetic.
 PN EP-578515-A.
 PD 12-JAN-1994.
 PF 24-MAY-1993; 401328.
 PR 26-MAY-1992; US-888233.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Rajorath J, Harris LJ, Heiao K, Ku-Chuan H;
 DR WPI; 94-010334/02.
 PT Humanised monoclonal antibodies prepn. - using comparative model PT building, by computer database searching
 PS Disclosure; Fig 3; 68pp; English.
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18 CC antibody 60.3 was prepared. The variable (V) region sequences from CC both the heavy (H) and light (L) chains were determined from cDNA CC (amplified by PCR), and spliced onto human constant (C) regions, CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected CC by ELISA), and examined in binding assays. The results from CC competition and inhibition assays showed that the chimeric Ab was CC as effective as the murine 60.3 MAb. The deduced murine VH and VL CC protein sequences were compared to the protein sequence data base, CC and two human Ig protein sequences were selected to be used as CC templates. A murine 60.3 Fv was modeled according to the deduced CC VH and VL protein sequences. Based on the 60.3 Fv model and the two CC human template sequences selected from the protein data base, a CC humanised Fv was modeled. Construction of the humanised 60.3 was CC done by piecing 5 pairs of complementary oligonucleotides together CC (spanning the entire V region) to form the VH and VL. These were CC then attached onto vectors containing genes for appropriate C regions CC to form humanised Ab (IgG1, kappa). The humanised proteins were again CC expressed in Aq8.653 cells and binding assays were done. FACS analyses CC indicated that the humanised Ab recognised cells expressing CD18.
 CC About a dozen of the humanised 60.3 Ab master wells were transferred CC and assayed for Ig.
 SQ Sequence 99 BP; 26 A; 28 C; 19 G; 26 T;

Query Match 85.2%; Score 23; DB 9; Length 99;
 Best Local Similarity 96.0%; Pred. No. 5.85e-04;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 66 tcgagagatcctcattctgtcg 90
 |||||
 Qp 25 TCGAGAGATCCTCACTTCTGTC 1

RESULT 7
 ID Q55000 standard; DNA; 334 BP.

AC Q55000;
 DT 06-JUL-1994 (first entry)
 DE Humanised anti-CD18 Ab 60.3 light chain.
 KW Monoclonal antibody; MAb; heavy chain; light chain;
 KW constant region; variable region; amplification; primer;
 KW polymerase chain reaction; PCR; chimera; Ig;
 KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.
 OS Chimeric; Homo sapiens.
 OS Chimeric; Mus sp.
 PN EP-578515-A.
 PD 12-JAN-1994.
 PF 24-MAY-1993; 401328.
 PR 26-MAY-1992; US-888233.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Bajorath J, Harris LJ, Heiao K, Ku-Chuan H;
 DR WPI; 94-010334/02.
 DR P-PSDB; R47492.
 PT Humanised monoclonal antibodies prepn. - using comparative model
 PT building, by computer database searching
 PS Disclosure; Page 18-19; 68pp; English.
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18
 CC antibody 60.3 was prepared. The variable (V) region sequences from
 CC both the heavy (H) and light (L) chains were determined from cDNA
 CC (amplified by PCR), and spliced onto human constant (C) regions,
 CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
 CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected
 CC by ELISA), and examined in binding assays. The results from
 CC competition and inhibition assays showed that the chimeric Ab was
 CC as effective as the murine 60.3 MAb. The deduced murine VH and VL
 CC protein sequences were compared to the protein sequence data base,
 CC and two human Ig protein sequences were selected to be used as
 CC templates. A murine 60.3 Fv was modeled according to the deduced
 CC VH and VL protein sequences. Based on the 60.3 Fv model and the two
 CC human template sequences selected from the protein data base, a
 CC humanised Fv was modeled. Construction of the humanised 60.3 was
 CC done by piecing 5 pairs of complementary oligonucleotides together
 CC (spanning the entire V region) to form the VH and VL. These were
 CC then attached onto vectors containing genes for appropriate C regions
 CC to form humanised Ab (IgG1, kappa). The humanised proteins were again
 CC expressed in Aq8.653 cells and binding assays were done. FACS analyses
 CC indicated that the humanised Ab recognised cells expressing CD18.
 CC About a dozen of the humanised 60.3 Ab master wells were transferred
 CC and assayed for Ig.
 SQ Sequence 334 BP; 90 A; 79 C; 80 G; 85 T;

Query Match 85.2%; Score 23; DB 9; Length 334;
 Best Local Similarity 96.0%; Pred. No. 5.85e-04;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaagaatgagatctctcgga 301
 |||||
 QY 1 CAGCAAGTAAATGAGATCTCTCGGA 25

RESULT 8
 ID Q55002 standard; DNA; 334 BP.
 AC Q55002;
 DT 06-JUL-1994 (first entry)
 DE Murine anti-CD18 Ab 60.3 light chain.
 KW Monoclonal antibody; MAb; heavy chain; light chain;
 KW constant region; variable region; amplification; primer;
 KW polymerase chain reaction; PCR; chimera; Ig;
 KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.
 OS Mus sp.

PN EP-578515-A.
 PD 12-JAN-1994.
 PF 24-MAY-1993; 401328.
 PR 26-MAY-1992; US-888233.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Bajorath J, Harris LJ, Heiao K, Ku-Chuan H;
 DR WPI; 94-010334/02.
 DR P-PSDB; R47494.
 PT Humanised monoclonal antibodies prepn. - using comparative model
 PT building, by computer database searching
 PS Disclosure; Page 21; 68pp; English.
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18
 CC antibody 60.3 was prepared. The variable (V) region sequences from
 CC both the heavy (H) and light (L) chains were determined from cDNA
 CC (amplified by PCR), and spliced onto human constant (C) regions,
 CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
 CC expressed in tissue culture (Aq8.653 mouse myeloma cells, detected
 CC by ELISA), and examined in binding assays. The results from
 CC competition and inhibition assays showed that the chimeric Ab was
 CC as effective as the murine 60.3 MAb. The deduced murine VH and VL
 CC protein sequences were compared to the protein sequence data base,
 CC and two human Ig protein sequences were selected to be used as
 CC templates. A murine 60.3 Fv was modeled according to the deduced
 CC VH and VL protein sequences. Based on the 60.3 Fv model and the two
 CC human template sequences selected from the protein data base, a
 CC humanised Fv was modeled. Construction of the humanised 60.3 was
 CC done by piecing 5 pairs of complementary oligonucleotides together
 CC (spanning the entire V region) to form the VH and VL. These were
 CC then attached onto vectors containing genes for appropriate C regions
 CC to form humanised Ab (IgG1, kappa). The humanised proteins were again
 CC expressed in Aq8.653 cells and binding assays were done. FACS analyses
 CC indicated that the humanised Ab recognised cells expressing CD18.
 CC About a dozen of the humanised 60.3 Ab master wells were transferred
 CC and assayed for Ig.
 SQ Sequence 334 BP; 88 A; 85 C; 81 G; 80 T;

Query Match 85.2%; Score 23; DB 9; Length 334;
 Best Local Similarity 96.0%; Pred. No. 5.85e-04;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaagaatgagatctctcgga 301
 |||||
 QY 1 CAGCAAGTAAATGAGATCTCTCGGA 25

RESULT 9
 ID Q30757 standard; cDNA; 393 BP.
 AC Q30757;
 DT 30-MAR-1993 (first entry)
 DE p64-k4.
 KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
 KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
 KW plasmid; p64-k4; p64-h2; ss.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT sig_peptide 1..60
 FT /*tag= a
 FT mat_peptide 61..393
 FT /*tag= b
 PN W09219759-A.
 PD 12-NOV-1992.
 PE 24-APR-1992; J00544.
 PR 25-APR-1991; JP-095476.
 PR 19-FEB-1992; JP-032084.

PA (CHUS) CHUGAI SEIYAKU KK.
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
 DR P-PSDB; R29008.
 PT Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 PS Disclosure; Page 124-125; 207pp; Japanese.
 CC The sequences given in Q30757-58 were used in example to illustrate
 CC the production of a human antibody which recognises human
 CC interleukin-6 receptor (IL-6R). The antibody comprises light (L)
 CC chain and heavy (H) chain variable regions which were derived from a
 CC mouse monoclonal antibody produced from the hybridoma AUK64-7 which
 CC contained the plasmids p64-k4 and p64-h2.
 SQ Sequence 393 BP; 93 A; 101 C; 100 G; 99 T;

Query Match 85.2%; Score 23; DB 5; Length 393;
 Best Local Similarity 100.0%; Pred. No. 5.85e-04;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 337 cagcaaaagtgaagatcctcc 359
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 QY 1 CAGCAAAAGTAATGAGATCCTCC 23

RESULT 10
 ID Q36609 standard; DNA; 393 BP.
 AC Q36609;
 DT 02-JUN-1993 (first entry)
 DE Anti-CD4 antibody MF 3.10 light chain variable region.
 KW immunosuppression; tissue transplantation; graft; L chain; V region;
 KW T-helper cell inhibition; transplant rejection; MAb;
 KW interleukin-2 receptor; ss.
 FH Key Location/Qualifiers
 FT sig peptide 1..60
 FT /*tag= a
 FT mat_peptide 61..393
 FT /*tag= b
 FT /note= "JL region begins at position 361"
 PN DE4143214-A.
 PD 28-JAN-1993.
 PF 30-DEC-1991; 143214.
 PR 25-JUL-1991; DE-124759.
 PR 30-DEC-1991; DE-143214.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 PI Kaluza B, Riethmuller G, Scheuer W, Weidle U;
 DR WPI; 93-037582/05.
 DR P-PSDB; R32123.
 PT Synergistic antibody compsn. for use as immunosuppressant -
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
 PT alpha- or anti-IL2R beta antibodies
 PS Claim 5; Page 11; 18pp; German.
 CC This sequence encodes the light chain variable region of a preferred
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic
 CC composition. Mab MT 3.10 is deposited as clone 3.101/sB10 (ECACC
 CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R
 CC alpha or beta antibody. Individually the antibodies are strongly
 CC inhibiting and when used together their immunosuppressive properties
 CC are improved; they synergistically inhibit T-helper cell
 CC proliferation to effectively inhibit transplant rejection at low
 CC doses without significantly reducing the general immune response.
 CC See Q36607-Q36616.
 SQ Sequence 393 BP; 100 A; 105 C; 98 G; 90 T;

Query Match 85.2%; Score 23; DB 6; Length 393;
 Best Local Similarity 96.0%; Pred. No. 5.85e-04;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 337 cagcaaaagtgaagatcctccga 361
 |||||
 QY 1 CAGCAAAAGTAATGAGATCCTCCGA 25

RESULT 11
 ID Q51746 standard; cDNA; 91 BP.
 AC Q51746;
 DT 31-MAY-1994 (first entry)
 DE Oligonucleotide probe MK14-A
 KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
 KW ss.
 OS Synthetic.
 PN EP-571911-A.
 PD 01-DEC-1993.
 PF 24-MAY-1993; 108325.
 PR 26-MAY-1992; US-889651.
 PA (BECT) BECTON DICKINSON CO.
 PI Shank DD, Spears PA;
 DR WPI; 93-378844/48.
 DT New oligonucleotide probes specific for Mycobacteria - used for
 PT detection and amplification of Mycobacteria nucleic acid in
 PT samples
 PS Claim 3; Page 14; 23pp; English.
 CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
 CC (Q51735). It hybridized to all spp. of mycobacteria tested, but
 CC cross reacted to a few non-mycobacterial spp. The probe may
 CC be useful as an initial screen for mycobacterial infection.
 CC See also Q51735-45 and Q51747-59.
 SQ Sequence 91 BP; 5 A; 17 G; 15 C; 4 T;

Query Match 81.5%; Score 22; DB 9; Length 91;
 Best Local Similarity 0.0%; Pred. No. 2.31e-03;
 Matches 0; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

Db 34 hvhsvvvvhhvhhvhhvhh 55
 :
 Cp 27 CCTCGGAGGATCCTCATTTACT 6

RESULT 12
 ID Q12684 standard; DNA; 336 BP.
 AC Q12684;
 DT 01-OCT-1991 (first entry)
 DE Murine IB4 light chain-2 variable region.
 KW Monoclonal antibody; complementarity determining region; CDR;
 KW integrin; hybridoma IB4; protein REI; Gal/Rei; Ig; ss.
 PN EP-438312-A.
 PN EP-440351-A.
 PD 24-JUL-1991.
 PF 17-JAN-1991; 300367.
 PR 19-JAN-1990; US-467692.
 PR 20-DEC-1990; US-627421.
 PA (MERI) MERCK & CO INC.
 PI Law WF, Mark GE, Schmidt JA, Singer II;
 DR WPI; 91-216985/30.
 DR P-PSDB; R13089.
 PT New recombinant immunoglobulin(s) reactive with leukocyte CD18
 PT antigen - comprise human heavy chain framework and murine
 PT complementarity regions useful in treatment of inflammation

ps Disclosure; Fig 25; 77pp; English.
 CC A recombinant human Ig comprises a human heavy chain framework
 CC and murine CDRs (with the heavy chain framework mutated at sites
 CC near the CDRs), a human light chain framework and murine CDRs.
 CC It has a mean IC50 nearly equal to that of the murine monoclonal
 CC antibody from which the CDRs were derived. It is designated
 CC mutated Gal/Rel. The human Ig is capable of binding to a human
 CC CD18 integrin.
 CC The murine CDRs are obt'd. from murine hybridoma 1B4
 CC (ATCC HB 10164). The light chain framework is derived from
 CC human myeloma protein REI (EP-239400).
 CC See also Q12682-84 and EP-438310.
 CC Sequence 336 BP; 80 A; 87 C; 85 G; 84 T;
 SQ

Query Match	81.5%;	Score 22;	DB 2;	Length 336;
Best Local Similarity	100.0%;	Pred. No. 2.31e-03;		
Matches	22;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Db 277 cagcaagtaatgaggatcctc 298
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QV 1 CAGCAAAGTAATGAGGATCCTC 22

RESULT 13

ID	Q51746 standard; cDNA; 91 BP.	
AC	Q51746;	
DT	31-MAY-1994 (first entry)	
DE	Oligonucleotide probe MK14-A	
KW	Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;	
KW	ss.	
OS	Synthetic.	
PN	EP-571911-A.	
PD	01-DEC-1993.	
PF	24-MAY-1993; 108325.	
PR	26-MAY-1992; US-889651.	
PA	(BECT) BECTON DICKINSON CO.	
PI	Shank DD, Spears PA;	
PI	WPI; 93-378844/48.	
PT	New oligo:nucleotide probes specific for Mycobacteria - used for	
PT	detection and amplification of Mycobacteria nucleic acid in	
PT	samples	
PS	Claim 3; Page 14; 23pp; English.	
CC	Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14-	
CC	(Q51735). It hybridized to all spp. of mycobacteria tested, but	
CC	cross reacted to a few non-mycobacterial spp. The probe may	
CC	be useful as an initial screen for mycobacterial infection.	
CC	See also Q51735-45 and Q51747-59.	
SO	Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;	

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Query Match      77.8%; Score 21; DB 9; Length 91;
Best Local Similarity 0.0%; Pred. No. 8.97e-03;
Matches         0: Conservative 23; Mismatches 2; Indels 0; Gaps 0;
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Db 18 vvshhhsvhvvhvhsvvv 42
::: :: : ::::: :::
Qv 3 GCAAGTAATGAGGATCCTCCAGG 27

14
PAGE

14
AC501

ID	Q42987	standard; DNA; 396 bp.
AC	Q42987;	
DT	30-SEP-1993	(first entry)
DE	Mouse 4C10 anti-idiotypic Ab light chain V region gene.	
RW	Polymerase chain reaction; MAF1; monoclonal antibody; hybridoma;	

KW	immuno-modulator; cancer; treatment; diagnosis; melanoma;
KW	anti-cancer immunity; enhancement; suppression;
KW	organ transplant rejection; ss.
OS	Mus musculus.
FH	Key
FT	Location/Qualifiers
FT	1..396
FT	/*tag= a
FT	sig peptide 1..60
FT	/*tag= b
FT	/note= "region coding for cleavable leader sequence"
FT	mat peptide 61..396
FT	/*tag= c
FT	misc_feature 151..153
FT	/*tag= d
FT	/note= "C substituted for C at nucleotide 152 due
FT	to PCR amplification of the gene sequence"
FT	W09310221-A.
PN	27-MAY-1993.
PD	27-MAY-1993.
PF	12-NOV-1992; U10166.
PF	13-NOV-1991; US-791934.
PR	(REGC) UNIV CALIFORNIA.
PA	Hastings A, Irie RF, Morrison SL.
PI	WPI; 93-182538/22.
DR	Chimeric murine-human anti-idiotype monoclonal antibodies -
PT	useful as immuno-modulators for treating and diagnosing cancers,
PT	and for suppressing organ transplant rejection and auto-immune
PT	diseases
PS	Disclosure; Page 29-30; 46pp; English.
CC	The sequence is that of the 4C10 anti-idiotype Ab light chain V region
CC	gene which was used in the construction of a murine/human monoclonal
CC	anti-idiotype antibody (MAIA). The MAIA elicits an anti-ganglioside
CC	response and produces antibodies which induce cytotoxic destruction
CC	of cancer cells bearing the gangliosides. It can be used for treating
CC	cancers partic. melanomas. It can also be used as an immunomodulator to
CC	enhance anti-cancer immunity, suppress organ transplant rejection and
CC	suppress autoimmune disease. The MAIA can also be used in the diagnosis
CC	of cancers.
SQ	Sequence 396 BP; 97 A; 96 C; 105 G; 98 T;
Query Match	77.8%; Score 21; DB 7; Length 396;
Best Local Similarity	88.9%; Pred. No. 8.97e-03;
Matches	24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 337 cagcaagtaatgagatcccaagtgg 363
|||
Qv 1 CAGCAAGTATGAGGATCTCCGAGG 27

DEC 11 1955

RESUL	ID	Q80292	standard; DNA; 645 BP.
13	AC	Q80292;	
	DT	08-JUL-1995	(first entry)
	DE	Monoclonal antibody 28C5 light chain.	
	KW	CD14 receptor; monoclonal antibody; 28C5; hybridoma;	
	KW	antiseptic; therapeutic; ds.	
	OS	Homo sapiens.	
	FH	Key	Location/Qualifiers
	FT	mat_peptide	1..645
	FT	/*tag=	a
	PN	W09428025-A.	
	PD	08-DEC-1994.	
	PF	27-MAY-1994;	U05898.
	PR	28-MAY-1993;	US-070160.
	PA	(SCRI)	SCRIPPS RES INST.

Mar 19 08:32

US-08-612-929-27.mg

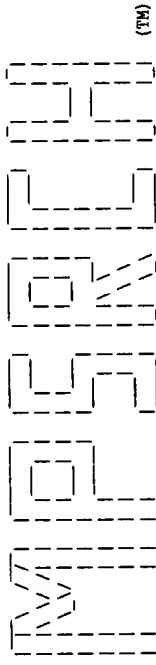
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PI Leturcq DJ, Mathison JC, Moriarty AM, Tobias PS;
PI Ulevitch RJ;
DR WPI; 95-022719/03.
DR P-PSDB; R64202.
PT Hybridoma cell lines produce MAb which inhibit CD14-mediated cell
PT activation - for detecting CD14 in a sample and to inhibit the
PT binding of LPS to CD14.
PS Disclosure; Fig 3; 91pp; English.
CC Anti-human soluble CD14 receptor MAb 28C5 may be used to
CC detect CD14 in cell samples, to inhibit binding of LPS to
CC CD14 or a LPS/CD14 complex to a cell, to inhibit CD14-mediated
CC activation of a cell expressing CD14 receptor, and for sepsis
CC therapy.
SQ Sequence 645 BP; 180 A; 170 C; 150 G; 145 T;

Query Match 77.8%; Score 21; DB 13; Length 645;
Best Local Similarity 92.0%; Pred. No. 8.97e-03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 268 caccaagtaatgagatccgacga 292
|||||
Qy 1 CAGCAAGTAATCAGGATCCTCCGA 25

Search completed: Wed Mar 19 08:34:29 1997
Job time : 14 secs.



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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:32:59 1997; MaePar time 55.50 Seconds
Tabular output not generated. 400.704 Million cell updates/sec

Title: >US-08-612-929-27
Description: (1-27) from US08612929.seq
Perfect Score: 27
N.A. Sequence: 1 CAGCAAGTATGAGTCTCCGAGG 27
Comp: GTGCTTTCATTACTCTAGGAGCTCC

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0\$
Listing first 45 summaries

Database: emb1-new5
1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI
10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR
genbank94
16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7
23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5
30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2
37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLN1 43:PLN2
44:PLN3 45:PLN4 46:PLN5 47:PLN6 48:PLN7 49:PLN8 50:PRI1
51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8
58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1
64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8
71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4
78:VRL5 79:VRL6 80:VRL7 81:VRL8
genbank-new5
82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG
89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL
u-emb146_94
96:part1

Statistics: Mean 7.264; Variance 2.639; scale 2.752

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	23	85.2	195	66	MUSIGKAAAC	Mouse Igk chain mRNA,	3.50e-05
2	23	85.2	228	65	MMU18577	Mus musculus immunogl	3.50e-05
3	23	85.2	273	67	MUSIGKCMH	Mouse Ig rearranged k	3.50e-05
4	23	85.2	307	64	MMIGGLA	Mus musculus (DBA/1)	3.50e-05
5	23	85.2	336	67	MUSIGKCMK	Mouse Ig rearranged k	3.50e-05
6	23	85.2	336	64	MMIGLC310	M.musculus mRNA for I	3.50e-05
7	23	85.2	336	64	MMIGLC404	M.musculus mRNA for I	3.50e-05
8	23	85.2	393	70	S50265	Ig VL-anti-CD4 mAb M-	3.50e-05
9	23	85.2	394	64	MMU01973	Mus musculus Balb/c a	3.50e-05
10	23	85.2	841	67	MUSIGKVR3	Mouse Ig germline kap	3.50e-05
11	21	77.8	312	66	MUSIGKARK	Mouse Ig kappa-chain	1.59e-03
12	21	77.8	318	65	MMVLZD4	M.musculus mRNA for i	1.59e-03
13	21	77.8	333	63	MDIGKVB	M.domesticus Igk vari	1.59e-03
14	21	77.8	333	70	S54207	V kappa 21=immunoglob	1.59e-03
15	21	77.8	360	67	MUSIGKAF	Mouse Ig active kappa	1.59e-03
16	21	77.8	363	67	MUSL341GV	Mouse hybridoma Ig re	1.59e-03
17	21	77.8	363	67	MUSL931GV	Mouse hybridoma Ig re	1.59e-03
18	21	77.8	396	70	SYN4C10L	Murine/Human chimeric	1.59e-03
19	21	77.8	671	67	MUSIGKVS	Mouse Ig germline kap	1.59e-03
20	21	77.8	841	67	MUSIGKVR2	Mouse Ig germline kap	1.59e-03
21	21	77.8	900	40	I08223	Sequence 1 from paten	1.59e-03
22	20	74.1	195	66	MUSIGKAAAB	Mouse Igk chain mRNA,	1.01e-02
23	20	74.1	245	64	MMIGKCVRH	M.musculus immunoglob	1.01e-02
24	20	74.1	255	64	MMIGKCVRD	M.musculus immunoglob	1.01e-02
25	20	74.1	264	64	MMIGKCVRI	M.musculus immunoglob	1.01e-02
26	20	74.1	266	64	MMIGKCVRC	M.musculus immunoglob	1.01e-02
27	20	74.1	270	64	MMIGKCVRG	M.musculus immunoglob	1.01e-02
28	20	74.1	270	64	MMIGKCVRB	M.musculus immunoglob	1.01e-02
29	20	74.1	270	64	MMIGKCVRF	M.musculus immunoglob	1.01e-02
30	20	74.1	279	66	MUSIGKAAA	Mouse Igk chain mRNA,	1.01e-02
31	20	74.1	292	65	MMU18599	Mus musculus immunogl	1.01e-02
32	20	74.1	297	65	MMU29629	Mus musculus anti-DNA	1.01e-02
33	20	74.1	302	67	MUSIGLAEJ	Mouse Ig kappa-chain	1.01e-02
34	20	74.1	321	64	MMIGLT82	Mouse immunoglobulin	1.01e-02
35	20	74.1	322	64	MMIGLT83	Mouse immunoglobulin	1.01e-02
36	20	74.1	323	70	S52318	Ig VJ=anti-carcinoemb	1.01e-02
37	20	74.1	333	67	MUSIGLVW21	Mus musculus (clone V	1.01e-02
38	20	74.1	333	65	MMVLIE10	Mouse mRNA for kappa-	1.01e-02
39	20	74.1	333	70	S42888	Ig V kappa =immunogl	1.01e-02
40	20	74.1	333	67	MUSIGL5B	Mouse IgL chain H2L2	1.01e-02
41	20	74.1	336	67	MUSIGKCMJ	Mouse Ig rearranged k	1.01e-02
42	20	74.1	336	67	MUSIGKCMJ	Mouse Ig rearranged k	1.01e-02
43	20	74.1	469	67	MUSIGKEK	Mouse Ig aberrantly r	1.01e-02
44	20	74.1	694	67	MUSIGKAM2	Mouse Ig kappa aberr	1.01e-02
45	20	74.1	833	64	MMIGK2	Part of the gene for	1.01e-02

ALIGNMENTS

RESULT 1
LOCUS MUSIGKAAAC 195 bp mRNA
DEFINITION Mouse Igk chain mRNA, VJ1 region.
ACCESSION M57980
NID q196406
KEYWORDS J-region; V-region; anti-cytochrome c antibody;
immunoglobulin kappa-chain; immunoglobulin light chain.
SOURCE Mouse (BALB/c) secondary B cell hybridoma 2B5 mRNA, clone 2B5.F8.
ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 195)
AUTHORS Goshorn, S.C., Retzel, E. and Jemerson, R.
TITLE Common structural features among monoclonal antibodies binding the
same antigenic region of cytochrome c
JOURNAL J. Biol. Chem. 266 (4), 2134-2142 (1991)

MEDLINE 91115823

FEATURES
Location/Qualifiers

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/clone="ZB5.F8"
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CDS

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/db_xref="PID:g196407"

/translation="PKLLIYAASNLESGIPARFSGSGCTDTINHPVEEDGATYY
CQSNEDPRTFGGTKLEIKR"
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136..162
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BASE COUNT 52 a 50 c 51 g 42 t
ORIGIN Chromosome 6.

Query Match 85.2%; Score 23; DB 66; Length 195;
Best Local Similarity 96.0%; Pred. No. 3.50e-05;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 136 caccaagaatgagatcctcgga 160

|||||

QY 1 CAGCAAGTAATGAGATCCTCGA 25

RESULT 2

LOCUS MMU18577 228 bp mRNA ROD 21-JUN-1995
DEFINITION Mus musculus immunoglobulin kappa light chain, variable region
mRNA, clone BALB/c-51, partial cds.

ACCESSION U18577

NTD g619707

KEYWORDS mouse.

SOURCE Mus musculus

ORGANISM

Eukaryota; Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Mus.
1 (bases 1 to 228)
AUTHORS Roark, J.H., Kuntz, C.L., Nguyen, K.A., Caton, A.J. and Erikson, J.
TITLE Breakdown of B cell tolerance in a mouse model of systemic lupus
erythematosus

J. Exp. Med. 181 (3), 1157-1167 (1995)

MEDLINE 95173583

REFERENCE 2 (bases 1 to 228)

AUTHORS Roark, J.H.

TITLE Direct Submission

JOURNAL Submitted (14-DEC-1994) Jessica H. Roark, Wistar Institute, 3601
Spruce St., Philadelphia, PA 19104, USA

FEATURES Location/Qualifiers

1..228

source

/strain="BALB/c"

/organism="Mus musculus"

/cell_type="splenic B cell hybridoma"

/tissue_type="spleen"

/dev_stage="adult"

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CDS

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region"

/db_xref="PID:g619708"

/translation="YDGDSYNNWYQKPGQPPKLLIYAASNLESGIPARFSGSGTDT

FTLNHPVEEDAAITYCQSNEDPPTFGSGT"

BASE COUNT 61 a 57 c 57 g 53 t

ORIGIN

Query Match 85.2%; Score 23; DB 65; Length 228;

Best Local Similarity 100.0%; Pred. No. 3.50e-05;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 187 cagcaagaatgagatcctcc 209

|||||

QY 1 CAGCAAGTAATGAGATCCTCC 23

RESULT 3

LOCUS MUSIGKCM1 273 bp mRNA ROD 15-MAR-1989
DEFINITION Mouse Ig rearranged kappa-chain V-region mRNA from hybridoma

H37-63, partial cds.

ACCESSION M21525

NTD g196987

KEYWORDS C-region; V-region; immunoglobulin light chain;

immunoglobulin-kappa; rearranged gene.

SOURCE Mouse (strain BALB/c) hybridoma H37-63, cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 273)

AUTHORS Clarke, S.H., Huppi, K., Ruezinsky, D., Staudt, L., Gerhard, W. and

Weigert, M.

TITLE Inter- and intracolon diversity in the antibody response to

influenza hemagglutinin

J. Exp. Med. 161, 687-704 (1985)

MEDLINE 85159415

FEATURES Location/Qualifiers

source

1..273

/organism="Mus musculus"

Mar 19 08:32

US-08-612-929-27.rge

5

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CDS
<1..>273
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/db_xref="PID:q196988"
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BASE COUNT      69 a   72 c   66 g   65 t   1 others
ORIGIN
Chromosome 6.

Query Match      85.2%; Score 23; DB 67; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.50e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 214 cagcaaaagtaatgagatcctcc 236
|||||
QY 1 CAGCAAGTAATGAGATCCTCC 23

RESULT 4
LOCUS MMIGGL4 307 bp RNA ROD 05-AUG-1994
DEFINITION Mus musculus (DBA/1) mRNA for immunoglobulin gamma light chain
variable region.
ACCESSION Z26771
NID q436888
KEYWORDS immunoglobulin; immunoglobulin gamma; light chain joining region;
light chain variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryote; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 307)
AUTHORS Mo,J.A., Scheynius,A., Nilsson,S. and Holmdahl,R.
TITLE Germline encoded IgG antibodies bind mouse cartilage in vivo
epitope and idiotype specific binding and inhibition
JOURNAL Scand. J. Immunol. (1993) In press
REFERENCE 2 (bases 1 to 307)
AUTHORS Mo,J.A.
TITLE Direct Submission
JOURNAL Submitted (30-SEP-1993) to the EMBL/GenBank/DBJ databases, John A
Mo, Department of Medical and Physiological, Department of, Medical
and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE 3 (bases 1 to 307)
AUTHORS Mo,J.A., Scheynius,A., Nilsson,S. and Holmdahl,R.
TITLE Germline-encoded IgG antibodies bind mouse cartilage in vivo:
epitope- and idiotype-specific binding and inhibition
JOURNAL Scand. J. Immunol. 39 (2), 122-130 (1994)
MEDLINE 94126659
FEATURES
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Location/Qualifiers
1..307
/organism="Mus musculus"
/strain="DBA/1"
/dev_stage="Adult"
/tissue_type="Lymph node"
/cell_type="B cell hybridoma"
/cell_line="CIIF4 hybridoma"
/chromosome="6"
1..272
/note="Light chain variable region"
J_segment 273..307
J_segment /note="Joining region JK2"
BASE COUNT      81 a   77 c   77 g   72 t
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6

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ORIGIN
Query Match      85.2%; Score 23; DB 64; Length 307;
Best Local Similarity 100.0%; Pred. No. 3.50e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 250 cagcaaaagtaatgagatcctcc 272
|||||
QY 1 CAGCAAGTAATGAGATCCTCC 23

RESULT 5
LOCUS MUSIGKCMK 336 bp mRNA ROD 15-MAR-1989
DEFINITION Mouse Ig rearranged kappa-chain V-region mRNA from hybridoma
H37-77, partial cds.
ACCESSION M21524
NID q196985
KEYWORDS C-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa; rearranged gene.
SOURCE Mouse (strain BALB/c) hybridoma H37-77, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryote; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 336)
AUTHORS Clarke,S.H., Huppi,K., Ruzinsky,D., Staudt,L., Gerhard,W. and
Weigert,M.
TITLE Inter- and intracloal diversity in the antibody response to
influenza hemagglutinin
JOURNAL J. Exp. Med. 161, 687-704 (1985)
MEDLINE 85159415
FEATURES
source
Location/Qualifiers
1..336
/organism="Mus musculus"
<1..>336
/note="Ig kappa-chain VJ-regions"
/codon_start=1
/db_xref="PID:q196986"
/translation="DIETQSPASLAVSLQQRATISCRASESVYSGKSFHHYQKPK
GQPPKLLIYRASNLGSGIPARESGSGSRDTFTLTINPVEADVATYYCQSNEDPPYF
GAGTKLEIKR"
BASE COUNT      84 a   88 c   84 g   80 t
ORIGIN Chromosome 6.

Query Match      85.2%; Score 23; DB 67; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.50e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 277 cagcaaaagtaatgagatcctcc 299
|||||
QY 1 CAGCAAGTAATGAGATCCTCC 23

RESULT 6
LOCUS MMIGLC310 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T310) .
ACCESSION X65091
NID g52288
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryote; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
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```
Scutigornathi; Myomorpha; Muridae; Murinae; Mus.
1 (bases 1 to 336)
Direct Submission
Weissenhorn, W.
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

2 (bases 1 to 336)
Weissenhorn, W., Riethmueller, G., Weiss, E.M. and Rieber, E.P.
JOURNAL Structural characterization of CD4 mAb
Unpublished
Location/Qualifiers
source
1..336
/organism="Mus musculus"
/strain="Balb/c"
/cell_type="B-cell"
/cell_line="Hybridoma M-T310"
<1..>336
/codon_start=1
/product="alpha CD4 mAb immunoglobulin light chain VJ
region"
/db_xref="PID:g52289"
/translat="DIVLTQSPASIPMSLQGRATISCKASQSLDYGDSYMNYYQOKP
GQPKLLIYAASNLSEGPARESGSGCTDFTLNHPVEEDAAATYYCQSSDDPPTF
GGGKLEIKR"

BASE COUNT 89 a 90 c 81 g 76 t
ORIGIN
Query Match 85.2%; Score 23; DB 64; Length 336;
Best Local Similarity 96.0%; Pred. No. 3.50e-05;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaaaagttagtgagatcctccga 301
||||| ||||| ||||| ||||| |||||
Qy 1 CAGCAAGTAATCAGGATCCTCCGA 25

RESULT 7
LOCUS MWIGLC404 336 bp RNA ROD 07-MAY-1992
DEFINITION M.musculus mRNA for IG light chain VJ region (M-T404).
ACCESSION X65092
NID g52292
KEYWORDS Ig light chain; VJ domain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
1 (bases 1 to 336)
Weissenhorn, W.
Direct Submission
JOURNAL Submitted (10-MAR-1992) to the EMBL/GenBank/DBJ databases. W.
Weissenhorn, Institut fuer Immunologie, Goethestrasse 31, W-8000
Muenchen 2, FRG

2 (bases 1 to 336)
Weissenhorn, W., Riethmueller, G., Weiss, E.M. and Rieber, E.P.
JOURNAL Structural characterization of CD4 mAb
Unpublished
Location/Qualifiers
source
1..336
/organism="Mus musculus"
/strain="Balb/c"
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/cell_type="B-cell"
/cell_line="Hybridoma M-T404"
<1..>336
/codon_start=1
/product="alpha CD4 mAb immunoglobulin light chain VJ
region"
/db_xref="PID:g52293"
/translat="DIVLTQSPASIPMSLQGRATISCKASQSLDYGDSYMNYYQOKP
GQPKLLIYAASNLSEGPARESGSGCTDFTLNHPVEEDAAATYYCQSSDDPPTF
GGGKLEIKR"

BASE COUNT 89 a 90 c 81 g 76 t
ORIGIN
Query Match 85.2%; Score 23; DB 64; Length 336;
Best Local Similarity 96.0%; Pred. No. 3.50e-05;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaaaagttagtgagatcctccga 301
||||| ||||| ||||| ||||| |||||
Qy 1 CAGCAAGTAATCAGGATCCTCCGA 25

RESULT 8
LOCUS S50265 393 bp mRNA ROD 02-APR-1993
DEFINITION Ig VJ-anti-CD4 mAb M-T310 variable region light chain [J], chimeric
antibody] [mice, hybridoma cells, mRNA Partial, 393 nt].
ACCESSION S50265
NID g260765
KEYWORDS mice hybridoma cells.
SOURCE Mus sp.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 393)
AUTHORS Weissenhorn, W., Scheuer, W., Kaluza, B., Schwirzke, M., Reiter, C.,
Flieger, D., Lenz, H., Weiss, E.H., Rieber, E.P., Riethmuller, G. et.al.
TITLE Combinatorial functions of two chimeric antibodies directed to
human CD4 and one directed to the alpha-chain of the human
interleukin-2 receptor
JOURNAL Gene 121 (2), 271-278 (1992)
MEDLINE 93077041
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibsq 119503] from the original journal article.
This sequence comes from Fig. 1c.
FEATURES
source
location/Qualifiers
1..393
/organism="Mus sp."
/note="mice"
1..393
/partial
/gene="Ig VJ"
/note="Method: conceptual translation supplied by author.
This sequence comes from Fig. 1c."
/codon_start=1
/product="anti-CD4 mAb M-T310 variable region light chain"
/db_xref="PID:g260766"
/translat="METDTILLVLLWVPGSTGDIVLTQSPASIPMSLQGRATISCK
ASQSLDYGDSYMNYYQOKPGQPKLLIYAASNLSEGPARESGSGCTDFTLNHPV
EEEDAAATYYCQSSDDPPTFGGKLEIK"

BASE COUNT 100 a 105 c 98 g 90 t
ORIGIN
Query Match 85.2%; Score 23; DB 70; Length 393;
Best Local Similarity 96.0%; Pred. No. 3.50e-05;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 337 cagcaagaagtatgagatcctccga 361
|||||
Qy 1 CAGCAAGTAATGAGATCCTCCGA 25

RESULT 9
LOCUS MMU01973 394 bp mRNA ROD 24-SEP-1993
DEFINITION Mus musculus Balb/c anti-CD18 Ig light chain variable region mRNA,
partial cds.
ACCESSION U01973
NID 9403071
KEYWORDS .
SOURCE mouse.
ORGANISM Mus musculus
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Rodentia; Myomorpha; Muridae; Mus.
REFERENCE 1 (bases 1 to 394)
AUTHORS Hsiao,K., Bajorath,J. and Harris,L.J.
TITLE Humanization of 60.3, an anti-CD18 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 394)
AUTHORS Harris,L.J.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1993) Linda J. Harris, Molecular Immunology,
Bristol-Myers Squibb, Pharmaceutical Research Institute, 3005 First
Avenue, Seattle, WA 98121 USA
FEATURES
source
1..394
/strain="Balb/c"
/organism="Mus musculus"
/cell_line="60.3 hybridoma"
/cell_type="hybridoma (B-cell)"
/tissue_type="spleen"
/dev_stage="adult"
sig_peptide 1..60
/note="nucleotides 1-29 derived from PCR primer and may
not reflect mRNA sequence"
exon 1..49
/number=1
/product="partial signal peptide"
CDS 1..394
/partial
/note="V gene is identical to Vk2lc germline gene; uses
Jk1"
/codon_start=1
/product="Ig variable region, light chain"
/db_xref="PID:g403072"
/translation="METDTLLLVLLWPGSTGDIVLTQSPASIVSLQQRATISCR
ASEVSDYSGNSFMHWYQKPGQPKLLIYRASNLGSGIPARFSGSRTDTLTINPV
EADDVATYYCQSNEDPRTEGGTKLEIK"
exon 50..394
/number=2
/product="carboxyl end of signal peptide and mature heavy
chain"
misc_feature 61..135
/standard_name="FR1"
mat_peptide 61..393
/product="Ig variable region, light chain"
misc_feature 136..168
/standard_name="CDR1"
misc_feature 169..219
/standard_name="FR2"
misc_feature 220..228
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misc_feature 229..339
/standard_name="CDR2"
misc_feature 340..357
/standard_name="CDR3"
misc_feature 358..393
/standard_name="FR4"
BASE COUNT 99 a 100 c 98 g 97 t
ORIGIN
Query Match 85.2%; Score 23; DB 64; Length 394;
Best Local Similarity 96.0%; Pred. No. 3.50e-05;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 337 cagcaagaagtatgagatcctccga 361
|||||
Qy 1 CAGCAAGTAATGAGATCCTCCGA 25

RESULT 10
LOCUS MUSIGKVR3 841 bp DNA ROD 14-APR-1994
DEFINITION Mouse Ig germline kappa V-region 9.5kb-V-kappa, V-kappa-21C.
ACCESSION K02161
NID g197492
KEYWORDS C-region; V-region; germline; immunoglobulin light chain;
immunoglobulin-kappa; immunoglobulin-kappa subgroup vk-21.
SEGMENT 3 of 3
SOURCE Mouse BALB/c embryo DNA, clones KM23 and KE5e.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 841)
AUTHORS Heinrich,G., Traunecker,A. and Tonegawa,S.
TITLE Somatic mutation creates diversity in the major group of mouse
immunoglobulin kappa-light chains
JOURNAL J. Exp. Med. 159, 417-435 (1984)
MEDLINE 84113346
FEATURES
source
1..841
/organism="Mus musculus"
<198..246
/note="Ig kappa V-region 9.5kb-V-kappa"
/number=1
exon 198..246
/note="Ig kappa V-region 9.5kb-V-kappa signal peptide,
exon 1; putative"
join(198..246,486..793)
/partial
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/db_xref="PID:g197496"
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EADDVATYYCQSNEDP"
sig_peptide 198..246
/note="Ig kappa V-region 9.5kb-V-kappa signal peptide"
/codon_start=1
exon 198..246
/note="Ig kappa V-region 9.5kb-V-kappa, exon 1; putative"
join(198..246,486..496)
/note="Ig kappa V-region 9.5kb-V-kappa signal peptide"
/codon_start=1
intron 247..485
/note="VK9.5 intron A"
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exon	486..793	/note="Ig kappa V-region 9.5kb-V-kappa, exon 2; putative"
sig_peptide	486..496	
	/note="Ig kappa V-region 9.5kb-V-kappa signal peptide"	
exon	486..5794	/codon_start=1
	/note="Ig kappa V-region 9.5kb-V-kappa"	
exon	486..496	/number=2
mat_peptide	497..794	/note="Ig kappa V-region 9.5kb-V-kappa signal peptide, exon 2; putative"
	/partial	
idna	795..5841	/note="Ig kappa V-region 9.5kb-V-kappa mature peptide"
misc_signal	796..823	/note="V-J intervening DNA (5' end +/- 1 bp)"
	796..823	/note="putative recombination recognition sequence; putative"
BASE COUNT	218 a 196 c 191 g 236 t	
ORIGIN	About 39 kb after segment 2; chromosome 6.	
Query Match	85.2%; Score 23; DB 67; Length 841;	
Best Local Similarity	100.0%; Pred. No. 3.50e-05;	
Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	773 cagcaaaagtaatgaggtactctcc 795	
Qy	1 CAGCAAAAGTAATGAGGTCTCTCC 23	
RESULT	11	
LOCUS	MUSIGKABK 312 bp mRNA	ROD 15-SEP-1990
DEFINITION	Mouse Ig kappa-chain (anti-insulin Ab 127) mRNA V region, partial cds.	
ACCESSION	M34529	
MID	g196507	
KEYWORDS	V-region; immunoglobulin heavy chain; immunoglobulin-kappa; processed gene.	
SOURCE	Mouse (strain Balb/c), cDNA to mRNA.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.	
AUTHORS	Evlonu,U.K., Nell,L.J. and Thomas,J.W.	
TITLE	V-H and V-L gene usage by murine IgG antibodies that bind autologous insulin	
JOURNAL	J. Immunol. 144, 3091-3098 (1990)	
MEDLINE	90217518	
FEATURES	Location/Qualifiers	
source	1..312	/organism="Mus musculus"
	<1..312	/note="Ig kappa-chain V-region"
CDS	/codon_start=1	
	/db_xref="PID:g196508"	
	/translation="DIVLTQSPASIVSLQGRATISCRASESVDSYGNFSFMHWYQRP GQPKLLIYRASNLSEGIPIARESGCSGRDTFLINPVADVASVYCCQSNSEEPFT GG"	
BASE COUNT	78 a 81 c 77 g 76 t	
ORIGIN		
Query Match	77.8%; Score 21; DB 66; Length 312;	

Best Local Similarity 95.7%; Pred. No. 1.59e-03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaaatgaatgaggaacttc 299
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Qy 1 CAGCAAGTAATGAGGATCCTCC 23
|||||

RESULT 12
LOCUS MWVL2D4 318 bp RNA ROD 16-MAY-1995
DEFINITION M.musculus mRNA for immunoglobulin light chain variable region (VL2D4).
ACCESSION X86545
NID g809058
KEYWORDS immunoglobulin; immunoglobulin light chain; kappa chain; light chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 318)
Cerato,E., Birkle,S., Portoukalian,J. and Aubry,J.
JOURNAL Unpublished
AUTHORS Cerato,E.M.
TITLE Direct Submission
JOURNAL Submitted (24-APR-1995) to the EMBL/GenBank/DBJ databases. E.M. Cerato, INSERM U211, Institut de Biologie, 9 quai Moncousu, 44035 Nantes Cedex 01, FRANCE

FEATURES
source Location/Qualifiers
1..318
/organism="Mus musculus"
/strain="BALB/c"
/dev_stage="adult"
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/cell_type="B cell hybridoma"
/cell_line="2D4 hybridoma"
/chromosome="12"
/rearranged
V_region 16..318
/note="anti-ganglioside asialo GM2 immunoglobulin"
/product="immunoglobulin light chain variable region VL 2D4"

BASE COUNT 75 a 84 c 80 g 79 t
ORIGIN

Query Match 77.8%; Score 21; DB 65; Length 318;
Best Local Similarity 92.0%; Pred. No. 1.59e-03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 262 cagcaataatgaggaatttcga 286
|||||
Qy 1 CAGCAAGTAATGAGGATCCTCCGA 25
|||||

RESULT 13
LOCUS MDIGKVB 333 bp RNA ROD 05-NOV-1994
DEFINITION M.domesticus Igk variable region.
ACCESSION Z22133
NID g297695
KEYWORDS anti-DNA antibody; Igk gene; Igk variable region; immunoglobulin.
SOURCE western European house mouse.
ORGANISM Mus musculus domesticus
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 333)

AUTHORS Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.

TITLE Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice

JOURNAL J. Exp. Med. 176 (3), 761-779 (1992)

MEDLINE 92381444

REFERENCE 2 (bases 1 to 333)

AUTHORS Marion,T.N.

TITLE Direct Submission

JOURNAL Submitted (23-MAR-1993) to the EMBL/GenBank/DBJ databases. Tony N. Marion, Microbiology and Immunology, University of, Tennessee, Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA

FEATURES

source

1..333

/organism="Mus domesticus"

/strain="(NZB x NZW)F1"

/dev stage="somatic variant"

/tissue_type="spleen"

/cell_type="hybridoma"

/cell_line="202p.38"

/isolates="mouse #202"

/chromosome="6"

/sex="Female"

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/gene="Igk"

/codon start=1

/function="kappa light chain variable region for anti-DNA antibody; Vk21 family"

/product="immunoglobulin variable region"

/db xref="PID:g297696"

/translation="DIVLTQSPASIVSLGQRATISCRASESDNYG1SPMNWFQOKP

GGPKLLIYASNQGSPARFSGSGTDFSLIHVEEDDAATYYCQQSIEDPPTF

GGGTKLEIK"

BASE COUNT 84 a 86 c 84 g 78 t 1 others

ORIGIN

Query Match 77.8%; Score 21; DB 63; Length 333;

Best Local Similarity 92.0%; Pred. No. 1.59e-03;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 277 cagcaaaagttaaggaggtctccga 301

||||||| ||||| ||||| |||||

QY 1 CAGCAAAAGTAATGAGGATCCTCGA 25

RESULT 14

LOCUS S54207 333 bp mRNA ROD 26-MAR-1993

DEFINITION V kappa 21=immunoglobulin light chain variable region [mice, HIV-1 BRU immunized BALB/c, mRNA Partial, 333 nt].

ACCESSION S54207

NID g264866

KEYWORDS mice HIV-1 BRU immunized BALB/c.

SOURCE Mus sp.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 333)

AUTHORS Pirofski,L.A., Thomas,E.K. and Scharff,M.D.

TITLE Variable region gene utilization and mutation in a group of neutralizing murine anti-human immunodeficiency virus type 1 principal neutralizing determinant antibodies

JOURNAL AIDS Res. Hum. Retroviruses 9 (1), 41-49 (1993)

MEDLINE 93152285

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 124489] from the original journal article. This sequence comes from Fig. 2.

FEATURES

source

1..333

/organism="Mus sp."

/note="mice"

1..333

/partial

/gene="V<kappa>21"

/notes="mismatch(62[I->M]); Description: immunoglobulin light chain variable region, anti-HIV-1 monoclonal antibody 110.3; Method: conceptual translation supplied by author. This sequence comes from Fig. 2. Author-given protein sequence is in conflict with the conceptual translation. anti-HIV-1 monoclonal antibody 110.3"

/codon start=1

/product="immunoglobulin light chain variable region"

/db xref="PID:g264867"

/translation="DVVLTPQSPASIVSLGQRATISCKASQSDYDGDSTYMNWYQOKP

GQPPKLLIHAASNLVSCIPARFSGSGTDFTLIHVVEEDAAATYYCQQSIEDPPTF

GGGTKLEIK"

BASE COUNT 87 a 85 c 85 g 76 t

ORIGIN

Query Match 77.8%; Score 21; DB 70; Length 333;

Best Local Similarity 95.7%; Pred. No. 1.59e-03;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 277 cagcaaaagtattgaggtactcc 299

||||||| ||||| ||||| |||||

QY 1 CAGCAAAAGTAATGAGGATCTCC 23

RESULT 15

LOCUS MUSIGKAF 360 bp mRNA ROD 30-AUG-1991

DEFINITION Mouse Ig active kappa chain mRNA V-region (V-D-J).

ACCESSION M61046

NID g196679

KEYWORDS anti-CD4; immunoglobulin light chain; monoclonal antibody.

SOURCE Mouse, cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 360)

AUTHORS Attanasio,R., Dilley,D., Buck,D.W., Maino,V.C., Lohman,K.L., Kanda,P. and Kennedy,R.C.

TITLE Structural characterization of a cross-reactive idiotype shared by monoclonal antibodies specific for the human CD4 molecule

JOURNAL J. Biol. Chem. 266, 14611-14619 (1991)

MEDLINE 91317827

FEATURES

source

1..360

/organism="Mus musculus"

/strain="BALB/c"

/sub species="domesticus"

/cell_line="SP20/spleen fusion hybridoma"

/sequenced_mol="cDNA to mRNA"

70..114

/note="CDR1"

/product="anti-human CD4 antibody"

160..180

misc_feature

misc_feature

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15

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/note="CDR2"
/product="anti-human CD4 antibody"
misc_feature 277..303
/note="CDR3"
/product="anti-human CD4 antibody"
BASE COUNT 95 a 98 c 84 g 83 t
ORIGIN
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Query Match 77.8%; Score 21; DB 67; Length 360;
Best Local Similarity 92.0%; Pred. No. 1.59e-03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 277 caacaaagttagagatcctccga 301
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Qy 1 CAGCAAGTAAATGAGGATCCTCCGA 25
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Search completed: Wed Mar 19 08:33:57 1997
Job time : 58 secs.

WATERMAN

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MParch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:38:19 1997; MasPar time 67.22 Seconds
Tabular output not generated. 295.243 Million cell updates/sec

Title: >US-08-612-929-53

Description: (1-45) from US08612929.seq

Perfect Score: 45

N.A. Sequence: 1 AAGCGCTCCCAAGCTGTCAATATGATGCTGATGATATATACAC 45

Comp: TTCGGGAGGGTTCCAACTATACACTATACCACTATCAATATACCTTG

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

EST-STS
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98
99:EST99

Database:

EST-STS-TWO
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124
125:EST125 126:EST126 127:EST127 128:EST128 129:EST129

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7
136:STS8 137:STS9 138:STS10 139:STS11 140:STS12
141:STS13 142:STS14 143:STS15 144:STS16 145:STS17
146:STS18 147:STS19 148:STS20 149:STS21 150:STS22
151:STS23 152:STS24 153:STS25 154:STS26 155:STS27
156:STS28 157:STS29 158:STS30 159:STS31 160:STS32
161:STS33 162:STS34 163:STS35 164:STS36 165:STS37
166:STS38 167:STS39 168:STS40 169:STS41 170:STS42
171:STS43 172:STS44 173:STS45 174:STS46

Statistics: Mean 7.747; Variance 2.176; scale 3.560

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	22	48.9	313	1	ATTS2998	A. thaliana transcrib 1.47e-05
2	19	42.2	292	131	G06364	human STS WI-7035. 1.41e-02
3	19	42.2	353	33	H88129	ys75d12.sl Homo sapie 1.41e-02
4	19	42.2	362	174	HS690296	human STS SHGC-6155 c 1.41e-02
5	19	42.2	362	134	GI7690	human STS SHGC-6155 c 1.41e-02
6	19	42.2	389	166	H599314	yz84g03.rl Homo sapie 1.41e-02
7	19	42.2	389	142	N79899	yz84g03.rl Homo sapie 1.41e-02
8	19	42.2	389	71	N79899	yz84g03.rl Homo sapie 1.41e-02
9	19	42.2	463	57	N36147	yz29c03.sl Homo sapie 1.41e-02
10	18	40.0	182	108	T25334	EST060 Homo sapiens c 1.22e-01
11	18	40.0	259	35	H96107	yt97c12.sl Homo sapie 1.22e-01
12	18	40.0	269	51	M78099	EST01689 Homo sapiens 1.22e-01
13	18	40.0	299	22	H52906	SW31CA458SK Brugia ma 1.22e-01
14	18	40.0	300	116	T54600	yb41a05.sl Homo sapie 1.22e-01
15	18	40.0	309	112	T41640	10221 Arabidopsis tha 1.22e-01
16	18	40.0	322	80	R30940	yh60c03.sl Homo sapie 1.22e-01
17	18	40.0	324	104	T07002	EST04891 Homo sapiens 1.22e-01
18	18	40.0	330	21	H48510	yr33f08.sl Homo sapie 1.22e-01
19	18	40.0	334	48	HUM224A03B	Human aorta cDNA 5'-e 1.22e-01
20	18	40.0	335	87	R55511	yj79h09.sl Homo sapie 1.22e-01
21	18	40.0	338	74	R10829	yf37b10.sl Homo sapie 1.22e-01
22	18	40.0	376	98	R91466	yq08a11.sl Homo sapie 1.22e-01
23	18	40.0	385	107	T19193	d08013t Homo sapiens 1.22e-01
24	18	40.0	387	128	T98507	ye60g02.sl Homo sapie 1.22e-01
25	18	40.0	396	96	R84415	yp89h09.sl Homo sapie 1.22e-01
26	18	40.0	406	93	R76483	y161c11.rl Homo sapie 1.22e-01
27	18	40.0	409	61	N49078	yy79c04.sl Homo sapie 1.22e-01
28	18	40.0	411	164	H5666293	za14h10.sl Homo sapie 1.22e-01
29	18	40.0	416	100	R96162	yt84c11.sl Homo sapie 1.22e-01
30	18	40.0	423	57	N34383	yy12h06.sl Homo sapie 1.22e-01
31	18	40.0	427	66	N63295	yz88h06.sl Homo sapie 1.22e-01
32	18	40.0	438	27	H67932	yu53c04.rl Homo sapie 1.22e-01
33	18	40.0	441	17	H38046	yp58c10.rl Homo sapie 1.22e-01
34	18	40.0	445	97	R88605	ym93e02.rl Homo sapie 1.22e-01
35	18	40.0	454	133	G13723	human STS SHGC-1250 c 1.22e-01
36	18	40.0	459	87	R55337	yg88c08.sl Homo sapie 1.22e-01
37	18	40.0	470	163	HS591325	yz93d03.rl Homo sapie 1.22e-01
38	18	40.0	473	71	N80390	za14h10.rl Homo sapie 1.22e-01
39	18	40.0	492	28	H72500	ys07e04.rl Homo sapie 1.22e-01
40	18	40.0	517	117	T59660	yb66f11.sl Homo sapie 1.22e-01
41	18	40.0	535	89	R60158	yh12d10.sl Homo sapie 1.22e-01
42	18	40.0	565	63	N53488	yy42f11.sl Homo sapie 1.22e-01

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3

43 18 40.0 581 56 N32030 yw96e02.sl Homo sapie 1.22e-01
44 18 40.0 587 54 N25532 yw76c05.sl Homo sapie 1.22e-01
45 18 40.0 601 8 H05802 y177d08.sl Homo sapie 1.22e-01

ALIGNMENTS

RESULT 1
LOCUS ATTS2998 313 bp RNA EST 31-MAY-1994
DEFINITION A. thaliana transcribed sequence; clone FA1102; 5' end.
ACCESSION Z33940
NID 9496427
KEYWORDS expressed sequence tag; partial cDNA sequence.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryotae; mitochondrial eukaryotes; Chlorophyta/Embryophyta
group; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Dilleniidae; Capparales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 313)
AUTHORS Philipps,G. and Gigot,C.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-1994) to the EMBL/GenBank/DBJ databases. CNRS,
GDR-1003 ACS, INRA, Laboratoire de Biologie Moleculaire, BP 27,
31326 Castanet-Tolosan cedex, France.
E-mail:gdr-svpetoulouse.inra.fr. On behalf of: Laboratoire de
Biologie Moleculaire des Plantes - CNRS, Gigot Claude / I512, 12
Rue du General Zimmer, 67084 Strasbourg Cedex, France.
E-mail:philippes@scilla.u-strasbg.fr

REFERENCE 2 (bases 1 to 313)
AUTHORS CNRS.
TITLE The Arabidopsis thaliana transcribed genome: the GDR cDNA program
JOURNAL Unpublished
COMMENT Cloning vector: Lambda ZAPII;
Physiological condition: leaves strips incubated 2/3/4 days
in liquid culture medium. full automatic.

FEATURES
source
1..313
/organism="Arabidopsis thaliana"
/clone="FA1102"
/tissue type="sliced leaves of A.thaliana ecotype
columbia"
/clone lib="Strasbourg-A"
BASE COUNT 74 a 76 c 60 g 99 t 4 others
ORIGIN

Query Match 48.9%; Score 22; DB 1; Length 313;
Best Local Similarity 86.7%; Pred. No. 1.47e-05;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 242 cctccacaagtggtattatgaagtgata 271
||||||| | ||||||||| |||||
Qy 5 CCTCCAAAGTGTGATTATGATGATGATA 34

RESULT 2
LOCUS G06364 292 bp DNA STS 19-OCT-1995
DEFINITION human STS WI-7035.
ACCESSION G06364
NID g859609
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human STSs derived from sequences in dbEST and the Unigene
collection.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Mar 19 08:38

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4

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 292)
AUTHORS Hudson,T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
JOURNAL Unpublished (1995)
COMMENT

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TAATTAAGTGTTCCTCCACTTAAAC
Primer B: ATTTGGGATTAATAAGTGAAACCA
STS size: 200
PCR Profile:

Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

Prepared with primer pairs derived from V00564 --- Unigene.

FEATURES
source
1..292
Location/Qualifiers
/organism="Homo sapiens"
/note="human"
STS
1..200
/map="738_B_6; 812_E_2; 815_D_4; 884_F_7; 907_A_8;
924_A_1; 929_A_6; 940_B_4; 945_B_5; 945_D_1; 946_D_1;
841_A_10; 846_E_11; 825_C_(2,11)"
primer_bind
1..25
/map="738_B_6; 812_E_2; 815_D_4; 884_F_7; 907_A_8;
924_A_1; 929_A_6; 940_B_4; 945_B_5; 945_D_1; 946_D_1;
841_A_10; 846_E_11; 825_C_(2,11)"
primer_bind
complement(176..200)
/map="738_B_6; 812_E_2; 815_D_4; 884_F_7; 907_A_8;
924_A_1; 929_A_6; 940_B_4; 945_B_5; 945_D_1; 946_D_1;
841_A_10; 846_E_11; 825_C_(2,11)"
BASE COUNT 92 a 32 c 124 t 12 others
ORIGIN

Query Match 42.2%; Score 19; DB 131; Length 292;
Best Local Similarity 77.1%; Pred. No. 1.41e-02;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
JOURNAL
COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 415/7259687
Fax: 415/7259689
Email: myers@shgc.stanford.edu

Primer A: TTGTGCTATTTCCAGAGAA
Primer B: GCTCAATGGCTTATCATCTG
STS size: 268
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Chromosome 13.
Location/Qualifiers
1..362
/organism="Homo sapiens"
/note="human"
52..319
/map="13"
52..71
/map="13"
complement(300..319)
/map="13"

BASE COUNT 104 a 75 c 54 g 113 t 16 others
ORIGIN

Query Match 42.2%; Score 19; DB 134; Length 362;
Best Local Similarity 76.5%; Pred. No. 1.41e-02;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 21 tcanatcatcatcatcatcatcatcatcttg 54

||||| ||| |||| ||||| ||||| ||| |||

Cp 43 TCATATAACTATCATCACCATCATATCAACACTTTC 10

RESULT 6

ID HS899314 standard; RNA; EST; 389 BP.
AC N79899;
DT 04-APR-1996 (Rel. 47, Created)
DT 13-APR-1996 (Rel. 47, Last updated, Version 3)
DE yz84g03.r1 Homo sapiens cDNA clone 289780 5' similar to contains
DE Alu repetitive element;.
RW EST.
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.
RN [1]
RP 1-389
RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
RA Trevasaki E., Waterston R., Williamson A., Wohlmann P., Wilson R.;
RT "The WashU-Merck EST Project";
RL Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu High quality sequence stops: 380 Source: IMAGE
CC Consortium, LNL This clone is available royalty-free through LNL
CC ; contact the IMAGE Consortium (info@image.llnl.gov) for further
CC information. NCBI gi: 1242600
FH Key Location/Qualifiers
FT source 1..389
FT /organism="Homo sapiens"
FT /clone="289780"
FT /note="human"
FT mRNA <1..>389
SQ Sequence 389 BP; 92 A; 87 C; 108 G; 101 T; 1 other;

Query Match 42.2%; Score 19; DB 166; Length 389;
Best Local Similarity 85.2%; Pred. No. 1.41e-02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 224 ccacatcatccagcacttggaggcc 250

||||| | || ||||| |||||

Cp 29 CCATCATATCAACACTTTCGGAGGCC 3

RESULT 7

LOCUS N79899 389 bp mRNA EST 02-APR-1996
DEFINITION yz84g03.r1 Homo sapiens cDNA clone 289780 5' similar to contains
Alu repetitive element;.

ACCESSION N79899

NID g1242600

KEYWORDS EST.

SOURCE
human clone=289780 primer=reverse ET library=Soares multiple
sclerosis 2NBHSP vector=pT7T3D (Pharmacia) with a modified
polylinker V TYPE: phagemid:host=DH10B (ampicillin resistant)
Rsitel=Not I Rsite2=Eco RI 46 year old male. 1st strand cDNA was
primed with a Not I - oligo(dT) primer
[5'-TCTTACCAATCTGAAGTGGGAGCGCGCATTTTCTTTTCTTTT-3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pT7 vector (Pharmacia). Library went
through one round of normalization to a Cot = 5. Library
constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4
multiple sclerosis lesions from one patient was kindly provided by
Dr. Kevin G. Becker (NINDS/NIH).

ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrápoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 380

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 1242600

Location/Qualifiers

FEATURES

source

1..389
/organism="Homo sapiens"
/clone="289780"
/note="human"

<1..>389

BASE COUNT

92 a 87 c 108 g 101 t 1 others

ORIGIN

Query Match 42.2%; Score 19; DB 142; Length 389;

Best Local Similarity 85.2%; Pred. No. 1.41e-02;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 224 ccatacatccagcactttggaggcc 250

||||| | | | | | | | | | | | | | | |

Cp 29 CCATCATATCAACACTTTGGGAGGCC 3

RESULT 8

LOCUS

N79899 389 bp mRNA EST 29-MAR-1996

DEFINITION yz84g03.r1 Homo sapiens cDNA clone 289780 3' similar to contains

Alu repetitive element;.

ACCESSION

N79899

NID

g1242600

KEYWORDS

EST.

SOURCE

human clone=289780 primer=ml3 -40 forward library=Soares multiple
sclerosis 2NBHSP vector=pT73D (Pharmacia) with a modified
polylinker V TYPE: phagemid host=DHI0B (ampicillin resistant)
Rsitel=Not I Rsite2=Eco RI 46 year old male. 1st strand cDNA was
primed with a Not I - oligo(dT) primer
[5'-GTGTACCAATCTGAAGTGGAGCGCGGCAATTTTTTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pT7T vector (Pharmacia). Library went
through one round of normalization to a Cot = 5. Library
constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4
multiple sclerosis lesions from one patient was kindly provided by
Dr. Kevin G. Becker (NINDS/NIH).

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrápoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 380

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

1..389
/organism="Homo sapiens"
/clone="289780"
/note="human"

<1..>389

BASE COUNT

92 a 87 c 108 g 101 t 1 others

ORIGIN

Query Match 42.2%; Score 19; DB 71; Length 389;

Best Local Similarity 85.2%; Pred. No. 1.41e-02;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 224 ccatacatccagcactttggaggcc 250

||||| | | | | | | | | | | | | | | |

Cp 29 CCATCATATCAACACTTTGGGAGGCC 3

RESULT 9

LOCUS

N36147 463 bp mRNA EST 16-JAN-1996

DEFINITION yY29c03.sl Homo sapiens cDNA clone 272644 3' similar to contains

Alu repetitive element;contains element MER22 repetitive element ;.

ACCESSION

N36147

NID

g1157289

KEYWORDS

EST.

SOURCE

human clone=272644 primer=ml3 -40 forward library=Soares melanocyte
2NBH vector=pT7T3D (Pharmacia) with a modified polylinker
host=DHI0B (ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Male.
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGGCAATTTTTTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pT7T vector (Pharmacia). Library
constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal
forekin melanocytes (FS374) was kindly provided by Dr. Anthony P.
Albino.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 463)

REFERENCE
AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE
The WashU-Merck EST Project

JOURNAL
Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 362
Source: IMAGE Consortium, LIND

This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.lind.gov) for further information.

FEATURES

source

1..463

/organism="Homo sapiens"

/clone="272644"

/note="human"

<1..>463

BASE COUNT 115 a 123 c 86 g 139 t

ORIGIN

Query Match 42.2%; Score 19; DB 57; Length 463;
Best Local Similarity 88.0%; Pred. No. 1.41e-02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 284 ggcctcccaagtgttttagat 308

|||||

Qy 3 GGCCTCCAAAGCTTGATTATCAT 27

RESULT 10

LOCUS T25334 182 bp mRNA EST 21-AUG-1995

DEFINITION EST060 Homo sapiens cDNA clone BL29-60.

ACCESSION T25334

NID 9559978

KEYWORDS EST.

SOURCE

human clone=BL29-60 library=BL29 Burkitt's lymphoma, Pascalis
Sideras vector=lambda ZAP 2 primer=47 Rsite1=EcoRI Rsite2=EcoRI
oligo dT-primed cDNA prepared from polyA RNA from BL29 cell line.
Size fractionated from 300bp to 3000bp. cDNA cloned into lambda Zap
using EcoRI linkers in random orientation.

Homo sapiens

ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 182)

Sanders R., Larsson, C., Wallin, E., Islam, K.B. and Smith, C.I.E.

Partial sequencing and chromosome mapping of clones from a human

Burkitt's lymphoma cDNA library

Unpublished (1994)

Other ESTs: EST060R

Map: Chromosome 3

Contact: Sanders R

Pharmacia Biotech
Bjoerksgatan 30, S-751 82 Uppsala, Sweden
Tel: 18-165194, 18-166019
Fax: 18-166396
Email: RS026918@suppb.t.pharmacia.se.

FEATURES

source

1..182

/organism="Homo sapiens"

/clone="BL29-60"

/note="human"

<1..>182

/gene="D3S2969E"

/map="3"

mRNA

BASE COUNT 78 a 31 c 16 g 57 t

ORIGIN

Query Match 40.0%; Score 18; DB 108; Length 182;
Best Local Similarity 76.5%; Pred. No. 1.22e-01;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 44 ttaacattaccatcatctctcatcaacatt 77

|||||

Cp 44 TTATATAACTATCACCATCAATCAACACTTT 11

RESULT 11

LOCUS H96107 259 bp mRNA EST 07-DEC-1995

DEFINITION yt97cl2.sl Homo sapiens cDNA clone 232246 3' similar to contains

Alu repetitive element;.

ACCESSION H96107

NID g1109249

KEYWORDS EST.

SOURCE

clone=232246 primer=Promega -21ml3 library=Soares pineal gland
N3HPG vector=pt7T3D (Pharmacia) with a modified polylinker
host=DHI10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTCAAGTGGAGGGCGCGCTTTTTTTTTTTT 3',
double-stranded cDNA was size selected, ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pT73 vector (Pharmacia). Library
constructed by Bento Soares and M.Fatima Bonaldo.

Homo sapiens

ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 259)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 249

Source: IMAGE Consortium, LIND

Mar 19 08:38

US-08-612-929-53.fst

13

This clone is available royalty-free through LML; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.

FEATURES

source

Location/Qualifiers

1..259

/organism="Homo sapiens"

/clone="232246"

<1..>259

BASE COUNT

ORIGIN

51 a 79 c 67 g 60 t 2 others

Query Match

Best Local Similarity 100.0%; Pred. No. 1.22e-01;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 210 ggcctcccaagtgttga 227

|||||

Qy 3 GGCTCCCAAGTGTGA 20

RESULT 12

LOCUS

DEFINITION EST01689 Homo sapiens cDNA clone HHCPC14 similar to Alu repetitive element.

ACCESSION M78099

NID 9273836

KEYWORDS EST.

SOURCE

human clone=HHCPC14 library-Subtracted Hippocampus, Stratagene (cat. #936205) vector=lamdazAP-II primer=M13 Forward The hippocampus library (#4 above) was subtracted with a fibroblast cell line cDNA library (Stratagene cat. #936209; M138 lung fibroblast cell line; oligo-dT + random primed cDNA synthesis; lamdazAP-II vector, 1.0kb average insert size.) by the method of Sive & St. John (Nucl. Acids Res. 16:10937, 1988).

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 269)

Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Kelley,J.M.,

Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C.

Sequence identification of 2,375 human brain genes

Nature 355 (6361), 632-634 (1992)

92168112

Contact: Kerlavage AR

The Institute for Genomic Research

932 Clopper Road, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

Location/Qualifiers

source

1..269

/organism="Homo sapiens"

/clone="HHCPC14"

/note="human"

<1..>269

/gene="D051098E"

BASE COUNT

ORIGIN

76 a 52 c 51 g 87 t 3 others

Query Match

Best Local Similarity 100.0%; Pred. No. 1.22e-01;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 79 ggcctcccaagtgttga 96

|||||

Qy 3 GGCTCCCAAGTGTGA 20

RESULT 13

LOCUS

DEFINITION SW31CA458K Brugia malayi cDNA clone SW31CA458 5'.

ACCESSION H52906

NID 992906

KEYWORDS EST.

SOURCE

clone=SW31CA458 primer=pBluescript SK library=Brugia malayi infective larva cDNA (SAM94WL-Bml3) strain=TRS Labs vector=lambda UniZap XR host=XLI-Blue MRF' Rsitel=EcoR I Rsite2=Xho I Lymphatic filarial nematode parasite of humans. mRNA was prepared from third stage infective larvae of Brugia malayi isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNapol I. The library had 1.6 x 10E6 independent recombinants and average insert size was 900 base pairs. The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email swilliams@smith.smith.edu.

ORGANISM

Brugia malayi

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Pseudocoelomata; Nematoda; Secernentea; Spirurida; Spirurida; Spirurina; Filarioidea; Onchocercidae; Onchocercinae; Brugia.

1 (bases 1 to 299)

REFERENCE

AUTHORS

Blaxter,M.L., Raghavan,N., Ghosh,I., Guiliano,D., Lu,W.,

Williams,S.A., Slatko,B. and Scott,A.L.

Genes expressed in Brugia malayi infective third stage larvae

Mol. Biochem. Parasitol. (1996) In press

COMMENT

Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA

Tel: 4135853826

Fax: 4135853786

Email: swilliams@smith.smith.edu.

Location/Qualifiers

FEATURES

source

1..299

/organism="Brugia malayi"

/clone="SW31CA458"

/strain="TRS Labs"

<1..>299

BASE COUNT

ORIGIN

129 a 31 c 61 g 73 t 5 others

Query Match

Best Local Similarity 40.0%; Score 18; DB 22; Length 299;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 102 ttgataatcgtgatgataagaa 129

|||||

Qy 17 TTGATTATGATGCTGATATATCAA 44

RESULT 14

LOCUS

DEFINITION T54600 300 bp mRNA EST 08-FEB-1995

yb41a05.s1 Homo sapiens cDNA clone 73712 3' contains Alu repetitive element.

Mar 19 08:38

US-08-612-929-53.fst

15

ACCESSION T54600
NTID 9656461
KEYWORDS EST.
SOURCE

human clone=73712 library=Stratagene fetal spleen (#937205)
vector=pBluescript SK- host=SOIR cells (kanamycin resistant)
primer=21ml3 Reitel=EcORI Reitel2=XhoI Pooled fetal spleens. Cloned
unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; 5' adaptor sequence: 5'-CAATTCCGACGAC-3'; 3'
adaptor sequence: 5'-CTCGAGTTTTTTTTTTTTTTTT-3'.

ORGANISM

Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 300)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, C., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE

WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 238

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found.

FEATURES

source

1..300

/organism="Homo sapiens"

/clone="73712"

/note="human"

BASE COUNT 92 a 68 c 88 g 42 t 10 others

ORIGIN

Query Match 40.0%; Score 18; DB 116; Length 300;
Best Local Similarity 83.3%; Pred. No. 1.22e-01;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 252 atcgnaagcaacantttggaggc 275

||||| || ||||| ||||| ||||| |||||

Cp 27 ATCATATCAACACTTTCGGAGGC 4

RESULT 15

LOCUS T41640 309 bp mRNA EST 07-AUG-1995

DEFINITION 10221 Arabidopsis thaliana cDNA clone 62E2TM.

ACCESSION T41640

NTID 9931282

KEYWORDS EST.

SOURCE

thale cress clone=62E2TM library=lambdapl2 strain=var columbia
vector=lambdapl2 Zip-Lox Reitel=Sal Reitel2=Not Lambdapl2 is a cDNA
library derived from equal quantities of 4 pools of mRNA. The mRNA
sources were 1) 7 day germinated etiolated seedlings; 2) tissue
culture grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants
as 3 but aerial tissue (stems, flowers and siliques. The vector is
BRU's lambda Zip-Lox. The cDNA inserts were directionally cloned
with Sal-Not arms using oligo dT primed cDNA.

Mar 19 08:38

US-08-612-929-53.fst

16

ORGANISM

Arabidopsis thaliana
Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;
Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 309)

AUTHORS

Newman, T., de Bruijn, F. J., Green, P., Keegstra, K., Kende, H.,

McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomasow, M.,

Retzel, E. and Somerville, C.

Genes galore: a summary of methods for accessing results from

large-scale partial sequencing of anonymous Arabidopsis cDNA clones

Plant Physiol. 106, 1241-1255 (1994)

JOURNAL

COMMENT

Contact: Thomas Newman

MSU-DOE Plant Research Laboratory

Michigan State University

MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.

Lansing, MI

Tel: 517-353-0854

Fax: 517-353-9168

Email: 22313tcn81bm.cl.msu.edu.

FEATURES

source

1..309

/organism="Arabidopsis thaliana"

/clone="62E2TM"

/strain="var columbia"

/note="thale cress"

BASE COUNT 93 a 53 c 71 g 77 t 15 others

ORIGIN

Query Match 40.0%; Score 18; DB 112; Length 309;
Best Local Similarity 80.0%; Pred. No. 1.22e-01;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 210 ttttgantatgatngtgatgngat 234

||||| ||||| ||||| ||||| ||

Qy 15 TGTTCATTATGATGCGTAGATTAT 39

Search completed: Wed Mar 19 08:39:35 1997

Job time : 76 secs.

PT and IgE-mediated allergic conditions
 PS Disclosure; Page 71-72; 97pp; English.
 CC A humanized antibody light chain variable region and signal
 CC sequence is given in R75355. The signal sequence is also
 CC provided in R70194. The sequences of the 3 CDRs
 CC are identical to mouse anti-human IL-4 Mab 3B9 light chain
 CC CDRs (given in R70195-97).
 SQ Sequence 393 BP; 97 A; 98 G; 105 G; 93 T;

Query Match 100.0%; Score 45; DB 14; Length 393;
 Best Local Similarity 100.0%; Pred. No. 7.56e-14;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 127 aaggctcccaagtgtgattatgattatgattatgattatgattatgaac 171
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 1 AAGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAAC 45

RESULT 2

ID Q83508 standard; DNA; 63 BP.
 AC Q83508;
 DT 20-SEP-1995 (first entry)
 DE IL-4 CDR1 gene fragment.
 KW Humanized antibody; antibody engineering; monoclonal antibody;
 KW Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;
 KW complementarity determining region; ss.
 OS Synthetic.
 PN W09507301-A.
 PD 16-MAR-1995.
 PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Example 3; Page 28; 97pp; English.
 CC A humanized antibody was designed to contain mouse CDRs (from
 CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A
 CC synthetic heavy chain was made using the oligonucleotides given
 CC in Q83498-502 and amplified by PCR using the primers given in
 CC Q83503-04. The construct was ligated into vector pCD, along
 CC with a signal sequence (Q83494) and an IgG1 human constant
 CC region. The CDR gene regions of a pre-existing light chain
 CC framework were replaced with synthetic IL-4 CDR genes constructed
 CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),
 CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into
 CC the vector. The anti-IL4 engineered antibody was expressed in
 CC COS and CHO cells.
 SQ Sequence 63 BP; 17 A; 16 C; 11 G; 19 T;

Query Match 97.8%; Score 44; DB 14; Length 63;
 Best Local Similarity 100.0%; Pred. No. 2.71e-13;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 gtttcataactatcaccatcataatcaacactttggaggcct 62
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Cp 45 GTTCATATACTATCACCATCAATCAACACTTTGGGAGGCCT 2

RESULT 3

Query Match 97.8%; Score 44; DB 14; Length 63;
 Best Local Similarity 100.0%; Pred. No. 2.71e-13;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 gtttcataactatcaccatcataatcaacactttggaggcct 62
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Cp 45 GTTCATATACTATCACCATCAATCAACACTTTGGGAGGCCT 2

ID Q83507 standard; DNA; 67 BP.
 AC Q83507;
 DT 20-SEP-1995 (first entry)
 DE IL-4 CDR1 gene fragment.
 KW Humanized antibody; antibody engineering; monoclonal antibody;
 KW Mab; interleukin-4; IL-4; allergy; heavy chain; CDR;
 KW complementarity determining region; ss.
 OS Synthetic.
 PN W09507301-A.
 PD 16-MAR-1995.
 PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Example 3; Page 28; 97pp; English.
 CC A humanized antibody was designed to contain mouse CDRs (from
 CC anti-IL-4 Mab 3B9 Mab) within a human antibody framework. A
 CC synthetic heavy chain was made using the oligonucleotides given
 CC in Q83498-502 and amplified by PCR using the primers given in
 CC Q83503-04. The construct was ligated into vector pCD, along
 CC with a signal sequence (Q83494) and an IgG1 human constant
 CC region. The CDR gene regions of a pre-existing light chain
 CC framework were replaced with synthetic IL-4 CDR genes constructed
 CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),
 CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into
 CC the vector. The anti-IL4 engineered antibody was expressed in
 CC COS and CHO cells.
 SQ Sequence 67 BP; 20 A; 12 C; 17 G; 18 T;

Query Match 97.8%; Score 44; DB 14; Length 67;
 Best Local Similarity 100.0%; Pred. No. 2.71e-13;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 aggcctcccaagtgtgattatgattatgattatgattatgaac 49
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 2 AGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAAC 45

RESULT 4

ID Q65554 standard; cDNA; 333 BP.
 AC Q65554;
 DT 27-JAN-1995 (first entry)
 DE Mouse anti-HIV mu5.5 light chain variable region cDNA.
 KW Immunoglobulin; light chain; anti-HIV antibody; neutralisation;
 KW human immunodeficiency virus; variable region; VL chain; murine; ds.
 OS Mus musculus.

FH Key Location/Qualifiers
 FT misc.feature 70..114
 FT /tag= a
 FT /note= "encodes CDR1"
 FT misc.feature 160..180
 FT /tag= b
 FT /note= "encodes CDR2"
 FT misc.feature 277..303
 FT /tag= c
 FT /note= "encodes CDR3"
 PN J06125783-A.
 PD 10-MAY-1994.

Mar 19 08:36
US-08-612-929-53.rdg

```

Qy 1 AAGCCCTCCCAAGCTGCTATGATGCTGATAGTTATATGAAC 45

RESULT 6
ID Q70376 standard; cDNA to mRNA; 333 BP.
AC Q70376;
DT 13-MAR-1995 (first entry)
DE Chimeric anti HIV antibody light chain variable region.
KW Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS: treatment;
KW prophylaxis; Mus musculus; Homo sapiens; ss.
KW Chimeric Homo sapiens
OS Chimeric Mus musculus.
FH Key Location/Qualifiers
FT CDS 1..333
FT /*tag= a
FT /product= Antibody light chain variable region.
FN W09415969-A.
PD 21-JUL-1994.
PE 14-JAN-1993; J00039.
PR 14-JAN-1993; AU-032671.
PR 14-JAN-1993; W0-J00039.
PA (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
PI Tokiyoshi S;
PI WPI; 94-249145/30.
DR P-FSDB; R60306.
PT Recombinant chimeric anti HIV antibody - useful for the treatment
PT and prevention of HIV
PS Claim 14; Figure 12; 51pp; Japanese.
CC The recombinant antibody light chain has neutralising activity
CC against HIV. Chimeric antibodies comprising both mouse and human
CC sequences are useful in the treatment/prevention of AIDS caused by
CC HIV. This sequence is derived from the mu5.5 anti HIV monoclonal
CC antibody producing cell.
SQ Sequence 333 BP; 95 A; 90 C; 88 G; 60 T;

Query Match 91.1%; Score 41; DB 12; Length 333;
Best Local Similarity 95.6%; Pred. No. 1.23e-11;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 70 aagccgcagcaagctgtattatgattatgctggtgatgattatgaac 114
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 1 AAGCCCTCCCAAGCTGCTATGATGCTGATAGTTATATGAAC 45

RESULT 7
ID Q65558 standard; cDNA; 333 BP.
AC Q65558;
DT 30-JAN-1995 (first entry)
DE Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.
KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
KW human immunodeficiency virus; variable region; VL chain; murine;
KW chimeric; humanised; ds.
KW Chimeric Mus musculus.
OS Chimeric Homo sapiens.
FH Key Location/Qualifiers
FT misc feature 70..114
FT /*tag= a
FT /note= "encodes murine CDR1"
FT misc feature 160..180
FT /*tag= b
FT /note= "encodes murine CDR2"
FT misc feature 277..303

```


FT /*tag= c
 FT /note= "encodes murine CDR3"
 PN J06125783-A.
 PD 10-MAY-1994.
 PF 28-DEC-1991; 359808.
 PR 28-DEC-1991; JP-359808.
 PA (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.
 DR WPI; 94-187942/23.
 DR P-PSDB; R55127.
 PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
 PT and recombinant antibody consisting of the H- and L-chains,
 PT useful in AIDS therapy
 PS Claim 5; Fig 12; 22pp; Japanese.
 CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
 CC The heavy and light chain variable regions from these antibodies
 CC were sequenced (Q65551-Q65554). The murine anti-HIV CDRs were
 CC introduced into human framework regions to construct chimeric
 CC antibodies (Q65555-Q65558).
 SQ Sequence 333 BP; 95 A; 90 C; 88 G; 60 T;

Query Match 91.1%; Score 41; DB 11; Length 333;
 Best Local Similarity 95.6%; Pred. No. 1.23e-11;
 Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 70 aaggccagcaaaagttgattatgatggtgatgtatgatgaac 114
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 1 AAGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAC 45

RESULT 8
 ID N90492 standard; DNA; 334 BP.
 AC N90492;
 DT 20-OCT-1989 (first entry)
 DE Gene fragment of immunoglobulin L chain variable region.
 KW Gene fragment; immunoglobulin; L chain variable region; HIV.
 OS Mus musculus
 FH Key Location/Qualifiers
 FT CDS 1..333
 FT /*tag= a
 PN EP-327000-A.
 PD 09-AUG-1989.
 PF 30-JAN-1989; 101583.
 PR 30-JAN-1988; JP-20255.
 PR 08-JUL-1988; JP-171385.
 PA (KAGA) The Chemo-Sero-Therapeutic Research Institute.
 PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,
 PI Takatsuki K;
 DR WPI; 89-229050/32.
 PT Chimeric anti-human immune virus antibodies - contg. mouse variable
 PT regions and human constant regions for diagnosis, treatment and
 PT prevention of AIDS
 PS Claim 6; page 15; 33pp; English.
 CC The gene fragment encodes an L chain variable region from an
 CC immunoglobulin with anti-HIV neutralising activity. It is used, with an
 CC H chain variable region gene fragment (see N90491), to produce a chimeric
 CC anti-HIV antibody with mouse variable regions and human constant regions.
 CC The antibody retains its original specificity, but have much lower
 CC antigenicity to humans. See also P90541, N90493 and N90495.
 SQ Sequence 334 BP; 91 A; 83 C; 81 G; 79 T;

Query Match 91.1%; Score 41; DB 1; Length 334;
 Best Local Similarity 95.6%; Pred. No. 1.23e-11;
 Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 70 aaggccagcaaaagttgattatgatggtgatgtatgatgaac 114
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 1 AAGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAC 45

RESULT 9
 ID Q73986 standard; cDNA; 393 BP.
 AC Q73986;
 DT 20-SEP-1995 (first entry)
 DE Humanized antibody 3B9 light chain.
 KW Humanized antibody; antibody engineering; monoclonal antibody;
 KW MAb; interleukin-4; IL-4; allergy; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..393
 FT /*tag= a
 FT sig_peptide 1..60
 FT /*tag= b
 FT mat_peptide 61..393
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 PN W09507301-A.
 PD 16-MAR-1995.
 PF 07-SEP-1994; U01308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR P-PSDB; R75355.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Fig.5; 97pp; English.
 CC A humanized antibody light chain variable region and signal
 CC sequence is given in R75355. The signal sequence is also
 CC provided in R70194. The sequences of the first 2 CDRs
 CC are identical to mouse anti-human IL-4 MAb 3B9 light chain
 CC CDRs (given in R70195-96), but the third (R70201) differs
 CC by a single amino acid from the native mouse CDR (R70197).
 SQ Sequence 393 BP; 97 A; 96 G; 108 G; 92 T;

Query Match 91.1%; Score 41; DB 14; Length 393;
 Best Local Similarity 95.6%; Pred. No. 1.23e-11;
 Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 127 aaggccagcaaaagttgattatgatggtgatgtatgatgaac 171
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 Qy 1 AAGGCTCCCAAGTGTGATTATGATGCTGATGATTATATGAC 45

RESULT 10
 ID Q83490 standard; cDNA; 396 BP.
 AC Q83490;
 DT 20-SEP-1995 (first entry)
 DE Mouse MAb 3B9 light chain.
 KW Chimeric antibody; humanized antibody; antibody engineering;
 KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT CDS 1..396
 FT /*tag= a
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PF 11-OCT-1989; 010415.
PR 17-OCT-1988; US-260558.
PA (BECT) Becton Dickinson Co.
PI Hinton R, Oi VT;
DR WPI; 90-126329/17.
DR P-PSDB; R04132.
PT New chimeric variants of murine antibody anti-leucine -
PT contg. human antibody regions, and DNA encoding sequences.
PS Claim 1; Fig 2; 12pp; English.
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
CC used to form chimeric mouse-variable, human-constant region Abs
CC suggested as being useful as a vaccine to HIV. 246 T;
SQ Sequence 900 BP; 261 A; 206 C; 187 G; 246 T;

Query Match 91.1%; Score 41; DB 1; Length 900;
Best Local Similarity 95.6%; Pred. No. 1.23e-11;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 618 aagggcagccaagtgtgattatgattggtgatgtatgatgaac 662
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RESULT 14

ID Q36609 standard; DNA; 393 BP.
AC Q36609;
DT 02-JUN-1993 (first entry)
DE Anti-CD4 antibody MF 3.10 light chain variable region.
KW immunosuppression; tissue transplantation; graft; L chain; V region;
KW T-helper cell inhibition; transplant rejection; MAB;
KW interleukin-2 receptor; ss.
FH Key Location/Qualifiers
FT sig_peptide 1..60
FT /*tag= a
FT mat_peptide 61..393
FT /*tag= b
FT /note= "J1 region begins at position 361"
PN DE143214-A.
PD 28-JAN-1993.
PE 30-DEC-1991; 143214.
PR 25-JUL-1991; DE-124759.
PR 30-DEC-1991; DE-143214.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
PI Kaluza B, Riethmuller G, Scheuer W, Weidle U;
DR P-PSDB; R32123.
PT Synergistic antibody compen. for use as immunosuppressant -
PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
PT alpha- or anti-IL2R beta antibodies
PS Claim 5; Page 11; 18pp; German.
CC This sequence encodes the light chain variable region of a preferred
CC anti-CD4 monoclonal antibody for use in the claimed synergistic
CC composition. Mab MT 3.10 is deposited as clone 3.101/sB10 (ECACC
CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R
CC alpha or beta antibody. Individually the antibodies are strongly
CC inhibiting and when used together their immunosuppressive properties
CC are improved; they synergistically inhibit T-helper cell
CC proliferation to effectively inhibit transplant rejection at low
CC doses without significantly reducing the general immune response.
CC See Q36607-Q36616.
SQ Sequence 393 BP; 100 A; 105 C; 98 G; 90 T;

Query Match 86.7%; Score 39; DB 6; Length 393;
Best Local Similarity 93.3%; Pred. No. 1.52e-10;

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Matches 42; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 130 aagggcagccaagtgtgattatgattggtgatgtatgatgaac 174
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QY 1 AAGGCTCCCAAGTGTGATTATGATGCTGCTAGTATATGAAC 45

RESULT 15

ID T04019 standard; cDNA; 717 BP.
AC T04019;
DT 02-JUL-1996 (first entry)
DE Anti-EGFR single chain antibody (Clone 4 B 2).
KW Single chain antibody; antibody; epidermal growth factor receptor;
KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
KW assessment; phage antibody library; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 1..717
FT /*tag= a
FT /product= Single chain antibody.
PN M09525167-A1.
PD 21-SEP-1995.
PF 16-MAR-1995; E00978.
PR 17-MAR-1994; EP-104160.
PR 02-DEC-1994; EP-118970.
PA (MERE) MERCK PATENT GMBH.
PI Adan J, Ansell KH, Bendig MM, Blasco F, Guesow D;
PI Kettleborough AC, Mitjans F, Pluats J, Rosell E;
DR WPI; 95-336972/43.
DR P-PSDB; R79866.
PT Anti-EGFR antibodies and single chain Fv antibody fragments -
PT obtained from phage-antibody libraries, useful for diagnosis and
PT therapy of tumours
PS Claim 4; Page 57; 93pp; English.
CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies
CC and antibodies constructed from anti-EGFR antibody fragments can be
CC used for diagnosis of tumours and assessment of tumour growth in
CC vitro and in vivo. They may also be used in a pharmaceutical
CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
CC The antibodies and fragments are derived from mice but are humanised
CC so as to cause minimum reaction against them. They are produced
CC using the phage antibody library. (See T04011-T04026 and
CC R79858-R79873)
SQ Sequence 717 BP; 165 A; 169 C; 213 G; 170 T;

Query Match 86.7%; Score 39; DB 18; Length 717;
Best Local Similarity 93.3%; Pred. No. 1.52e-10;
Matches 42; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 472 aagggcagccaagtgtgattatgattggtgatgtatgatgaac 516
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QY 1 AAGGCTCCCAAGTGTGATTATGATGCTGCTAGTATATGAAC 45

Search completed: Wed Mar 19 08:37:58 1997
Job time : 15 secs.

WATERMAN

(TM)

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HPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:36:16 1997; MacPar time 63.91 Seconds
Tabular output not generated. 579,960 Million cell updates/sec

Title: >US-08-612-929-53

Description: (1-45) from US08612929.seq

Perfect Score: 45

N.A. Sequence: 1 AAGGCTCCCAAGTCTGATTATGATGTCATAGTATATGAC 45

Comp: TTCGGAGGGTTTCACAACTACTACCACTATCAATATCTTG

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: 1:BCT 2:FON 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PIN 9:PRI

10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

genbank94

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7

23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5

30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2

37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PIN1 43:PIN2

44:PIN3 45:PIN4 46:PIN5 47:PIN6 48:PIN7 49:PIN8 50:PRI1

51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8

58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1

64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8

71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4

78:VRL5 79:VRL6 80:VRL7 81:VRL8

genbank-new5

82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG

89:PIN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL

u-embl46.94

96:part1

Statistics: Mean 8.084; Variance 4.056; scale 1.993

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	41	91.1	245	64	MMIGKCVRH	M.musculus immunoglob	9.84e-14
2	41	91.1	255	64	MMIGKCVRD	M.musculus immunoglob	9.84e-14
3	41	91.1	262	64	MMIGKCVRE	M.musculus immunoglob	9.84e-14
4	41	91.1	264	64	MMIGKCVRI	M.musculus immunoglob	9.84e-14
5	41	91.1	266	64	MMIGKCVRC	M.musculus immunoglob	9.84e-14
6	41	91.1	270	64	MMIGKCVRF	M.musculus immunoglob	9.84e-14
7	41	91.1	270	64	MMIGKCVRB	M.musculus immunoglob	9.84e-14
8	41	91.1	270	64	MMIGKCVRG	M.musculus immunoglob	9.84e-14
9	41	91.1	279	66	MUSIGKAAAA	Mouse Igk chain mRNA	9.84e-14
10	41	91.1	286	65	MMU29628	Mus musculus anti-DNA	9.84e-14
11	41	91.1	297	65	MMU29629	Mus musculus anti-DNA	9.84e-14
12	41	91.1	333	67	MMU07207	Mus musculus clone 31	9.84e-14
13	41	91.1	333	67	MUSIGL5B	Mouse Igl chain H2L2	9.84e-14
14	41	91.1	333	70	S42888	Ig V kappa =immunoglob	9.84e-14
15	41	91.1	333	70	S54207	V kappa 21=immunoglob	9.84e-14
16	41	91.1	336	66	MUSIGKAAW	Mouse Ig rearranged k	9.84e-14
17	41	91.1	350	66	MUSIGKABBC	Mouse Ig kappa chain	9.84e-14
18	41	91.1	354	67	MUSL711GKV	Mouse hybridoma Ig re	9.84e-14
19	41	91.1	360	67	MUSIGKAF	Mouse Ig active kappa	9.84e-14
20	41	91.1	363	67	MUSL341GKV	Mouse hybridoma Ig re	9.84e-14
21	41	91.1	363	67	MUSL931GKV	Mouse hybridoma Ig re	9.84e-14
22	41	91.1	363	67	MUSL2021GK	Mouse hybridoma Ig re	9.84e-14
23	41	91.1	900	40	I08223	Sequence 1 from paten	9.84e-14
24	40	88.9	318	66	MUSIGGVKB	Mouse immunoglobulin	5.00e-13
25	39	86.7	292	65	MMU18599	Mus musculus immunogl	2.52e-12
26	39	86.7	333	65	MMVLI1E10	Mouse mRNA for kappa-	2.52e-12
27	39	86.7	336	64	MMIGLC404	M.musculus mRNA for I	2.52e-12
28	39	86.7	336	64	MMIGLC310	M.musculus mRNA for I	2.52e-12
29	39	86.7	342	62	S78338	Ig V=anti-CD19 antib	2.52e-12
30	39	86.7	393	70	S50265	Ig V=anti-CD4 mAb M-	2.52e-12
31	37	82.2	351	66	MUSIGKABBH	Mouse Ig kappa chain	6.20e-11
32	37	82.2	388	64	MMU07814	Mus musculus BALB/c a	6.20e-11
33	37	82.2	397	40	I08225	Sequence 5 from paten	3.03e-10
34	36	80.0	317	67	MUSIGVACR	Mus musculus Ig rearr	3.03e-10
35	36	80.0	353	66	MUSIGKABBD	Mouse Ig kappa chain	3.03e-10
36	35	77.8	351	66	MUSIGKABBF	Mouse Ig kappa chain	1.46e-09
37	35	77.8	353	66	MUSIGKABBG	Mouse Ig kappa chain	1.46e-09
38	34	75.6	313	70	S74550	Ig V kappa =rheumatoi	6.98e-09
39	34	75.6	336	67	MUSIGVACP	Mus musculus Ig rearr	6.98e-09
40	33	73.3	353	66	MUSIGKABBE	Mouse Ig kappa chain	3.29e-08
41	31	68.9	238	65	MMU18563	Mus musculus immunogl	7.01e-07
42	29	64.4	336	64	MMIGLC413	M.musculus mRNA for I	1.41e-05
43	25	55.6	271	65	MMU29627	Mus musculus anti-DNA	4.58e-03
44	25	55.6	333	12	MM51468	Mus musculus clone 4F	4.58e-03
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ALIGNMENTS

RESULT 1
LOCUS MMIGKCVRH 245 bp RNA ROD 13-OCT-1993
DEFINITION M.musculus immunoglobulin kappa light chain (DBA/1) gene, v region.
ACCESSION Z25456
NID 9407846
KEYWORDS Igk gene; immunoglobulin; light chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;

REFERENCE
1 (bases 1 to 264)
Mo, J. A., Bona, C. A. and Holmdahl, R.
Amino acid sequence of the variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen
Eur. J. Immunol. (1993) in press

JOURNAL
2 (bases 1 to 264)
Mo, J. A.
Direct Subcloning

REFERENCE	1 (bases 1 to 266)
AUTHORS	Mo, J.A., Bona, C.A. and Holmdahl, R.
TITLE	Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL	Eur. J. Immunol. (1993) In press
REFERENCE	2 (bases 1 to 266)
AUTHORS	Mo, J.A.
TITLE	Direct Submission
JOURNAL	Submitted (02-AUG-1993) to the EMBL/GenBank/DBJ databases. John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE	3 (bases 1 to 266)


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Db 13 aagcgccagcaagtgttgattatgatgtgatgtatgatgaac 57
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QY 1 AAGGCTCCCAAGTGTGATTATGATGCTGATGATGATATGAAC 45

RESULT 10
LOCUS MMU29628 286 bp mRNA ROD 08-DEC-1995
DEFINITION Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region,
hybridoma 52.60, partial cds.
ACCESSION U29628
NID g996124
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 286)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Light chain contribution to specificity in anti-DNA antibodies
JOURNAL J. Immunol. 155 (6), 3223-3233 (1995)
MEDLINE 95403997
REFERENCE 2 (bases 1 to 286)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology,
Princeton University, Princeton, NJ 08544, USA
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BASE COUNT 74 a 75 c 69 g 68 t
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Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 AAGGCTCCCAAGTGTGATTATGATGCTGATGATGATATGAAC 45

RESULT 11
LOCUS MMU29629 297 bp mRNA ROD 08-DEC-1995
DEFINITION Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region,
hybridoma 52.46B, partial cds.
ACCESSION U29629
NID g996126
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 297)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Light chain contribution to specificity in anti-DNA antibodies
JOURNAL J. Immunol. 155 (6), 3223-3233 (1995)
MEDLINE 95403997
REFERENCE 2 (bases 1 to 297)
AUTHORS Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology,
Princeton University, Princeton, NJ 08544, USA
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Best Local Similarity 95.6%; Pred. No. 9.84e-14;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 12
LOCUS MMU07207 333 bp mRNA ROD 08-OCT-1994
DEFINITION Mus musculus clone 3l anti-C5a Ig light chain V region mRNA,
partial cds.
ACCESSION U07207
NID g459212
KEYWORDS
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13

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SOURCE
ORGANISM      mouse.
Mus musculus
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Rodentia; Myomorpha; Muridae; Mus.

REFERENCE
AUTHORS      Ames,R.S., Tornetta,M.A., Jones,C.S. and Tsui,P.
TITLE        Isolation of neutralizing anti-C5a monoclonal antibodies from a
              filamentous phase monovalent Fab display library [published erratum
              appears in J Immunol Jul 15;153(2):910]
JOURNAL      J. Immunol. 152 (9), 4572-4581 (1994)
MEDLINE      94209678
REFERENCE    2 (bases 1 to 333)
AUTHORS      Ames,R.S.
TITLE        Direct Submission
JOURNAL      Submitted (28-FEB-1994) Robert S. Ames, Molecular Genetics,
              SmithKline Beecham Pharmaceuticals, 709 Swedeland Road, PO Box
              1539, King of Prussia, PA 19406-0939, USA
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Best Local Similarity 95.6%; Pred. No. 9.84e-14;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 13
LOCUS      MUSIGL5B      333 bp      DNA      ROD      01-NOV-1991
DEFINITION Mouse IgJ chain H2L2 V-region, partial cds.
ACCESSION  M80406
NID        q197577
KEYWORDS   V-region; immunoglobulin light chain.
SOURCE     Mus musculus (strain BALB/c, sub_species domesticus) (library:
           lambda-gt11) DNA.

ORGANISM
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE
AUTHORS      Matsushita,S., Maeda,H., Kimachi,K., Eda,Y., Maeda,Y., Hattori,T.,
              Tokiyoshi,S. and Takatsuki,K.
TITLE        Characterization of a mouse/human chimeric monoclonal antibody
              (C-beta-1) to a principal neutralizing domain of the human
              immunodeficiency virus type 1 envelope protein
              Unpublished (1991)
JOURNAL
FEATURES
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Location/Qualifiers
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14

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               /genes="0.5 beta-VL"
               /note="FR4"

BASE COUNT   91 a   82 c   81 g   79 t
ORIGIN
Query Match      91.1%; Score 41; DB 67; Length 333;
Best Local Similarity 95.6%; Pred. No. 9.84e-14;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 70 aagggcagcaagtggtgattgatggtgatgtatgatgaac 114
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 AAGGCCTCCCAAGTGTGATTGATTGATGCGTAGTATATGAAC 45

RESULT 14
LOCUS      S42888      333 bp      DNA      ROD      09-NOV-1992
DEFINITION Ig V kappa =immunoglobulin V kappa region [mice, hybridoma 54' CBI,
           Genomic, nt].
ACCESSION  S42888
NID        q254222
KEYWORDS   .
SOURCE     mice hybridoma 54' CBI.
           Mus sp.
           Unclassified.
REFERENCE   1 (bases 1 to 333)
AUTHORS      Matsushita,S., Maeda,H., Kimachi,K., Eda,Y., Maeda,Y., Murakami,T.,
              Tokiyoshi,S. and Takatsuki,K.
TITLE        Characterization of a mouse/human chimeric monoclonal antibody (C
              beta 1) to a principal neutralizing domain of the human
              immunodeficiency virus type 1 envelope protein
```

WUQSELEH

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPerch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:41:52 1997; MasPar time 57.47 Seconds
161.157 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-54
Description: (1-21) from US08612929.seq
Perfect Score: 21
N.A. Sequence: 1 ACCTCGGGTATGGCTGTTCC 21
Comp: TGGAGGCCATACCCACARAGG

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98
99:EST99
EST-STS-TWO
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124
125:EST125 126:EST126 127:EST127 128:EST128 129:EST129

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7
136:STS8 137:STS9 138:STS10 139:ueEST 140:gnEST1
141:gnEST2 142:gnEST3 143:gnEST4 144:gnEST5 145:gnEST6
146:gnEST7 147:gnEST8 148:gnEST9 149:gnEST10 150:gnEST11
151:gnEST12 152:gnEST13 153:gnEST14 154:gnEST15
155:gnEST16 156:gnSTS 157:enEST1 158:enEST2 159:enEST3
160:enEST4 161:enEST5 162:enEST6 163:enEST7 164:enEST8
165:enEST9 166:enEST10 167:enEST11 168:enEST12
169:enEST13 170:enEST14 171:enEST15 172:enEST16
173:enSTS1 174:enSTS2

Statistics: Mean 6.395; Variance 1.190; scale 5.375

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
	1	16	76.2	451	77	R21117	yg52ell.r1 Homo sapie	1.02e-04
c	2	15	71.4	311	103	T02032	wEST02753 Caenorhabdi	2.67e-03
c	3	15	71.4	313	6	CELK129A9R	C.elegans cDNA clone	2.67e-03
c	4	15	71.4	424	139	HS44035	ya46dl1.s2 Homo sapie	2.67e-03
c	5	15	71.4	424	76	R15814	ya46dl1.s2 Homo sapie	2.67e-03
c	6	15	71.4	460	102	R1CS14394A	Rice cDNA, partial se	2.67e-03
	7	14	66.7	241	5	CELK101B2R	C.elegans cDNA clone	6.06e-02
	8	14	66.7	312	103	S503B07	S.scrofa mRNA; expres	6.06e-02
c	9	14	66.7	333	4	CELK072C1R	C.elegans cDNA clone	6.06e-02
c	10	14	66.7	339	6	CELK130F5R	C.elegans cDNA clone	6.06e-02
c	11	14	66.7	343	18	H39637	yo56h08.r1 Homo sapie	6.06e-02
c	12	14	66.7	432	81	R35538	y64g04.r1 Homo sapie	6.06e-02
c	13	14	66.7	483	62	N52367	y229h06.s1 Homo sapie	6.06e-02
	14	13	61.9	144	85	R46854	yj54c02.r1 Homo sapie	1.17e+00
	15	13	61.9	190	34	H93158	y93a08.r1 Homo sapie	1.17e+00
	16	13	61.9	211	28	H73137	yu03f08.r1 Homo sapie	1.17e+00
c	17	13	61.9	226	95	R80495	yi97b04.r1 Homo sapie	1.17e+00
c	18	13	61.9	318	45	HSDECB07	H. sapiens partial cD	1.17e+00
c	19	13	61.9	335	3	CELK012D5R	C.elegans cDNA clone	1.17e+00
	20	13	61.9	356	80	R32847	yh71h02.s1 Homo sapie	1.17e+00
c	21	13	61.9	360	4	CELK072C6F	C.elegans cDNA clone	1.17e+00
c	22	13	61.9	360	6	CELK117F2F	C.elegans cDNA clone	1.17e+00
c	23	13	61.9	392	172	TG8022	TgESTzy36d09.r1 Toxop	1.17e+00
c	24	13	61.9	399	172	TG2653	TgESTzy25a10.s1 Toxop	1.17e+00
c	25	13	61.9	407	12	H20576	yn63b03.r1 Homo sapie	1.17e+00
c	26	13	61.9	417	73	R07483	ye97d01.s1 Homo sapie	1.17e+00
c	27	13	61.9	422	75	R14360	yf80b10.r1 Homo sapie	1.17e+00
c	28	13	61.9	425	24	H59423	yr37a02.s1 Homo sapie	1.17e+00
c	29	13	61.9	429	88	R59019	y96d02.r1 Homo sapie	1.17e+00
c	30	13	61.9	431	108	T24356	crs1483 Ricinus commu	1.17e+00
c	31	13	61.9	435	140	N60135	TgESTzy01h12.r1 Toxop	1.17e+00
c	32	13	61.9	438	87	R56041	yg91a05.s1 Homo sapie	1.17e+00
c	33	13	61.9	452	159	HS161338	zb69d04.r1 Soares fet	1.17e+00
c	34	13	61.9	452	154	W25161	zb69d04.r1 Soares fet	1.17e+00
c	35	13	61.9	453	69	N74979	za87d04.s1 Homo sapie	1.17e+00
c	36	13	61.9	458	144	N96464	Z1187 Arabidopsis tha	1.17e+00
c	37	13	61.9	463	97	R89039	ym98h12.s1 Homo sapie	1.17e+00
c	38	13	61.9	467	8	H05395	yl80c09.r1 Homo sapie	1.17e+00
c	39	13	61.9	518	163	HS611309	za55a05.s1 Homo sapie	1.17e+00
c	40	13	61.9	519	77	R20659	yf59f08.s1 Homo sapie	1.17e+00
c	41	13	61.9	561	80	R30154	12759 Arabidopsis tha	1.17e+00
c	42	13	61.9	563	164	HS644330	zb35g11.r1 Soares par	1.17e+00

43 13 61.9 569 171 MM9332 ma03d10.r1 Soares mou 1.17e+00
 44 13 61.9 958 169 MM1677 ma93g09.r1 Soares mou 1.17e+00
 c 45 13 61.9 4626 174 HSW5842 human chromosome 7 ST 1.17e+00

ALIGNMENTS

RESULT 1 R21117 451 bp mRNA EST 18-APR-1995
 LOCUS y052e11.r1 Homo sapiens cDNA clone 36023 5' similar to SP:S20969
 DEFINITION S20969 NA/CA,K ANTIFORTER - ;
 ACCESSION R21117
 NID g77598
 KEYWORDS EST.
 SOURCE human clone-36023 library=Soares infant brain LNB vector=Lafmid BA host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I Rsite2=Hind III Whole brain from a 73 days post natal female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGATTTCGGCGCGCAGCAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 451)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT

GDB: G00-408-524
 Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu
 High quality sequence stops: 303
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES Location/Qualifiers
 source 1..451
 /organism="Homo sapiens"
 /clone="36023"
 /note="human"

BASE COUNT 72 a 119 c 138 g 119 t 3 others
 ORIGIN

Query Match 76.2%; Score 16; DB 77; Length 451;
 Best Local Similarity 94.4%; Pred. No. 1.02e-04;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 324 cctcctgtatgggtgttt 341
 ||||| |||||
 Qy 2 CCTCGGTATGGGTGTT 19

RESULT 2 T02032 311 bp mRNA EST 10-NOV-1992
 LOCUS WES0702753 Caenorhabditis elegans cDNA clone CEESY50.
 ACCESSION T02032
 NID g278513
 KEYWORDS EST.

SOURCE Nematodes clone=CEESY50 library=Early embryo, Stratagene (cat. #937007) primer=M13 Forward.
 ORGANISM Caenorhabditis elegans
 Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae.

REFERENCE 1 (bases 1 to 311)
 AUTHORS McCombie,W.R., Kelley,J.M., Aubin,L., Goscochea,M., Fitzgerald,M.G., Wu,A., Adams,M.D., Dubnick,M., Kerlavage,A.R., Venter,J.C. and Fields,C.A.

JOURNAL Unpublished (1993) Contact: Kerlavage AR-The Institute for Genomic Research-932 Clopper Road,Gaithersburg,MD 20878-Tel: (301) 869 9056-Fax: (301) 869 9423 Email: arkerlavet@tigr.org

COMMENT

Contact: Kerlavage AR
 The Institute for Genomic Research
 932 Clopper Road, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlavet@tigr.org.

FEATURES Location/Qualifiers
 source 1..311
 /organism="Caenorhabditis elegans"
 /clone="CEESY50"
 /note="Nematodes"

BASE COUNT 138 a 23 c 71 g 67 t 12 others
 ORIGIN
 Query Match 71.4%; Score 15; DB 103; Length 311;
 Best Local Similarity 100.0%; Pred. No. 2.67e-03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 140 accataccggaggt 154
 |||||
 Cp 15 ACCCATACGGAGGT 1

RESULT 3 CEK129A9R 313 bp mRNA EST 12-DEC-1995
 LOCUS C-elegans cDNA clone yk129a9 : 3' end, single read.
 DEFINITION D64977
 ACCESSION g1117417

NID EST (expressed sequence tag).
 KEYWORDS Caenorhabditis elegans (strain CB1489 him-8(e1489),) (library: Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole animal cDNA to mRNA.

SOURCE Caenorhabditis elegans
 ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae; Rhabditoidea; Rhabditidae; Caenorhabditis.

REFERENCE 1 (bases 1 to 313)
 AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Sugimoto,A., Watanabe,H. and Nishigaki,A.

TITLE Toward an expression map of the C.elegans genome
 JOURNAL Unpublished (1995)
 COMMENT Submitted (23-Aug-1995) to DDBJ by: Yuji Kohara
 Gene Library Lab.

Mar 19 08:41

US-08-612-929-54.rst

5

National Institute of Genetics
Yata 1111, Mishima Shizuoka
411 Japan
Phone: 0559-81-6854
Fax : 0559-81-6855
Email:ykohara@dbj.nig.ac.jp.
Location/Qualifiers

FEATURES

source
1..313
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8 (el489)"
/dev_stage="varied"
/sequenced_mol="cDNA to mRNA"
/sex="Hermaphrodite, male"
/tissue type="whole animal"
/clone_lib="Yuji kohara unpublished cDNA"
134 a 31 c 75 g 65 t 8 others

ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 313;
Best Local Similarity 88.2%; Pred. No. 2.67e-03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 70 anaccatnccggaggt 86

Cp 17 ACACCCATACCGGAGGT 1

RESULT 4

ID HS44035 standard; RNA; EST; 424 BP.
AC T66440;
DT 08-MAR-1995 (Rel. 42, Created)
DT 08-APR-1995 (Rel. 43, Last updated, Version 3)
DE ya46dl1.s2 Homo sapiens cDNA clone 53316 3' similar to
DE SP:MDHC_MOUSE P14152 MALATE DEHYDROGENASE, CYTOPLASMIC ;
KW EST.
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RN [1]
RP 1-424
RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
RA Trevaskis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;
RT "The WashU-Merck EST Project";
RL Unpublished.
CC GDB: G00-426-252 Contact: Wilson RK WashU-Merck EST Project
CC Washington University School of Medicine 4444 Forest Park Parkway,
CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC Email: est@watson.wustl.edu High quality sequence stops: 359 Source:
CC IMAGE Consortium, L1NL This clone is available royalty-free through
CC L1NL ; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. NCBI gi: 696158
FH Key Location/Qualifiers
FT source 1..424
FT /organism="Homo sapiens"
FT /clone="53316"
FT /note="human"

SQ Sequence 424 BP; 130 A; 76 C; 84 G; 133 T; 1 other;

Query Match 71.4%; Score 15; DB 139; Length 424;
Best Local Similarity 85.7%; Pred. No. 2.67e-03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 393 ggaaccaccataggagggt 413
||||| ||||||| |||||||
Cp 21 GGAAACACCCATACCGGAGGT 1

RESULT 5

LOCUS R15814 424 bp mRNA EST 13-APR-1995
DEFINITION ya46dl1.s2 Homo sapiens cDNA clone 53316 3' similar to
SP:MDHC_MOUSE P14152 MALATE DEHYDROGENASE, CYTOPLASMIC ;.
ACCESSION R15814
NID g768229
KEYWORDS EST.
SOURCE human clone=53316 library=Soares infant brain L1NB vector=Lafmid BA
host=DHI108 (ampicillin resistant) primer=21ml3 Rsite1=Not I
Rsite2=Hind III Whole brain from a 73 days post natal female. 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AACTGGAGAAATTCGCCGCCAGGAATTTTTTTTTTTT 3']; double-stranded
cDNA was ligated to Hind III adaptors (Pharmacia), digested with
Not I and directionally cloned into the Not I and Hind III sites of
the Lafmid BA vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.Fatima
Bonaldo.

ORGANISM

Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 (bases 1 to 424)

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

GDB: G00-426-252
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 359
Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source
1..424
Location/Qualifiers
/organism="Homo sapiens"
/clone="53316"
/note="human"

BASE COUNT 130 a 76 c 84 g 133 t 1 others
ORIGIN

Query Match 71.4%; Score 15; DB 76; Length 424;
Best Local Similarity 85.7%; Pred. No. 2.67e-03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 393 ggaaccaccataggagggt 413

Cp 21 GGAAACACCCATACCGGAGGT 1

Mar 19 08:41

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RESULT 6
LOCUS   RICS14394A 460 bp mRNA EST 27-JUL-1995
DEFINITION Rice cDNA, partial sequence (S14394_1A).
ACCESSION D48269
NID      9701978
KEYWORDS EST (expressed sequence tag).
SOURCE   Oryza sativa (strain Nipponbare, ) Green shoot (8 days old) cDNA to
          mRNA.

ORGANISM Oryza sativa
          Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
          Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
          Liliopsida; Poales; Poaceae; Oryza.
REFERENCE 1 (bases 1 to 460)
AUTHORS   Sasaki, T., Miyao, A. and Yamamoto, K.
TITLE     Rice cDNA from shoot
JOURNAL   Unpublished (1995)
COMMENT   PROJECT = 'RGP'
          Submitted (14-Feb-1995) to DDBJ by:
          Takuji Sasaki
          Rice Genome Research Program
          National Institute of Agrobiological Resources
          2-1-2 Kanondai
          Tsukuba Ibaraki
          Japan 305
          Phone: 0298-38-7441
          Fax : 0298-38-7468.

FEATURES             Location/Qualifiers
     source
     1..460
        /organism="Oryza sativa"
        /strain="Nipponbare"
        /dev_stage="Green shoot (8 days old)"
        /sequenced_mol="cDNA to mRNA"

BASE COUNT  111 a 116 c 109 g 120 t 4 others
ORIGIN

```

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Query Match      71.4%; Score 15; DB 102; Length 460;
Best Local Similarity 94.1%; Pred. No. 2.67e-03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 104 cctccggtatgggggtt 120
      |||||
QY 2 CCTCCGGTATGGGTGTT 18

Query Match      71.4%; Score 15; DB 102; Length 460;
Best Local Similarity 94.1%; Pred. No. 2.67e-03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

RESULT 7
LOCUS   CELK101B2R 241 bp mRNA EST 12-DEC-1995
DEFINITION C.elegans cDNA clone yk101b2 : 3' end, single read.
ACCESSION D66478
NID      g1116862
KEYWORDS EST (expressed sequence tag).
SOURCE   Caenorhabditis elegans (strain CB1489 him-8(e1489), ) (library:
          Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole
          animal cDNA to mRNA.

ORGANISM Caenorhabditis elegans
          Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
          Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
          Rhabditidae; Caenorhabditis.
REFERENCE 1 (bases 1 to 241)
AUTHORS   Kohara, Y., Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and
          Nishigaki, A.
TITLE     Toward an expression map of the C.elegans genome
JOURNAL   Unpublished (1995)
COMMENT   Submitted (23-Aug-1995) to DDBJ by:
          Yuji Kohara

```

Mar 19 08:41

US-08-612-929-54.rst

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Gene Library Lab.
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Yata 1111, Mishima Shizuoka
411 Japan
Phone: 0559-81-6854
Fax : 0559-81-6855
Email: ykohara@dbj.nig.ac.jp.

FEATURES             Location/Qualifiers
     source
     1..241
        /organism="Caenorhabditis elegans"
        /strain="CB1489 him-8(e1489)"
        /dev_stage="varied"
        /sequenced_mol="cDNA to mRNA"
        /sex="Hermaphrodite, male"
        /tissue_type="whole animal"
        /clone_lib="Yuji kohara unpublished cDNA"

BASE COUNT  101 a 31 c 55 g 53 t 1 others
ORIGIN

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```

Query Match      66.7%; Score 14; DB 5; Length 241;
Best Local Similarity 100.0%; Pred. No. 6.06e-02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 191 gtatgggtgtttcc 204
      |||||
QY 8 GTATGGGTGTTTCC 21

RESULT 8
LOCUS   SS03B07 312 bp RNA EST 30-AUG-1995
DEFINITION S.scrofa mRNA; expressed sequence tag (5'; clone o3b07).
ACCESSION F14577
NID      g972417
KEYWORDS cofilin; EST; expressed sequence tag.
SOURCE   pig.

ORGANISM Sus scrofa
          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
          Vertebrata; Sarcotrygii; Mammalia; Eutheria; Artiodactyla;
          Suiformes; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 312)
AUTHORS   Winteroe, A.K., Fredholm, M. and Davies, W.
TITLE     Evaluation and characterization of a porcine small intestine cDNA
          library
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 312)
AUTHORS   Winteroe, A.K.
TITLE     Direct Submission
JOURNAL   Submitted (26-JUL-1995) to the EMBL/GenBank/DBJ databases.

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```

Submitted (26-JUL-1995) to the EMBL/GenBank/DBJ databases.
Winteroe A.K., The Royal Veterinary and Agricultural University,
Department of Animal Science and Animal Health, Division of Animal
Genetics, Bulowsvej 13, 1870 Frederiksberg C, DENMARK

FEATURES             Location/Qualifiers
     source
     1..312
        /organism="Sus scrofa"
        /tissue_type="small intestine"
        /clone_lib="directionally cloned cDNA in X11-blue MRF"
        /clones="o3b07"
        /note="expressed sequence tag; pid:e196635"
        /codon_start=1
        /product="cofilin"
        /db_xref="PID:g972418"
        /translation="MAGVAVSGYIKVENDMKVRSSTPEEVKKRKYAVLFCIXEDK
          KNIILEEGKEIILVGDVGQXVDPYATFYATFKMLPKDCRYLYDATYETKSKKXLUFI

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US-08-612-929-54.fst

9

```

BASE COUNT      72 a      73 c      96 g      60 t      11 others
ORIGIN
FW*
Query Match      66.7%; Score 14; DB 103; Length 312;
Best Local Similarity 84.2%; Pred. No. 6.06e-02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 5 cctccgggtggtgctgtc 23
    ||||| ||| ||| ||
Qy 2 CCTCCGGGTATGGGTGTTTC 20

RESULT 9
LOCUS      CELK072C1R      333 bp      mRNA      EST      11-DEC-1995
DEFINITION C.elegans cDNA clone yk72c1 : 3' end, single read.
ACCESSION  D66007
NID        q1116169
KEYWORDS   EST(expressed sequence tag).
SOURCE     Caenorhabditis elegans (strain CB1489 him-8(e1489), ) (library:
           Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole
           animal cDNA to mRNA.
ORGANISM   Caenorhabditis elegans
           Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
           Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
           Rhabditidae; Caenorhabditis.
REFERENCE  1 (bases 1 to 333)
AUTHORS    Kohara,Y., Motohashi,T., Tabara,H., Sugimoto,A., Watanabe,H. and
           Nishigaki,A.
TITLE      Toward an expression map of the C.elegans genome
JOURNAL    Unpublished (1995)
COMMENT    Submitted (23-Aug-1995) to DDBJ by:
           Yuji Kohara
           Gene Library Lab.
           National Institute of Genetics
           Yata 1111, Mishima Shizuoka
           411 Japan
           Phone: 0559-81-6854
           Fax : 0559-81-6855
           Email:ykohara@dbj.nig.ac.jp.
FEATURES   Location/Qualifiers
            source
              1..333
              /organism="Caenorhabditis elegans"
              /strain="CB1489 him-8(e1489)"
              /dev stage="varied"
              /sequenced_mol="cDNA to mRNA"
              /sex="Hermaphrodite, male"
              /tissue type="whole animal"
              /clone lib="Yuji kohara unpublished cDNA"
              /clone lib="Yuji kohara unpublished cDNA"

BASE COUNT      150 a      27 c      80 g      70 t      6 others
ORIGIN

Query Match      66.7%; Score 14; DB 4; Length 333;
Best Local Similarity 93.3%; Pred. No. 6.06e-02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 123 accatnccggaggt 137
    ||||| ||||| |||
Cp 15 ACCCATACCGGAGGT 1

RESULT 10
LOCUS      CELK130F5R      339 bp      mRNA      EST      12-DEC-1995
DEFINITION C.elegans cDNA clone yk130f5 : 3' end, single read.
```

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ACCESSION  D65087
NID        q1117514
KEYWORDS   EST(expressed sequence tag).
SOURCE     Caenorhabditis elegans (strain CB1489 him-8(e1489), ) (library:
           Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole
           animal cDNA to mRNA.
ORGANISM   Caenorhabditis elegans
           Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
           Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
           Rhabditidae; Caenorhabditis.
REFERENCE  1 (bases 1 to 339)
AUTHORS    Kohara,Y., Motohashi,T., Tabara,H., Sugimoto,A., Watanabe,H. and
           Nishigaki,A.
TITLE      Toward an expression map of the C.elegans genome
JOURNAL    Unpublished (1995)
COMMENT    Submitted (23-Aug-1995) to DDBJ by:
           Yuji Kohara
           Gene Library Lab.
           National Institute of Genetics
           Yata 1111, Mishima Shizuoka
           411 Japan
           Phone: 0559-81-6854
           Fax : 0559-81-6855
           Email:ykohara@dbj.nig.ac.jp.
FEATURES   Location/Qualifiers
            source
              1..339
              /organism="Caenorhabditis elegans"
              /strain="CB1489 him-8(e1489)"
              /dev stage="varied"
              /sequenced_mol="cDNA to mRNA"
              /sex="Hermaphrodite, male"
              /tissue type="whole animal"
              /clone lib="Yuji kohara unpublished cDNA"
              /clone lib="Yuji kohara unpublished cDNA"

BASE COUNT      132 a      37 c      76 g      91 t      3 others
ORIGIN

Query Match      66.7%; Score 14; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 6.06e-02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 194 gtatgggtgtttcc 207
    ||||| ||||| |||||
Qy 8 GTATGGGTGTTTCC 21

RESULT 11
LOCUS      H39637      343 bp      mRNA      EST      16-AUG-1995
DEFINITION yos6h08.r1 Homo sapiens cDNA clone 181983 5'.
ACCESSION  H39637
NID        g915689
KEYWORDS   EST.
SOURCE     human clone=181983 library=Soares breast 3NBH8est vector=pf7T3D
           (Pharmacia) with a modified polylinker host=DH10B (ampicillin
           resistant) primer=M13RF1 Rsite1=Not I Rsite2=Eco RI Adult human.
           1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
           TGTTACCAATCTGAGTGGAGCGGCCCTTTTCTTTTCTTTT 3'].
           double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
           digested with Not I and cloned into the Not I and Eco RI sites of a
           modified pf7T3 vector (Pharmacia). library went through one round
           of normalization to a Cot = 20. library constructed by Bento Soares
           and M.Fatima Bonaldo.
ORGANISM   Homo sapiens
           Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
           Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
```


Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 343)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence stops: 297
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source

1..343
/organism="Homo sapiens"
/clone="181983"
/note="human"

BASE COUNT 82 a 92 c 89 g 75 t 5 others
ORIGIN

Query Match 66.7%; Score 14; DB 18; Length 343;
Best Local Similarity 85.0%; Pred. No. 6.06e-02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 155 ggaacacaccacacacagtgg 174
||||||| ||| |

Cp 21 GGAACACCCATACCGGAGG 2

RESULT 12
LOCUS R35538 432 bp mRNA EST 02-MAY-1995
DEFINITION y964g04.r1 Homo sapiens cDNA clone 37508 5'.

ACCESSION R35538

NID g792439

KEYWORDS EST.

SOURCE human clone=37508 library=Soares infant brain IN18 vector=Lafmid BA
host=DH10B (ampicillin resistant) primer=M13Rpl Rsite1=Not I
Rsite2=Hind III Whole brain from a 73 days post natal female. 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AACTGGACAAATTCGGCGCCGCGAGATTTTTTTTTTTT 3']; double-stranded
cDNA was ligated to Hind III adaptors (Pharmacia), digested with
Not I and directionally cloned into the Not I and Hind III sites of
the Lafmid BA vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.Fatima
Bonaldo.

ORGANISM

Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 432)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

COMMENT

GDB: G00-410-049
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 302
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source

1..432
/organism="Homo sapiens"
/clone="37508"
/note="human"

BASE COUNT 92 a 120 c 119 g 94 t 7 others
ORIGIN

Query Match 66.7%; Score 14; DB 81; Length 432;
Best Local Similarity 80.0%; Pred. No. 6.06e-02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 407 acntcgccgtggtgttc 426

||||| ||| ||| ||| ||| ||| |||

Qy 1 ACCTCCGCTATCGGTGTTTC 20

RESULT 13

LOCUS N52367 483 bp mRNA EST 15-FEB-1996

DEFINITION y22906.s1 Homo sapiens cDNA clone 284507 3'.

ACCESSION N52367

NID g1193533

KEYWORDS EST.

SOURCE human clone=284507 primer=m13 -40 forward library=Soares multiple
sclerosis 2NBHSP vector=pT73D (Pharmacia) with a modified
polylinker V TYPE: phagemid host=DH10B (ampicillin resistant)
Rsite1=Not I Rsite2=Eco RI 46 year old male. 1st strand cDNA was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pT7 vector (Pharmacia). Library went
through one round of normalization to a Cot = 5. Library
constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4
multiple sclerosis lesions from one patient was kindly provided by
Dr. Kevin G. Becker (NINDS/NIH).

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 483)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

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US-08-612-929-54.rst

15

Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality.

FEATURES

source
1..190
/organism="Homo sapiens"
/clone="Z31830"
<1..>190
3 a 44 c 64 g 54 t 25 others
BASE COUNT
ORIGIN
Query Match 61.9%; Score 13; DB 34; Length 190;
Best Local Similarity 84.2%; Pred.No. 1.17e+00;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 2 cctccgggtggtgtctc 20
||||||| ||| ||| ||
Qy 2 CCTCCGGTATGGGTGTTTC 20

Search completed: Wed Mar 19 08:42:58 1997
Job time : 66 secs.

US-08-612-929-54

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MParch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:41:17 1997; MasPar time 10.34 Seconds
177.156 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-54
Description: (1-21) from US08612929.seq
Perfect Score: 21
N.A. Sequence: 1 ACCTCGGTATGGCTGTTCC 21
Comp: TGGAGGCCATACCCACARAGG

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.199; Variance 2.769; scale 1.878

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.
1	21	100.0	117 14	Q83498 Heavy chain variable	9.79e-04
2	21	100.0	423 14	Q83493 Humanized antibody 3B	9.79e-04
c 3	20	95.2	91 9	Q51746 Oligonucleotide probe	4.23e-03
4	15	71.4	91 9	Q51746 Oligonucleotide probe	4.48e+00
c 5	14	66.7	10897 20	T09187 MuTu putative oncogen	1.65e+01
6	13	61.9	32 17	T06048 Primer for subcloning	5.81e+01
7	13	61.9	85 7	Q44071 HUH-G14.	5.81e+01
8	13	61.9	85 7	Q44055 HUH-G4.	5.81e+01

c 9	13	61.9	330 18	T19543 Human gene signature	5.81e+01
c 10	13	61.9	354 7	Q42266 Encodes gamma chain V	5.81e+01
c 11	13	61.9	354 13	Q75544 Humanized antibody he	5.81e+01
c 12	13	61.9	354 7	Q42267 Encodes gamma chain V	5.81e+01
c 13	13	61.9	357 12	Q70373 Chimeric anti HIV ant	5.81e+01
c 14	13	61.9	357 11	Q65555 Mouse-human chimeric	5.81e+01
c 15	13	61.9	357 12	Q70369 Anti HIV antibody hea	5.81e+01
c 16	13	61.9	357 11	Q65551 Mouse anti-HIV mu39.1	5.81e+01
c 17	13	61.9	360 19	T09300 Murine anti-Protein C	5.81e+01
c 18	13	61.9	414 6	Q34573 Plasmid pXOM1.	5.81e+01
c 19	13	61.9	417 19	T09299 Murine anti-Protein C	5.81e+01
c 20	13	61.9	417 18	T19077 Human gene signature	5.81e+01
c 21	13	61.9	423 14	Q83492 Chimeric antibody 3B9	5.81e+01
c 22	13	61.9	425 7	Q44060 H65 heavy chain varia	5.81e+01
c 23	13	61.9	483 14	Q83491 Mouse MAb 3B9 heavy c	5.81e+01
c 24	13	61.9	723 7	Q42284 V-J(kappa)/(Gly)4Ser	5.81e+01
c 25	13	61.9	723 7	Q42285 V-J(gamma)/(Gly)4Ser	5.81e+01
c 26	13	61.9	738 12	Q70612 IL-6 binding inhibito	5.81e+01
c 27	13	61.9	769 6	Q37624 Vdelta1 (genomic).	5.81e+01
c 28	13	61.9	1065 17	T02472 Cowpox virus T2-equiv	5.81e+01
c 29	13	61.9	1107 11	Q68716 GDI D4 cDNA.	5.81e+01
c 30	13	61.9	1159 7	Q40592 JSC1 precursor DNA.	5.81e+01
c 31	13	61.9	1405 13	Q79667 Escherichia coli glyA	5.81e+01
c 32	13	61.9	1406 13	Q75378 DNA encoding the E. c	5.81e+01
c 33	13	61.9	2054 2	Q11648 D-aminopeptidase gene	5.81e+01
c 34	13	61.9	2559 2	Q13850 Phibacilin PSBX fragmen	5.81e+01
c 35	13	61.9	2896 4	Q24135 Vector comprising alp	5.81e+01
c 36	13	61.9	3273 13	Q78178 Ammonia monooxygenase	5.81e+01
c 37	13	61.9	8808 22	T32227 Plasmid pBE146.	5.81e+01
c 38	13	61.9	9643 1	N80859 Sequence of entire HI	5.81e+01
c 39	13	61.9	9672 3	Q20616 ROD HIV-2 isolate com	5.81e+01
c 40	13	61.9	11141 20	T15820 TBE virus strain Neud	5.81e+01
c 41	13	61.9	12364 2	Q13607 ACV synthetase gene,	5.81e+01
c 42	13	61.9	12364 2	Q13547 ACVS gene pcbAB.	5.81e+01
c 43	12	57.1	84 22	T15288 cDNA encoding rat pre	1.96e+02
c 44	12	57.1	4234 15	Q87819 Agmenellum quadruplic	1.96e+02
c 45	12	57.1	6513 22	T18986 Drosophila para volta	1.96e+02

ALIGNMENTS

RESULT	ID	AC	DT	DE	KW	KW	OS	PN	PF	PR	PR	PA	PA	PI	DR	PT	PT	CC	
1	Q83498	Q83498	20-SEP-1995 (first entry)	Heavy chain variable region fragment.	Humanized antibody; antibody engineering; monoclonal antibody;	MAB; interleukin-4; IL-4; allergy; heavy chain; ss.	Synthetic.	W09507301-A.	16-MAR-1995.	07-SEP-1994; U10308.	07-SEP-1993; US-117366.	14-OCT-1993; US-136783.	(SMIK) SMITHKLINE BEECHAM CORP.	(SMIK) SMITHKLINE BEECHAM PLC.	Gross MS, Holmes SD, Sylvester DR;	WPI; 95-123387/16.	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions	Example 3; Page 61; 97pp; English.	A humanized antibody was designed to contain mouse CDRs (from anti-IL-4 MAb 3B9 MAB) within a human antibody framework. A

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US-08-612-929-S4.rmg

3

CC synthetic heavy chain was made using the oligonucleotides given
 CC in Q83498-502 and amplified by PCR using the primers given in
 CC Q83503-04. The construct was ligated into vector pCD, along
 CC with a signal sequence (Q83494) and an IgG1 human constant
 CC region. The CDR gene regions of a pre-existing light chain
 CC framework were replaced with synthetic IL-4 CDR genes constructed
 CC from oligonucleotides given in Q83505-08 (CDR1), Q83509-10 (CDR2),
 CC and Q83511-12 (CDR3). The synthetic VL (Q73986) was ligated into
 CC the vector. The anti-IL4 engineered antibody was expressed in
 CC COS and CHO cells.
 SQ Sequence 117 BP; 18 A; 40 C; 28 G; 31 T;

Query Match 100.0%; Score 21; DB 14; Length 117;
 Best Local Similarity 100.0%; Pred. No. 9.79e-04;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 acctccggtatgggtttcc 109
 |||||
 QY 1 ACCTCCGGTATGGGTTCCTCC 21

RESULT 2

ID Q83493 standard; cDNA; 423 BP.
 AC Q83493;
 DE 20-SEP-1995 (first entry)
 DT Humanized antibody 3B9 heavy chain.
 KW Humanized antibody; antibody engineering; monoclonal antibody;
 KW MAb; interleukin-4; IL-4; allergy; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..423
 FT /*tag= a
 FT sig_peptide 1..57
 FT /*tag= b
 FT mat_peptide 58..423
 FT /*tag= c
 PN W09507301-A.
 PD 16-MAR-1995.
 PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR P-PSDB; R70192.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Fig.4; 9pp; English.
 CC A humanized antibody heavy chain variable region and signal
 CC sequence is given in R70192. The signal sequence is also
 CC provided in R70193. The CDR sequences of the construct are
 CC identical to the native CDRs of mouse anti-human IL-4 MAb
 CC 3B9 (R70198-200).
 SQ Sequence 423 BP; 84 A; 131 C; 102 G; 106 T;

Query Match 100.0%; Score 21; DB 14; Length 423;
 Best Local Similarity 100.0%; Pred. No. 9.79e-04;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 151 acctccggtatgggtttcc 171
 |||||
 QY 1 ACCTCCGGTATGGGTTCCTCC 21

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US-08-612-929-S4.rmg

4

RESULT 3

ID Q51746 standard; cDNA; 91 BP.
 AC Q51746;
 DT 31-MAY-1994 (first entry)
 DE Oligonucleotide probe MK14-A
 KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
 KW ss.
 OS Synthetic.
 PN EP-571911-A.
 PD 01-DEC-1993.
 PF 24-MAY-1993; 108325.
 PR 26-MAY-1992; US-889651.
 PA (BECT) BECTON DICKINSON CO.
 PI Shank DD, Spears PA;
 DR WPI; 93-378844/48.
 PT New oligonucleotide probes specific for Mycobacteria - used for
 PT detection and amplification of Mycobacteria nucleic acid in
 PT samples
 PS Claim 3; Page 14; 23pp; English.
 CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
 CC (Q51735). It hybridized to all spp. of mycobacteria tested, but
 CC cross reacted to a few non-mycobacterial spp. The probe may
 CC be useful as an initial screen for mycobacterial infection.
 CC See also Q51735-45 and Q51747-59.
 SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 95.2%; Score 20; DB 9; Length 91;
 Best Local Similarity 0.0%; Pred. No. 4.23e-03;
 Matches 0; Conservative 20; Mismatches 0; Indels 0; Gaps 0;

Db 22 vshhshvhhvhhvhhvsvvv 41
 Cp 21 GGAAACACCATACCGGAGG 2

RESULT 4

ID Q51746 standard; cDNA; 91 BP.
 AC Q51746;
 DT 31-MAY-1994 (first entry)
 DE Oligonucleotide probe MK14-A
 KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
 KW ss.
 OS Synthetic.
 PN EP-571911-A.
 PD 01-DEC-1993.
 PF 24-MAY-1993; 108325.
 PR 26-MAY-1992; US-889651.
 PA (BECT) BECTON DICKINSON CO.
 PI Shank DD, Spears PA;
 DR WPI; 93-378844/48.
 PT New oligonucleotide probes specific for Mycobacteria - used for
 PT detection and amplification of Mycobacteria nucleic acid in
 PT samples
 PS Claim 3; Page 14; 23pp; English.
 CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
 CC (Q51735). It hybridized to all spp. of mycobacteria tested, but
 CC cross reacted to a few non-mycobacterial spp. The probe may
 CC be useful as an initial screen for mycobacterial infection.
 CC See also Q51735-45 and Q51747-59.
 SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 71.4%; Score 15; DB 9; Length 91;

Best Local Similarity 0.0%; Pred. No. 4.48e+00;
Matches 0; Conservative 18; Mismatches 3; Indels 0; Gaps 0;

Db 26 havhvhvhhvhhvhhvhhv 46

Oy 1 ACCTCGGTATGGGTGTTCC 21

RESULT 5

ID T09187 standard; DNA; 10897 BP.
AC T09187;
DE MuTu putative oncogene MN genomic DNA.
KW MuTu; endogenous; cellular component; MN; HeLa cell; diagnosis;
KW lymphocytic choriomeningitis virus; LCMV; putative oncogene;
KW treatment; neoplastic; pre-neoplastic; disease; antisense therapy;
KW antibody; vaccine; vertebrate; immunisation; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_feature 1973
FT /tag= a
FT /note= *given as *? in specification*
FT exon 3536..3950
FT /tag= b
FT /number= 1
FT exon 5125..5154
FT /tag= c
FT /number= 2
FT exon 5350..5518
FT /tag= d
FT /number= 3
FT exon 5650..5792
FT /tag= e
FT /number= 4
FT exon 5882..5974
FT /tag= f
FT /number= 5
FT exon 7375..7441
FT /tag= g
FT /number= 6
FT exon 8776..8933
FT /tag= h
FT /number= 7
FT exon 9446..9590
FT /tag= i
FT /number= 8
FT exon 9705..9731
FT /tag= j
FT /number= 9
FT exon 10349..10430
FT /tag= k
FT /number= 10
FT exon 10561..10751
FT /tag= l
FT /number= 11
PN W09534650-A2.
PD 21-DEC-1995.
PF 15-JUN-1995; US-260190.
PR 07-JUN-1995; US-447504.
PR 07-JUN-1995; US-487077.
PR 07-JUN-1995; US-481658.
PR 07-JUN-1995; US-486756.
PR 07-JUN-1995; US-485049.

PR 07-JUN-1995; US-485862.
PR 07-JUN-1995; US-485863.
PA (CIBA) CIBA CORNING DIAGNOSTICS CORP.
PA (VIRO-) INST VIROLOGY.
PI Pastorek J, Pastorekova S, Zavada J;
DR WPI; 96-049679/05.
PT MN gene, protein and nucleic acid fragments - used as primers and
PT probes in the detection of MN antigens and antibodies, and in the
PT treatment of (pre)neoplastic disease
PS Claim 1; Fig 3; 102pp; English.
CC The present sequence is the complete MuTu endogenous cellular
CC component, MN, genomic DNA, which was isolated from lymphocytic
CC choriomeningitis virus (LCMV) infected HeLa cells. Persistent LCMV,
CC the exogenous MuTu transmissible agent (MX), infection increases
CC the expression level of the MN gene. MN is a putative oncogene,
CC and can therefore be used in the development of prods. for the
CC diagnosis and treatment of neoplastic (NP), or pre-NP diseases.
CC NP diseases can be treated using DNA antisense to MN transcribed
CC mRNA, anti-MN protein antibodies can be used for the diagnosis NP
CC or pre-NP diseases and a vaccine contg. immunogenic amounts of the
CC MN protein can be used to immunise a vertebrate against a NP
CC disease associated with MN antigen expression. 2647 G; 2857 T;
SQ Sequence 10897 BP; 2634 A; 2738 C; 2647 G; 2857 T;

Query Match 66.7%; Score 14; DB 20; Length 10897;
Best Local Similarity 85.0%; Pred. No. 1.65e+01;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1541 gaaactccctactctgaggt 1560

||||| ||| |||| |||||
Cp 20 GAACACCCATACCGAGGT 1

RESULT 6

ID T06048 standard; cDNA; 32 BP.
AC T06048;
DT 18-MAR-1996 (first entry)
DE Primer for subcloning PM95 antigen sequence.
KW Blowfly larvae; blowfly strike; antigen; PM95; vaccine;
KW prophylaxis; treatment; Lucilla cuprina; antibody; ss.
OS Synthetic.
PN AU9517609-A.
PD 02-NOV-1995.
PF 21-APR-1995; 017609.
PR 22-APR-1994; AU-005235.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PI Casu RE, Eisenmann CH, Tellam RL;
DR WPI; 96-000017/01.
PT DNA encoding the blowfly larvae PM95 antigen - used to produce
PT antigenic compns. for use in vaccines for the prophylaxis or
PT treatment of blowfly strike in sheep
PS Example 7; Page 34; 63pp; English.
CC Host cells transformed with the PM95 antigen coding sequence can be
CC used for the production of the antigen for its use in a vaccine.
CC The vaccine is used for the prophylaxis or treatment of blowfly
CC strike in sheep. The antigen can also be used to produce antibodies
CC which can be used to provide passive immunisation against blowfly
CC strike. Two primers (T06048, T06049) were used to subclone the PM95
CC antigen gene into a baculovirus transfer vector.
SQ Sequence 32 BP; 6 A; 8 C; 10 G; 8 T;

Query Match 61.9%; Score 13; DB 17; Length 32;
Best Local Similarity 88.2%; Pred. No. 5.81e+01;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 8 tccgcagtggtgtttc 24
 |||| |||||
 Qy 4 TCCGCTATCGGTGTTT 20

RESULT 7
 ID Q44071 standard; DNA; 85 BP.
 AC Q44071;
 DT 28-OCT-1993 (first entry)
 DE HUH-G14.
 KW Antibody; variable domain; light; L; heavy; H; PCR;
 KW polymerase chain reaction; H65; monoclonal antibody; MAB; ss.
 OS Synthetic.
 PN W09311794-A.
 PD 24-JUN-1993.
 PF 14-DEC-1992; U10906.
 PR 13-DEC-1991; US-808464.
 PA (XOMA) XOMA CORP.
 PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
 DR WPI; 93-213827/26.
 PT Antibodies prepn. used for treatment of auto-immune diseases - by
 PT replacement of critical residues to reduce immunogenicity but
 PT retain binding affinity, etc.
 PS Example 6; Fig 7b; 160pp; English.
 CC Example 6 describes the construction of the gene encoding the
 CC humanised H65 heavy chain contg. the moderate risk residues.
 CC The humanised heavy chain was assembled from the oligonucleotides
 CC given in Q44070-75.
 SQ Sequence 85 BP; 25 A; 21 C; 18 G; 21 T;

Query Match 61.9%; Score 13; DB 7; Length 85;
 Best Local Similarity 88.2%; Pred. No. 5.81e+01;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 47 ctccagtggtgtttt 63
 |||| |||||
 Qy 3 CTCCGCTATCGGTGTTT 19

RESULT 8
 ID Q44055 standard; DNA; 85 BP.
 AC Q44055;
 DT 28-OCT-1993 (first entry)
 DE HUH-G4.
 KW Antibody; variable domain; light; L; heavy; H; PCR;
 KW polymerase chain reaction; H65; monoclonal antibody; MAB; ss.
 OS Synthetic.
 PN W09311794-A.
 PD 24-JUN-1993.
 PF 14-DEC-1992; U10906.
 PR 13-DEC-1991; US-808464.
 PA (XOMA) XOMA CORP.
 PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
 DR WPI; 93-213827/26.
 PT Antibodies prepn. used for treatment of auto-immune diseases - by
 PT replacement of critical residues to reduce immunogenicity but
 PT retain binding affinity, etc.
 PS Example 2b; Fig 7a; 160pp; English.
 CC Example 2b describes the construction of the gene encoding the
 CC humanised H65 heavy chain variable region. The humanised V- and
 CC J-segments of the heavy chain were assembled from six oligonucleotides
 CC (Q44052-57). The oligonucleotides were amplified with PCR primers
 CC (Q44058-59). The DNA sequence of the assembled V/J-region is given

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CC in Q44060.
 SQ Sequence 85 BP; 23 A; 22 C; 18 G; 22 T;
 Query Match 61.9%; Score 13; DB 7; Length 85;
 Best Local Similarity 88.2%; Pred. No. 5.81e+01;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 47 ctccagtggtgtttt 63
 |||| |||||
 Qy 3 CTCCGCTATCGGTGTTT 19

RESULT 9
 ID T19543 standard; cDNA to mRNA; 330 BP.
 AC T19543;
 DT 28-JUN-1996 (first entry)
 DE Human gene signature HUMGS00607.
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; ss.
 OS Homo sapiens.
 PN W09514772-A1.
 PD 01-JUN-1995.
 PF 11-NOV-1994; J01916.
 PR 12-NOV-1993; JP-355504.
 PA (MATS/) MATSUBARA K.
 PA (OKUB/) OKUBO K.
 PI Matsubara K, Okubo K;
 DR WPI; 95-206931/27.
 PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of corresp. mRNA in specific human
 PT tissues

PS Claim 1; Page 413; 2245pp; Japanese.
 CC A single-stranded DNA (or its complementary strand or the corresp.
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
 CC given in T19001-T26837 and which is able to hybridise to part of
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
 CC sequences were obtained from 3'-directed cDNA libraries prepared
 CC from various human tissues; synthesis of cDNA was initiated from the
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
 CC untranslated sequence is unique to a particular mRNA species, almost
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
 CC is constructed so as to reflect accurately the relative abundance of
 CC different mRNAs in the particular tissue from which it was derived.
 CC The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS
 CC sequences) as a means of diagnosing abnormal cell function or for
 CC recognising different cell types.
 SQ Sequence 330 BP; 61 A; 80 C; 84 G; 89 T;

Query Match 61.9%; Score 13; DB 18; Length 330;
 Best Local Similarity 84.2%; Pred. No. 5.81e+01;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 85 gaaccaccagcgagg 103
 |||| ||||| |||||
 Cp 20 GAAACACCCATACCGAGG 2

RESULT 10
 ID Q42266 standard; cDNA; 354 BP.
 AC Q42266;
 DT 13-SEP-1993 (first entry)

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DE Encodes gamma chain V-region of hel H65 antibody fragment.
KW Type I ribosome-inactivating protein; ricin; momordin;
KW immunoconjugate; autoimmune disease; cell killing; toxin;
KW human engineered antibody; variable region; heavy chain;
KW cell targeting; chimeric antibody; ss.
OS Synthetic.
PN W09309130-A.
PD 13-MAY-1993.
PF 04-NOV-1992; U09487.
PR 04-NOV-1991; US-787567.
PR 19-JUN-1992; US-901707.
PA (XOMA) XOMA CORP.
PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP.
DR WPI; 93-167617/20.
PT Analogues of type I ribosome inactivating protein - useful as
PT cytotoxic agents, immuno toxins for treating auto immune diseases,
PT cancer, graft versus host disease and selective cell killing in-vivo
PS Example 5; Page 117; 163pp; English.
CC The invention covers analogues of the plant type I RIP gelonin
CC which have a non-naturally occurring Cys residue in a position
CC which enables the analogue to be conjugated via a disulphide
CC linkage to a molecule which specifically binds to a target cell.
CC Pref. target-cell binding molecules are antibodies or their
CC fragments. Human engineered H65 antibody fragments (i.e. selected
CC murine-encoded amino acids are replaced to make the H65 antibody
CC less immunogenic to humans) were conjugated to various gelonin
CC analogues. The resulting immunoconjugates can be used as cytotoxic
CC therapeutic agents.
SQ Sequence 354 BP; 88 A; 89 C; 98 G; 79 T;

Query Match 61.9%; Score 13; DB 7; Length 354;
Best Local Similarity 88.2%; Pred. No. 5.81e+01;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 153 aaacaccacacactggag 169
||||| ||| |||
Cp 19 AAACACCCATACCGGAG 3

RESULT 11
ID Q75544 standard; DNA; 354 BP.
AC Q75544;
DE Humanised antibody hel gamma chain.
KW Type I ribosome-inactivating proteins; RIPs; humanised antibodies;
KW hel gamma chain; cytotoxic therapeutic agents; autoimmune disease;
KW cancer; graft-versus-host disease; ss.
OS Synthetic.
PN W09426910-A.
PD 24-NOV-1994.
PF 12-MAY-1994; U05348.
PR 12-MAY-1993; US-064691.
PA (XOMA) XOMA CORP.
PI Better MD, Carroll SS, Studnicka GW, Carroll SF;
DR WPI; 95-006804/01.
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins
PT - which are suitable for use as components of cytotoxic
PT therapeutic agents.
PS Example 7; Page 171; 221pp; English.
CC Q75544 encodes the humanised antibody hel gamma chain, which was
CC conjugated to gelonin type I ribosome-activating proteins (RIPs),
CC to produce immunoconjugate cytotoxic therapeutic agents
CC (CTAs). CTAs can be used in the treatment of diseases where
CC the elimination of a particular cell type is desired, such as

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CC autoimmune disease, cancer and graft-versus-host disease.
SQ Sequence 354 BP; 88 A; 89 C; 98 G; 79 T;
Query Match 61.9%; Score 13; DB 13; Length 354;
Best Local Similarity 88.2%; Pred. No. 5.81e+01;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 153 aaacaccacacactggag 169
||||| ||| |||
Cp 19 AAACACCCATACCGGAG 3
RESULT 12
ID Q42267 standard; cDNA; 354 BP.
AC Q42267;
DT 13-SEP-1993 (first entry)
DE Encodes gamma chain V-region of he2 and he3 H65 antibody fragment.
KW Type I ribosome-inactivating protein; ricin; momordin;
KW immunoconjugate; autoimmune disease; cell killing; toxin;
KW human engineered antibody; variable region; heavy chain;
KW cell targeting; chimeric antibody; ss.
OS Synthetic.
PN W09309130-A.
PD 13-MAY-1993.
PF 04-NOV-1992; U09487.
PR 04-NOV-1991; US-787567.
PR 19-JUN-1992; US-901707.
PA (XOMA) XOMA CORP.
PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP.
DR WPI; 93-167617/20.
PT Analogues of type I ribosome inactivating protein - useful as
PT cytotoxic agents, immuno toxins for treating auto immune diseases,
PT cancer, graft versus host disease and selective cell killing in-vivo
PS Example 5; Page 118; 163pp; English.
CC The invention covers analogues of the plant type I RIP gelonin
CC which have a non-naturally occurring Cys residue in a position
CC which enables the analogue to be conjugated via a disulphide
CC linkage to a molecule which specifically binds to a target cell.
CC Pref. target-cell binding molecules are antibodies or their
CC fragments. Human engineered H65 antibody fragments (i.e. selected
CC murine-encoded amino acids are replaced to make the H65 antibody
CC less immunogenic to humans) were conjugated to various gelonin
CC analogues. The resulting immunoconjugates can be used as cytotoxic
CC therapeutic agents.
SQ Sequence 354 BP; 83 A; 86 C; 102 G; 83 T;

Query Match 61.9%; Score 13; DB 7; Length 354;
Best Local Similarity 88.2%; Pred. No. 5.81e+01;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 153 aaacaccacacactggag 169
||||| ||| |||
Cp 19 AAACACCCATACCGGAG 3
RESULT 13
ID Q70373 standard; cDNA to mRNA; 357 BP.
AC Q70373;
DT 13-MAR-1995 (first entry)
DE Chimeric anti HIV antibody heavy chain variable region.
KW Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS; treatment;
KW prophylaxis; Mus musculus; Homo sapiens; ss.
OS Chimeric Homo sapiens.

OS Chimeric Mus musculus.
 FT Key Location/Qualifiers
 FT CDS 1..357
 FT /tag= a
 FT /product= Antibody heavy chain variable region.
 PN W09415969-A.
 PD 21-JUL-1994.
 PF 14-JAN-1993; J00039.
 PR 14-JAN-1993; AU-032671.
 PR 14-JAN-1993; WO-J00039.
 PA (KAGA) CHERO SERO THERAPEUTIC RES INST.
 PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
 PI Tokiyoshi S;
 DR WPI; 94-249145/30.
 DR P-PSDB; R60303.
 PT Recombinant chimeric anti HIV antibody - useful for the treatment
 PT and prevention of HIV
 PS Claim 3; Figure 9; 51pp; Japanese.
 CC The recombinant antibody heavy chain has neutralising activity
 CC against HIV. Chimeric antibodies comprising both mouse and human
 CC sequences are useful in the treatment/prevention of AIDS caused by
 CC HIV. This sequence is derived from the mu39.1 anti HIV monoclonal
 CC antibody producing cell.
 SQ Sequence 357 BP; 95 A; 88 C; 100 G; 74 T;

Query Match 61.9%; Score 13; DB 12; Length 357;
 Best Local Similarity 88.2%; Pred. No. 5.81e+01;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 153 aaacaccaatactggag 169
 ||||| |||| ||||
 Cp 19 AACACCCATACCGGAG 3

RESULT 14
 ID Q65555 standard; cDNA; 357 BP.
 AC Q65555;
 DT 30-JAN-1995 (first entry)
 DE Mouse-human chimeric anti-HIV mu39.1-derived heavy chain V region.
 KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
 KW human immunodeficiency virus; variable region; VH chain; murine;
 KW chimeric; humanised; ds.
 OS Chimeric Mus musculus.
 FT Key Location/Qualifiers
 FT misc_feature 91..105
 FT /tag= a
 FT /note= "encodes murine CDR1"
 FT misc_feature 148..198
 FT /tag= b
 FT /note= "encodes murine CDR2"
 FT misc_feature 295..324
 FT /tag= c
 FT /note= "encodes murine CDR3"
 PN J06125783-A.
 PD 10-MAY-1994.
 PF 28-DEC-1991; 359808.
 PR 28-DEC-1991; JP-359808.
 PA (KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.
 DR WPI; 94-187942/23.
 DR P-PSDB; R55124.
 PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
 PT and recombinant antibody consisting of the H- and L-chains,
 PT useful in AIDS therapy

PS Claim 1; Fig 9; 22pp; Japanese.
 CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
 CC The heavy and light chain variable regions from these antibodies
 CC were sequenced (Q65551-Q65554). The murine anti-HIV CDRs were
 CC introduced into human framework regions to construct chimeric
 CC antibodies (Q65555-Q65558).
 SQ Sequence 357 BP; 95 A; 88 C; 100 G; 74 T;

Query Match 61.9%; Score 13; DB 11; Length 357;
 Best Local Similarity 88.2%; Pred. No. 5.81e+01;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 153 aaacaccaatactggag 169
 ||||| |||| ||||
 Cp 19 AACACCCATACCGGAG 3

RESULT 15
 ID Q70369 standard; cDNA to mRNA; 357 BP.
 AC Q70369;
 DT 09-MAR-1995 (first entry)
 DE Anti HIV antibody heavy chain variable region.
 KW Antibody; heavy chain; light chain; human immunodeficiency virus;
 KW HIV; acquired immune deficiency syndrome; AIDS; treatment;
 KW prophylaxis; Mus musculus; Homo sapiens; ss.
 OS Mus musculus.
 FT Key Location/Qualifiers
 FT CDS 1..357
 FT /tag= a
 FT /product= Antibody heavy chain variable region.
 PN W09415969-A.
 PD 21-JUL-1994.
 PF 14-JAN-1993; J00039.
 PR 14-JAN-1993; AU-032671.
 PR 14-JAN-1993; WO-J00039.
 PA (KAGA) CHERO SERO THERAPEUTIC RES INST.
 PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
 PI Tokiyoshi S;
 DR WPI; 94-249145/30.
 DR P-PSDB; R60299.
 PT Recombinant chimeric anti HIV antibody - useful for the treatment
 PT and prevention of HIV
 PS Claim 4; Figure 1; 51pp; Japanese.
 CC The recombinant antibody heavy chain has neutralising activity
 CC against HIV. Chimeric antibodies comprising both mouse and human
 CC sequences are useful in the treatment/prevention of AIDS caused by
 CC HIV. This sequence is obtained from the mu39.1 anti HIV monoclonal
 CC antibody producing cell.
 SQ Sequence 357 BP; 104 A; 74 C; 94 G; 85 T;

Query Match 61.9%; Score 13; DB 12; Length 357;
 Best Local Similarity 88.2%; Pred. No. 5.81e+01;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 153 aaacaccaatactggag 169
 ||||| |||| ||||
 Cp 19 AACACCCATACCGGAG 3

Search completed: Wed Mar 19 08:41:32 1997
 Job time : 15 secs.

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RESULT 3
LOCUS S75897 438 bp mRNA ROD 14-JUN-1995
DEFINITION Ig VH=IgG heavy chain variable region [mice, Ric45.14 U1 hybridoma, secondary variant DMK, mRNA Partial, 438 nt].
ACCESSION S75897
NID g861529
KEYWORDS
SOURCE mice Ric45.14.U1 hybridoma secondary variant DMK.
ORGANISM Mus sp.
Unclassified.
REFERENCE 1 (bases 1 to 438)
AUTHORS Kobrin,B.J., Zivion,C., Zivion,D., Scharff,M.D. and Spira,G.
TITLE In vitro activation of a nonproductive immunoglobulin allele by a single base pair insertion
JOURNAL Hybridoma 13 (4), 257-261 (1994)
MEDLINE 95104873
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 161740] from the original journal article.

COMMENT Insertion of a single A converts nonproductive allele to productive one.

FEATURES
source Location/Qualifiers
1..438
/organism="Mus sp."
/note="mice"

CDS
307..438
/partial
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/note="Method: conceptual translation supplied by author.
This sequence comes from Fig. 3."

/codon_start=1
/product="IgG heavy chain variable region"
/db_xref="PID:g861530"

/translation="KNEYGSADFYWGQGTTLTVSAKTPPSVYVPLAPGSAQTNSMVT"

BASE COUNT 100 a 131 c 99 g 108 t
ORIGIN

Query Match 71.4%; Score 15; DB 70; Length 438;
Best Local Similarity 94.1%; Pred. No. 1.14e+01;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 100 acctcgtatggtgt 116
||||| |||||||||
QY 1 ACCTCCGTATGGGTGT 17

RESULT 4
LOCUS S77714S2 1661 bp DNA ROD 26-SEP-1995
DEFINITION Ifi56-interferon-alpha regulated gene [mice, Genomic, 1661 nt, segment 2 of 2].

ACCESSION S77715
NID g998618
KEYWORDS
SEGMENT 2 of 2
SOURCE mice.
ORGANISM Mus sp.

Unclassified.
REFERENCE 1 (bases 1 to 1661)
AUTHORS Bluyssen,H.A., Vlietstra,R.J., Faber,P.W., Smit,E.M., Hagemeijer,A. and Trapman,J.

TITLE Structure, chromosome localization, and regulation of expression of

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the interferon-regulated mouse Ifi54/Ifi56 gene family

JOURNAL Genomics 24 (1), 137-148 (1994)
MEDLINE 95203869
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 166055] from the original journal article.
This sequence comes from Fig. 2B.
Map location: 19D1.

FEATURES
Location/Qualifiers
source 1..1661
/organism="Mus sp."
/note="mice"

CDS
Join(S77714:320..324,66..1452)
/gene="Ifi56"

/note="Mismatch(94[1->T]); Description: interferon-alpha regulated gene; Method: conceptual translation supplied by author. This sequence comes from Fig. 2B. Author-given protein sequence is in conflict with the conceptual translation."
/codon_start=1
/db_xref="PID:g998619"

/translation="MGENADGQVWENLQLRCHFTWKLIFENNIDIPLEVRISQVQ
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FAKALKVEPEPENTGYAVAYRQDLDNFTISLEPRKAVRINPEDPYLKVLLAKL
QDLGEHVEAEHIEEALSSTCSQSVIRYAAKYFRKRVKALHLNRLAQSPSSG
YLHYQKGLCYKQIISQRTSRNQRQDQVQLAQAIHEFQETIKLRPTFEMATVC
MAEQVETIHQYEEAEFNAKNTLVAHIQDILHRYGRFLQFHQSEDKAITLYL
KCLKVEKSFARWKLITALEKVAERVCQNVHLVESTLLGLVYKLKQEKNAIFYE
KALRLTGEWNPAF"

BASE COUNT 463 a 382 c 401 g 415 t
ORIGIN

Query Match 71.4%; Score 15; DB 70; Length 1661;
Best Local Similarity 85.7%; Pred. No. 1.14e+01;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1169 acctcgcgtatgcccgtttcc 1189
||||| ||||| |||||
QY 1 ACCTCCGTATGGGTGTTC 21

RESULT 5
LOCUS HSU45983 1953 bp DNA PRI 02-APR-1996
DEFINITION Human G protein-coupled receptor GPR-CY6 gene, complete cds.

ACCESSION U45983
NID g1245056
KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1953)
AUTHORS Lautens,L.L., Tiffany,H.L., Gao,J.-L., Modi,W., Murphy,P.M. and Bonner,T.I.

TITLE Cloning, Tissue Distribution and Chromosomal Localization of two potential G-Protein-Linked Chemokine Receptors

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1953)
AUTHORS Bonner,T.I.

TITLE Direct Submission
JOURNAL Submitted (16-JAN-1996) Tom I. Bonner, Lab of Cell Biology, NIMH, Bldg 36, Rm 3A-17, MSC 4090, Bethesda, MD 20892-4090, USA

FEATURES
source Location/Qualifiers
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FT /organism="Homo sapiens"
FT /chromosome="3"
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267..1334 translation supplied by author."
FT /codon_start=1
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AIMATIPLVFYQVASEDGVLCYSFYNQOTLWKMKIETNFKNNILGLLIPETIFMFCYIKI
IKILHQKRCQNHKTKAIRLVLIVIASLFWPFPNVVLFSLHSMHLDGCSIQ
OLTYATHVTEIISFTHCCVNPVIYAFVGEKFKHLSEIFQKSCQIFNYLGRQMPRES
CEKSSCQHSRSSVDYIL"
BASE COUNT 550 a 423 c 412 g 568 t
ORIGIN
Query Match 71.4%; Score 15; DB 56; Length 1953;
Best Local Similarity 94.1%; Pred. No. 1.14e+01;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 117 acaccacacccgaggt 133
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Cp 17 ACACCCATACCGGAGGT 1
RESULT 6
ID HS459831 standard; DNA; PRI; 1953 BP.
AC U45983;
DT 03-APR-1996 (Rel. 47, Created)
DE 05-APR-1996 (Rel. 47, Last updated, Version 1)
DE HUMAN G protein-coupled receptor GPR-CY6 gene, complete cds.
KW .
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RN [1]
RP 1-1953
RA Lautens L.L., Tiffany H.L., Gao J.L., Modi W., Murphy P.M.,
RA Bonner T.I.;
RT "Cloning, Tissue Distribution and Chromosomal Localization of two
RT potential G-Protein-Linked Chemokine Receptors";
RL Unpublished.
RN [2]
RP 1-1953
RA Bonner T.I.;
RT ;
RL Submitted (16-JAN-1996) to the EMBL/GenBank/DBJ databases.
RL Tom I. Bonner, Lab of Cell Biology, NIMH, Bldg 36, Rm 3A-17, MSC
RL 4090, Bethesda, MD 20892-4090, USA
CC NCBI gi: 1245056
FH Key Location/Qualifiers
FH 1..1953
FT source
FT /organism="Homo sapiens"
FT /chromosome="3"
FT /map="3p22"
FT 267..1334
FT /note="G protein-coupled receptor; Method: conceptual
translation supplied by author. NCBI gi: 1245057"
FT /codon_start=1
FT /product="GPR-CY6"
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FT /db_xref="PID:g1245057"
FT /translation="MDYTLDSLVTVTVDYYPDIFSSPCDAELIQTNKLLLAIFYCL
FVFSLGNLSVLVWCKLRISITDYLNLIALSDLLFVFSFPQYIYLLDQWFGT
MCKVSGFYIGFYSSMFEITLMSVDRLAVHAYALKVTRTGMCTTLCIAWLTAL
ATIPLVFYQVASEDGVLCYSFYNQOTLWKMKIETNFKNNILGLLIPETIFMFCYIKI
HQLKRCQNHKTKAIRLVLIVIASLFWPFPNVVLFSLHSMHLDGCSIQQLTY
THVTEIISFTHCCVNPVIYAFVGEKFKHLSEIFQKSCQIFNYLGRQMPRESCKSS
CQHSRSSVDYIL"
SQ Sequence 1953 BP; 550 A; 423 C; 412 G; 568 T; 0 other;
Query Match 71.4%; Score 15; DB 9; Length 1953;
Best Local Similarity 94.1%; Pred. No. 1.14e+01;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 117 acaccacacccgaggt 133
||||||| |||||||
Cp 17 ACACCCATACCGGAGGT 1
RESULT 7
LOCUS HTVENVSP 3233 bp ss-RNA VRL 19-AUG-1992
DEFINITION Human T-cell leukemia virus I env gene, complete cds and protein 27
gene, 3' end.
ACCESSION M67514
NID g331123
KEYWORDS envelope-associated protein.
SOURCE Human T-cell leukemia virus I
ORGANISM Human T-cell leukemia virus type I
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
Retroviridae; Oncovirinae.
REFERENCE 1 (bases 1 to 3233)
AUTHORS Paine,E., Garcia,J., Philpott,T.C., Shaw,G.M. and Ratner,L.
TITLE Limited sequence variation in human T-lymphotropic virus type 1
isolates from North American and African patients
JOURNAL Virology 182, 111-123 (1991)
MEDLINE 91220642
FEATURES
source Location/Qualifiers
1..3233
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/sequenced_mol="RNA"
<1..81
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/translation="MPKTRRRPRRSQKRPPTPWVSFSL"
57..1523
/feature="env"
/codon_start=1
/product="envelope protein"
/db_xref="PID:g331125"
/translation="MGKFIATLILFFQFCPLILSDYSPSCCTLTIGVSSYHSKPCNPA
QPVCSWTLDLALSDAQALQPPCNLVSSYSYHATYSLYLFPHWIKKRNNGGYSA
SYSDPCSLEKCPYLGCSMTCPYTGAVSSPYKFKQDYNFQVSRNLINLHFSKCGEP
FSLVDAPGDPIMFINTEPSQLPPTAPPLPHSLDHIIEFSIPWKSLLTLVQLTL
QSTNYTCIVCIDRASLSLTHVLYSPNVSPSSSTP LLYPSLALPHLTPFNWTHC
FDPQIQAIYSSPCNSLILPPFSLSPVPTLGSRSRAVPVAVMLYSALAMCAGMAGGI
TCSMSTASGRSLHHEVDKDISQLTQAIYKHNKLIKIAQYAAQNRRLGLDLLEWEGGL
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QSSSISHDTTSGRELPSLLMGSTISMEMSGCASSATTTTSSNGCQTSRSINAPHP
PATRIORF TALFNSTSDSGEKKSRMKRSRTSPASRFALPGTTLIQRDGVARQT
WYKQETALGKGRNMRWAVLCRRSLYLCVESPAYTTEKTELGSHTRVDCNA
IVDJAYDMLSSSESKORHVRIVTONSEHILTELNTESEMLSWISVLOSSSEDIATG
SSVDENELSTGRNNNAVNSALLHNSQSIASLASSCSTATTSEFIANSQHTLQQQ
QQQQTQKQQTQWELSGAGIVSHLPTSKSFGGLSTTASSTTENAKNRLIMHYIARNS
QLOSPANKKMETDPSVTPSSSQTWATTSFHHHSQACP SRD IENCEAPTATATTP
KSGRKKKSKAAKQSGSGSGSSGSGQQAAGAPQVILGVRIADCP TSCEDHVPD
IVQACVCLVETYGMDTVGIYRIPGNTAAVNALKESLNRGFTSDLSKVESLDPRMD
VNVYSLLWELRKLPKLEPLITDKLYPFEIDANRISTHNRHLKRLNLRKLPRHYDT
LFLVLHLSIEKTSUDVNMKCNLALMFGPSIVRPSDDNMATWTHMSDQCKLIETL
IHYNLWFDSTEDVADPEQHPADQGNPLEPGYGVQPTGVSAASFNDMHNLRKA
NEDQAAAMNEKGKQIKNMLRNSRRKSKLKISTAPAAVNPWGTOPPTPNTS
AASVESAFCONQVEDIDAEIESRQTVSPQTSNGDACSRLDQSPSLESSLIP
DTSRTEPLGSSGVDDEAKAARKQEMYSAARRIF IAGAGAAAAATADAEKA
AIDALANHQSQHLHLASPAFEVLSEETREKIRMOKQSHDTELKASGELLKTSPT
KDLTDALSCSDYSTTSAPLSTNPP LAVACADQPNSSDYASSDPSPCARNPSTSPA
SRPNSLAIAPQALHATSSGSHQPMGRSOKILRLKLSRDPARRHTLSVDVDTLKEG
RLDKLARWFGIRKSPDVSDEVDKKNQEA PPLPAAAAPVIVRTSPNELTPVSGD
ELL"
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3' UTR 4323..4824

BASE COUNT 1469 a 1121 c 991 g 1243 t

ORIGIN

Query Match 71.4%; Score 15; DB 26; Length 4824;
Best Local Similarity 100.0%; Pred. No. 1.14e+01;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4643 acctcggatggt 4657

QY 1 ACCTCCGGTATGGGT 15
|||||

RESULT 10

ID MYPIORF standard; DNA; PHG; 8204 BP.

AC M12911;

DT 16-JUL-1988 (Rel. 16, Created)

DT 22-APR-1990 (Rel. 23, Last updated, Version 1)

DE Bacteriophage HP1 (mutant cl) from H.influenzae, partial cds.

KW

OS Bacteriophage HP1

OC Viridae; ds-DNA nonenveloped viruses; Myoviridae.

RN [1]

RP 1-8204

RX MEDLINE; 85128433.

RA Benjamin R.C., Fitzmaurice W.P., Huang P.C., Scocca J.J.;

RT "Nucleotide sequence of cloned DNA segments of the Haemophilus

RT influenzae bacteriophage HP1c1";

RL Gene 31:173-185(1984).

CC Nine open reading frames (orf's) corresponding to presumed

CC polypeptides of longer than 90 amino acids have been identified.

CC All share a common orientation which suggests a probable direction

CC of transcription.

FH Key Location/Qualifiers

FT source

FT 1..8204

FT /organism="Bacteriophage HP1"

SQ Sequence 8204 BP; 2682 A; 1536 C; 1840 G; 2146 T; 0 other;

Query Match

Best Local Similarity 71.4%; Score 15; DB 96; Length 8204;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2830 ggaacacaccataacgtag 2848

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|||||
Cp 21 GGAACACCCATACCGGAG 3

RESULT 11
LOCUS DROUBXX2 11215 bp DNA INV 11-MAY-1994
DEFINITION Drosophila melanogaster (clone DS05563), centromeric to Ubx gene,
DNA sequence.
ACCESSION L32750
NID 9485331
KEYWORDS bichorax complex.
SOURCE Drosophila melanogaster (library: Pl) DNA.
ORGANISM Drosophila melanogaster
Eukaryota; Animalia; Metazoa; Arthropoda; Uniramia; Insecta;
Pterygota; Neoptera; Holometabola; Diptera; Brachycera;
Cyclorhapha; Schizophora; Drosophiloidea; Drosophilidae.
REFERENCE 1 (bases 1 to 11215)
AUTHORS Martin, C.H., Bondoc, M.M., Chiang, A., Cloutier, T., Davis, C.A.,
Ericsson, C.L., Jaklevic, M.A., Kim, R.J., Lee, M.T., Li, M.,
Mayeda, C.A., Steiert-El Kheir, A. and Palazzolo, M.J.
TITLE Sequencing of the antennapedia complex of Drosophila melanogaster
JOURNAL Unpublished (1994)
COMMENT Sequence submitted by:
Human Genome Center and
Drosophila Genome Center
Lawrence Berkeley Laboratory
Berkeley, CA 94720
e-mail: seqgenome.lbl.gov.
Location/Qualifiers
1..11215
/organism="Drosophila melanogaster"
/sequenced_mol="DNA"
/tissue_lib="Pl"
misc_feature 1..11215
/gene="Ubx"
/note="Description: Ultrabithorax"
/db_xref="FlyBase:FBgn0003944"
BASE COUNT 3034 a 2457 c 2515 g 3209 t
ORIGIN
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Query Match 71.4%; Score 15; DB 29; Length 11215;
Best Local Similarity 85.7%; Pred. No. 1.14e+01;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 9765 accaccgtctctgggtttctc 9785

QY 1 ACCTCCGGTATGGGTGTTTCC 21
|||||

RESULT 12

LOCUS DMCCTGGEN 11216 bp DNA INV 19-FEB-1996

DEFINITION D.melanogaster Cctg gene.

ACCESSION X95602

NID g1199815

KEYWORDS CCT-gamma protein; Cctg gene.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;

Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila; Sophophora.

REFERENCE 1 (bases 1 to 11216)

AUTHORS Walkley, N.A. and Malik, A.N.

TITLE Drosophila melanogaster Pl genomic clone DS05563 contains the

chaperonin-encoding gene Cctg

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 11216)
AUTHORS Walkley,N.A.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1996) N.A. Walkley, School of Molecular & Medical
Bioscience, University of Wales, College of Cardiff, PO Box 911,
Cardiff CF1 3US, UK
COMMENT Related sequence L32750, FLYBASE FBgn0003944.
FEATURES Location/Qualifiers
source
1..11216
/organism="Drosophila melanogaster"
complement(join(534..1572,1639..2138,2224..2284,
2340..2377))
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/codon_start=1
/product="CCT-gamma protein"
/db_xref="PID:gl119816"
/translation="MFGGQPIVLISDNTKRESGRKVOLENIQAKAIADVIRTCIG
PQAMKMLDPMGGIVMTDNGNALIREITVQHPAKSMIEIARTODEVGDGTTTSVIV
LAGELAAAEFFLAQQHTPTVIRAYREALDIVHLQSQLQIDVRKAKWADVKR
ACVCTKEIGKNSDLAKIALDAVEVTLSNGRLEVDIKRYAKVEKIPGGAIEESCVL
KGMINKDTHKMRRLIENPRIVLDCSLEYKKGESQTNVELIGEQDFTRMLQIEE
FVQRICADIIAVKGDIVFTKGVSDLAQHYLLKAGITAIRLRKTDNLRIRACGATI
VNRFEELTEKDVGTGAGLEEVKKIGDEYFTVTECKEPAKCTILLRGASKDILNTER
NLQALHARNVILVLEPLVAGGVGEMAAQLLRKQKGPYTAVAHLEIIPRTLQAK
NCGANTRALTRAKHSHHTGGVCAWGDIGESGEIVDMNVKNITWEP LAKVLOTYKT
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complement(534..1572)
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/gene="Cctg"
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/number=1
exon complement(2340..2377)
/gene="Cctg"
/number=1

BASE COUNT 3034 a 2457 c 2515 g 3209 t 1 others
ORIGIN
Query Match 71.4%; Score 15; DB 27; Length 11216;
Best Local Similarity 85.7%; Pred. No. 1.14e+01;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 9766 accaccgtctgggtgttcc 9786
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QY 1 ACCTCGGTATGGGTGTTCC 21

RESULT 13
LOCUS CELK03c7 29989 bp DNA INV 09-NOV-1995
DEFINITION Caenorhabditis elegans cosmid K03C7.
ACCESSION U40059

NID g1055170
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans strain=Bristol N2.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.

REFERENCE 1 (bases 1 to 29989)
AUTHORS Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M., Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J., Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A., Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jlier,M., Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N., Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B., O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A., Saunders,D., Showkeen,R., Smaildon,N., Smith,A., Sonnhammer,E., Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M., Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans

JOURNAL Nature 368 (6466), 32-38 (1994)
MEDLINE 94150718
REFERENCE 2 (bases 1 to 29989)
AUTHORS Leimbach,D.
TITLE The sequence of C. elegans cosmid K03C7
JOURNAL Unpublished (1995)
REFERENCE 3 (bases 1 to 29989)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-1995) Robert Waterston
COMMENT Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1HQ, England
e-mail: tw@nematode.wustl.edu and jes@sanger.ac.uk
NEIGHBORING COSMID INFORMATION:
The 5' cosmid is F35A5, 400 bp overlap; 3' cosmid is 2C64, 500 bp overlap. Actual start of this cosmid is at base position 397 of CELK03c7; actual end is at 6975 of CEL2C64

NOTES:
Coding sequences below are predicted from computer analysis, using the program GeneFinder(P. Green and L. Hillier, ms in preparation).

FEATURES
source Location/Qualifiers
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PAKPKPTEDLADPPEPKPAAPKKKRPWEEDPDEPEEADYTMPAPKKPDTEDPA
DFLGGPKPKLAKAPAKKPTDKPKSKDVKEAPEAPEPKPAAPKKKRPWEEDP
DEPEEADFTWPAKKPDTEDPADP LGGPKKDKPLAKKAPSKPTDKPKDKLPKE
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PKLAKAPAKKTDRPKPKDAPKDKAPTPEEPKPVAPKPKWPPWEEDPDEPEEAD

FTMPAKKPDTEADPADLGGPNKKPKLAKKAPTKPADKPKSEEPKVPAPKKWRP
PWEEPDDEPADTVP IKPGEDEDEPADDEEPEAEDEPKKKPKKRRKRP
KKKPVPEKKEPTFPPVVPKAKWIAP IKKPEEP IPMPKPKTIAENKEERIPALR
YAKKPELEVTPVPWQVTAALITQEGMGAFKSRANVEVNF GDRP IVQGAVDK
TVPI LNDKSKANRSGMTAFCAPREIDONVVDHKKSGQIIPILAKGTTVPHGEY
GTIRQTDVYKDGKPKGMSHSGFI SRQFIANSKEXKAGSNLLDKRRTIISDALQ
SKECEAMPIAMFDGRAVETREGSEFSFRPIVMTNATGGYILMSYADEMKCKNIIPQVN
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CDS
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9874..9969))

/evidence=not experimental

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/map="X"

/note="contains similarity to the fork-head DNA binding

domain"

/codon_start=1

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EIIYQVILLHPYTHRRPDQMGQNSIRHNLSDFCVKLP LKQTSASGVGHFTVPV
ELSDKQTLRRNRQPPALAKKSDAGTTLSDRDRGSSGGETSPSPQSISPPNENP
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/map="X"

/codon_start=1

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ALALFQDPDEQCTEAMKNSDNDFLCLACEA"

BASE COUNT 10357 a 5252 c 6025 g 8355 t
ORIGIN

Query Match 71.44; Score 15; DB 26; Length 29989;

Best Local Similarity 89.5%; Pred. No. 1.14e+01;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1019 gaacacccaacccaagg 1037

||||| ||||| ||||| |||

Cp 20 GAAACACCCATACCGAGG 2

RESULT 14

LOCUS BRU24159 32355 bp DNA PHG 01-NOV-1995

DEFINITION Bacteriophage HP1 strain HP1cl, complete genome.

ACCESSION U24159 006847 M28366 M12911 M22941 M12910 M15313

NID g1046235

KEYWORDS

SOURCE Bacteriophage HP1.

ORGANISM Bacteriophage HP1

REFERENCE 1 Viruses; deDNA viruses, no RNA stage; Tailed phages; Myoviridae.

AUTHORS 1 (bases 1 to 32355)

Eposito, D., Fitzmaurice, W.P., Benjamin, R.C., Goodman, S.D. and

Scocca, J.J.

TITLE The complete nucleotide sequence of the genome of Bacteriophage

HP1, a temperate phage of Haemophilus influenzae

JOURNAL Unpublished (1995)

REFERENCE 2 (bases 1 to 6506)

AUTHORS Eposito, D. and Scocca, J.J.

TITLE Identification of an HP1 phage protein required for site-specific

excision

JOURNAL Mol. Microbiol. 13 (4), 685-695 (1994)

MEDLINE 95089704
REFERENCE 3 (bases 1 to 2363)
AUTHORS Goodman, S.D. and Scocca, J.J.
TITLE Nucleotide sequence and expression of the gene for the
site-specific integration protein from bacteriophage HP1 of
Haemophilus influenzae

JOURNAL J. Bacteriol. 171 (8), 4232-4240 (1989)

MEDLINE 89327135

REFERENCE 4 (bases 17471 to 25675)

AUTHORS Benjamin, R.C., Fitzmaurice, W.P., Huang, P.C. and Scocca, J.J.

TITLE Nucleotide sequence of cloned DNA segments of the Haemophilus

influenzae bacteriophage HP1cl

JOURNAL Gene 31 (1-3), 173-185 (1984)

MEDLINE 85128433

REFERENCE 5 (bases 1 to 2357; 32265 to 32355)

AUTHORS Fitzmaurice, W.P., Waldman, A.S., Benjamin, R.C., Huang, P.C. and

Scocca, J.J.

TITLE Nucleotide sequence and properties of the cohesive DNA termini from
bacteriophage HP1cl of Haemophilus influenzae Rd

JOURNAL Gene 31 (1-3), 197-203 (1984)

MEDLINE 85128435

REFERENCE 6 (bases 1 to 858)

AUTHORS Waldman, A.S., Goodman, S.D. and Scocca, J.J.

TITLE Nucleotide sequences and properties of the sites involved in

lysogenic insertion of the bacteriophage HP1cl genome into the

Haemophilus influenzae chromosome

JOURNAL J. Bacteriol. 169 (1), 238-246 (1987)

MEDLINE 87083373

REFERENCE 7 (bases 1 to 32355)

AUTHORS Eposito, D., Fitzmaurice, W.P., Benjamin, R.C., Goodman, S.D. and

Scocca, J.J.

TITLE Direct Submission

JOURNAL Submitted (04-APR-1995) Dominic Eposito, Biochemistry, The Johns

Hopkins University School of Public Health, 615 North Wolfe Street,

Baltimore, MD 21205, USA

FEATURES

source

1..32355

/organism="Bacteriophage HP1"

/strain="HP1cl"

misc_feature

1..9

/note="cosL; left cohesive end"

251..694

/note="attP; bacterial attachment site"

complement (698..1711)

misc_feature

/gene="int"

/codon_start=1

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/product="integrase"

/db_xref="PID:g459175"

/translation="MAVRKOTKNGKLAEVYVNGNASKRWF LTKGDALRFYNOAKQET

TSANDSVQVLESSDLPALSFYQWEDLHGKTLSDGKARLAKLNKLSNIGDPPANEF

NKAFADYRRRLDGEFSVKNKNPPKATVNRHAYLRVFNELKSLRKWTENPLDGC

VELAFERETELAFYERDIYRLAECDSNPDGLIVRICLATGARWSEATLTQSQ

VMPYKIFTFTWTKSKNRITVP LSKELFDMLPKRGLFNDAYESFNARVRAETELPKG

QUTHVLRHTFASHFMNMGGNLIVLKEILGHSTIEMTYAHFAPSHLESVAKFNPLSN

PAQ"

complement (1698..2315)

/note="orf1"

/codon_start=1

/transl_table=11

/db_xref="PID:g459176"

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KYTDWISSLTLLIMCTFAGVNSMKKQTPDLKSKVAKNIIDFTHAVLIPSKFQS

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/complement(2316..2522)
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WKGWKMALNRLGRCKYPNGGIDL"
/complement(2523..2756)
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/translacion="MAYTKYQVPPNIIANRKNITTAADYLDVQVWNAENGWEW"
RIDNFSFEKAGCLSGCKLTMTYKYITFRKEV"
/complement(2767..3060)
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DQDDVGFFYVLTIKLPNGRKKFKKEYHNGKIKNGKRRSDIKELKEYTSTH"
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FFPAELVRCVSETGARDLYAVAGNEP IFDSDDLKYFHTIKLESKGSFTVENKPFLL
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3636..3641
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3659..3664
/notes="P1 promoter"
3663..3668
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3687..3692
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3754..3993
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4050..4553
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/translacion="MTKSSPTFFOEYCEKHNLNTEEIOERFAILQYQAEVERDITDQ
HQQLSAIFAKWRENCPRQANDDETTSQYTGAEHQAI RDLFLASLKQSAEHAHSHQOS
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4572..4940
/notes="orf6"
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CDS
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FNHLSDEQGMKALADIEPFEDYISPDLTGDKLWHYNEKGIDKLTAFHANSALRTP
FPRALTRDFYNIIDPHTRCK"
4940..5125
/notes="orf7"
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KYITAGDNWINTYKFAH"
5137..5418
/notes="orf8"
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5469..5729
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/translacion="MTKFNLEQALQGAPVRLANGKAYIFADVUSLLAINEPYPLGGY
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5732..8059
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/transl_table=11
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DESCYTPQLQELFATNPVDFEE IEQKLENLPQRQREYFKLYLKA YRSVKDDGSJAF
LLGNKQRHANDYLRD ILDVRLQKVF SQYNVNVDF LQAFINTPQWLSVKDEMQQAVQ
FSTVPTREELAKHYNELHYSGFHELLIGTQOKQQLPYLITESKLKQWAEYMATAFI
RFQDCSHFLKNGIEKNEGDIQGYEYQLYKWCGEIAFSAGEFKI PHKEK IENDKRIKA
EHIDSTLRIITCEXWFKQMRDIQKRVEHIAIACGEVRANAASYISNQSFQEWQLQQ
RKHNDYLRAMII TENIDNPEQVELDFMFLKSSSNPALRRNEMWVRLRGLEAEENNN
EALFLTLTAPSSFHAGNGKWKLVNPRETONYLNKVQOQFRALLSKENIKFYGMRVA
EPHKDGTPHMHALAYVPAEHKEEVIRLFKOKALELDGNGEAGAEHRKVKCKDKTNGS
ATAYIAKYIAKNIDGFALAGEYSDDEPTLS LHDNALVRWASRWGIRQFYFGGASI
CVMBELRRLISQADDEIINKAQAAGIANDYAAVMEIOGGALAKRADOP IKLDYETK
PANKYGEQRKALIGLANRFS LKQVISRTEKQWQIKKRPQDFQAQRTESWERSSTANNSA
RSAPWTCVSNCRNSILEQKIKLLTQPICAPLSAQKLDYLFKYKRLTIDKYTALELTEN
DVOLVKNONNMWMTSLSPVSRNFQKIDFHKQRIQ"
8071..8370
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/db_xref="PID:g1046237"
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Note: remainder of annotations omitted.

Query Match 71.4%; Score 15; DB 41; Length 32355;
Beat Local Similarity 89.5%; Pred. No. 1.14e+01;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 20301 ggaacaccataacgtag 20319

|||||

Cp 21 GGAAACACCATACCGGAG 3

Mar 19 08:39

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RESULT 15
LOCUS CELZC21 36087 bp DNA INV 22-OCT-1993
DEFINITION C. elegans cosmid ZC21.
ACCESSION L16685 L18807
NTD 9289729
KEYWORDS breakpoint cluster region protein; dual bar protein;
transient receptor potential protein.
SOURCE Caenorhabditis elegans (strain Bristol N2) hermaphrodite mixed
whole animal DNA.
ORGANISM Caenorhabditis elegans
Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae.
REFERENCE 1 (bases 1 to 36087)
AUTHORS Sulston, J., Du, Z., Thomas, K., Wilson, R., Hillier, L., Staden, R.,
Halloran, N., Green, P., Thierry-Mieg, J., Qiu, L., Dear, S.,
Coulson, A., Craxton, M., Durbin, R., Berks, M., Metzstein, M.,
Hawkins, T., Ainscough, R. and Waterston, R.
TITLE The C.elegans genome sequencing project: A beginning
JOURNAL Nature 356, 37-41 (1992)
MEDLINE 92168156
REFERENCE 2 (bases 1 to 36087)
AUTHORS Du, Z. and Waterston, R.
TITLE Sequence of the C. elegans cosmid ZC21
JOURNAL Unpublished (1993) see COMMENT for author address
COMMENT Submitted by:
Nematode Sequencing Project
Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
MRC Laboratory of Molecular Biology,
Cambridge CB2 2QH, England
e-mail: rwenematode.wustl.edu and jes@cele.mrc-lmba.cam.ac.uk NOTE:
Coding sequences below are predicted from computer analysis, using
the program Genefinder (P. Green and L. Hillier, in preparation)
Neighboring cosmid information:
This sequence is the entire sequence of C. elegans cosmid ZC21.
Bases 1 to 200 of this cosmid correspond to bases 10234 to 10433 of
the C. elegans cosmid C04D8 entry (GenBank: L16687). Bases 1 to
200 of the GenBank entry for cosmid C02D5 (GenBank: CELC02D5)
correspond to bases 35888 to 36087 of this entry.
The end of the actual sequence of the C04D8 cosmid is at 7298 of
this entry.
The beginning of the actual C02D5 cosmid sequence is at 22573 of
this entry.
The beginning of the actual K10C7 cosmid sequence is at 30071 of
this entry.

FEATURES
source Location/Qualifiers
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/strain="Bristol N2"
/dev stage="mixed"
/sequenced mol="DNA"
/sex="hermaphrodite"
/tissue type="whole animal"
1540..1713
/note="putative"
/number=1
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/partial
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/note="putative"
/codon_start=1
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/translation="IASLASSCGSTATTSEFINSHQTLQ000000TNKHQQTWNELS
exon
CDS
join(14870...15023,15131...15373,16179..16710,16862...16973)
/partial
/standard_name="ZC21.3 protein"
/note="homology with dual bar protein; putative"
/codon_start=1
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/translation="IKNIKAREIKDYIKNGPESHKTEIFEILREKFIKGVKFKNFI
ILEIATSRRTSSGSSSYNTNGVQSDTDGSSNNQPGYLPDYGDRTYDQRIATQALN
KAFDTSGGAPSPPLTPAQOGMGSSSSTGAPSTTYSPTSYGVSSONTYNPSSASS
NVTNPSTSYGNTQSQNQNYVAYDTNQNSPFYYQRPVSTAQYNVLGVNAGFPQSSN

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exon
2360..2456
/partial
/note="ZC21.8: orphan; putative"
/number=2
misc_feature 3399
/note="possible trans-spliced leader site for ZC21.4"
join(3490..4296,4696..5541,5657..5802,5854..6064,
6551..6742)
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/note="homology with breakpoint cluster region protein;
putative"
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AAKGGCGSSGSSGQQQGAAGPQVLCVRIADPTGSCEDHVPMTIVQACVCVIE
TYGMDTVGIYRIPGNTAAVAALKESLSNRFSDVLSKVESLDPRWRDNNVSSLLKM
FLKLPPLLDKLYPFFIDANRISTHNRLLKRLPRPHYDTLRLTLVHLS
ITKUSDVMECRNLALMFGPSIVRPSDDNMATWTHMSDOCKIETLIHYNLMWDE
SSTTSDAVPEQHPADQGNPLEPGYGVPTGVSASFNDMNLIRKANEDQAAAMN
EGKGQIKNMLRNRNRDSSKSLKIESTAPAAVNPGRWQPTPSNTSAASVESAFCC
NYQERDIAETESQTVSPQMTSGADGASSTRLDQSPSLESSLSGLPDTSRTEPILG
SSGYDDDEAKAARKQEQEYSAHRIFTAGAAGAAAAATTADAEKAAIDALNHSQ
HLHLASSPAFVLSSEETREKIRMQKQSWHDTKELRSGELIKTYSPTKOLTDALSC
SDYSTTSSAPLSNPPILAVACADQPNSSSDYASDPSPCARNPSTSPASRPSNLAISP
AQLHATSSSGSHQPMRSQKIRLNTKLSRDPARRHTLSDVDTLKEGRDLKLRWFG
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4696..5541
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5657..5802
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5854..6064
/note="putative"
/number=5
7581..7714
/note="complement; putative"
/number=7
complement(join(7581..7714,7759..7855))
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/partial
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/note="putative"
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/translation="TKAKSGKGTNTAKS SGGNNGTNLNAKRSNTTQDDVKENLN IKNT
EKKRDEDDDEENP LAKITFKARLPKKVSGLL"
14870...15023
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/number=8
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/partial
/standard_name="ZC21.3 protein"
/note="homology with dual bar protein; putative"
/codon_start=1
/db_xref="PID:g289733"


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          ASSIQPQQQQQQYNNQYNNQNMNGYNNQPITLHQSIQSDNESNFNFIYFSLA
          TFALSDCIDYSE"
          15131..15373
          /note="putative"
          /number=9
exon      16179..16710
          /note="putative"
          /number=10
misc_feature 24684
          /note="possible trans-spliced leader site for ZC21.2"
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          26887..27067,27321...27890,28061..28264)
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          /note="homology with transient receptor potential protein;
          putative"
          /codon_start=1
          /db_xref="PID:g289732"
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          ERKSRVKSKHQAQLHGYYILSNLRFLEAAELGNKPTLOECDYDGDRIINWNCIL
          DSMGRTALEIADVNDENMEWVELLQQPDIRIGNALLCAIREGYRLVEVLVNHPIWTR
          EMLGDGMSQALDPSEAAAEYSYSDISPVILAAQLNQFEIIQMLIRKQASIEKPHRHS
          ICETCDREIRINDISLQYSIKRINTFRALAPAMWSITSPDILSAFKLSWDLQRLAFEE
          HEFRETQLSQCKQYSCDLLSQCRSEEVIAILNKDGNVDDNIDVWASKLSLSRL
          KLAIKYEQKAFVSHPHQQLLTSIWYEGIPYQRSGTWANFYAFLEFLWPIFCIMY
          ILMPSRLGRLVRSPFMKFFYYSVSFATFGLLTWATFEDRYEKGEGMGMTFRASDRG
          PPAWTVESLFTWIGLWSEIKQLWEEGKRYMQWNNWDLFIMICLYLCTISIRLS
          AYYITFREDPYRYVTYWTSEEPMLVNAELFAGVNFSAFRIIYLFQTNPYLGPDQ
          ISLGMILDVAKFCFIFVLIISSFSIGLAQLWYDPTDVCPLPGATCKHSSNVFSSI
          ADSVLTLWLSFSTKPEDVDVENHKITQWVQCQMFIMYHCTSIIIVLNLMLIAMWSH
          SFQIINDHADLEWKFHFKLWMAHFDEGSSLPDPFNIIIVTPKSLIYVMNCLFTVWVL
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          25082...25214
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exon      25738..26125
          /note="putative"
          /number=14
exon      26232..26381
          /note="putative"
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exon      26426..26563
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exon      26887..27067
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          /number=18
exon      27321..27890
          /note="putative"
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          DTYTSSFTPKLLPVFAQPPHSAARKTDTSMSPFINGTALDTSIVKPPRGVIRASQENL
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          30055..30276
          /note="putative"
          ...
          Note: remainder of annotations omitted.
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          Best Local Similarity 100.0%; Pred. No. 1.14e+01;
          Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
          Db 7064 acctccggtatgggt 7078
          QY 1 ACCTCCGGTATGGGT 15
          Search completed: Wed Mar 19 08:40:58 1997
          Job time : 64 secs.
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4
RESULT CELK059EXR 346 bp mRNA EST 11-DEC-1995
LOCUS C.elegans cDNA clone yk59e10 : 3' end, single read.
DEFINITION D45581
ACCESSION g1115748
NID EST (expressed sequence tag).
KEYWORDS Caenorhabditis elegans (strain CB1499 him-8(e1489),) (library:
SOURCE Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole
animal cDNA to mRNA.
ORGANISM Caenorhabditis elegans
Eukaryotes; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditidae; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
1 (bases 1 to 346)
AUTHORS Kohara, Y., Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and
Nishigaki, A.
TITLE Toward an expression map of the C.elegans genome
JOURNAL Unpublished (1995)
COMMENT Submitted (23-Aug-1995) to DDBJ by:
Yuji Kohara
Gene Library Lab.
National Institute of Genetics
Yata 1111, Mishima Shizuoka
411 Japan
Phone: 0559-81-6854
Fax : 0559-81-6855
Email:ykohara@dbi.nig.ac.jp.

FEATURES
source Location/Qualifiers
1..346
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/dev stage="varied"
/sequenced_mol="cDNA to mRNA"
/sex="Hermaphrodite, male"
/tissue_type="whole animal"
/cclone_lib="Yuji kohara unpublished cDNA"
BASE COUNT 128 a 66 c 48 g 96 t 8 others
ORIGIN

Query Match 35.4%; Score 17; DB 4; Length 346;
Best Local Similarity 69.0%; Pred. No. 3.42e-04;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 163 catctaattggacagataaagaattatcncgcccaagatgaa 204
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QY 3 CATCTACTGGGACGACGACAAACGTTTCAACCCGAGCCTGAA 44

RESULT 5
LOCUS H08860 352 bp mRNA EST 23-JUN-1995
DEFINITION Y193e06.s1 Homo sapiens cDNA clone 45751 3'.
ACCESSION H08860
NID 9873682
KEYWORDS EST.
SOURCE
human clone=45751 library=Soares infant brain LNB vector=Lafmid BA
host=DH10B (ampicillin resistant) primer=Promega -21m13 Reitel=Not
I Rsite2=Hind III Whole brain from a 73 days post natal female. 1st
strand cDNA was primed with a Not I - oligo(df) primer [5'
AACTCGAACAATTCGCGCCGACGAGAAATTTTTTTTTTTT 3']; double-stranded
cDNA was ligated to Hind III adaptors (Pharmacia), digested with
Not I and directionally cloned into the Not I and Hind III sites of
the Lafmid BA vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.Fatima
Bonaldo.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 352)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)

REFERENCE
AUTHORS
GDB: G00-418-292
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 234
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
Location/Qualifiers

Mar 19 08:44

US-08-612-929-55.rst

7

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source 1..352
/organism="Homo sapiens"
/clone="45751"
/note="human"
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Best Local Similarity 84.0%; Pred. No. 3.42e-04;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 216 gaagacgtcaaacggtacagccaga 240
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QY 13 GAGCAGCAGCAACGTTACACCGA 37

RESULT 6
ID H8506309 standard; RNA; EST; 422 BP.
AC N71506;
DT 20-MAR-1996 (Rel. 47, Created)
DT 13-APR-1996 (Rel. 47, Last updated, Version 2)
DE yw32d12.r1 Homo sapiens cDNA clone 253943 5'.
KW EST.
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RN [1]
RP 1-422
RA Hillier L., Clark N., Dubouque T., Elliston K., Hawkins M.,
RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
RA Parsons J., Rifkin L., Rohlfing T., Tan F., Trevasakis E.,
RA Waterston R., Williamson A., Wohlmann P., Wilson R.;
RT "WashU-Merck EST Project";
RL Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu High quality sequence stops: 150 Source: IMAGE
CC Consortium, L1NL This clone is available royalty-free through L1NL
CC ; contact the IMAGE Consortium (info@image.llnl.gov) for further
CC information. NCBI gi: 1228218
FH Key Location/Qualifiers
FT source 1..422
FT /organism="Homo sapiens"
FT /clone="253943"
FT /note="human"
FT <1..>422
SQ Sequence 422 BP; 136 A; 94 C; 96 G; 91 T; 5 other;
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Best Local Similarity 83.3%; Pred. No. 3.42e-04;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 228 ggntgacgacaaacggtgaacc 251
||| ||||||||| |||||
QY 11 GGCAGCAGCAACGTTACACCC 34

RESULT 7
LOCUS N71506 422 bp mRNA EST 15-MAR-1996
DEFINITION yw32d12.r1 Homo sapiens cDNA clone 253943 3'.
ACCESSION N71506
NID g1228218
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8

```
KEYWORDS EST.
SOURCE human clone=253943 primer=m13 -40 forward library=Morton Fetal
Cochlea vector=pBluescript SK- host-SOLR cells (kanamycin
resistant) Raitel=EcoRI Raitel2=XhoI The cDNA was oligo (dT) primed
with an XhoI restriction enzyme recognition site and an 18 base
poly dT sequence. For the 5' end, the synthesized cDNA termini
were treated with T4 DNA polymerase and EcoRI adaptors were ligated
to the blunt ends. adaptor linker: GAATTCGGCAGCAG.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 422)
AUTHORS Hillier L., Clark N., Dubouque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Tan F., Trevasakis E.,
Waterston R., Williamson A., Wohlmann P. and Wilson, R.
WashU-Merck EST Project
Unpublished (1995)
TITLE Contact: Wilson RK
JOURNAL WashU-Merck EST Project
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 150
Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
source 1..422
/organism="Homo sapiens"
/clone="253943"
/note="human"
mRNA <1..>422
BASE COUNT 136 a 94 c 96 g 91 t 5 others
ORIGIN
Query Match 35.4%; Score 17; DB 68; Length 422;
Best Local Similarity 83.3%; Pred. No. 3.42e-04;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 228 ggntgacgacaaacggtgaacc 251
||| ||||||||| |||||
QY 11 GGCAGCAGCAACGTTACACCC 34

RESULT 8
LOCUS N71506 422 bp mRNA EST 02-APR-1996
DEFINITION yw32d12.r1 Homo sapiens cDNA clone 253943 5'.
ACCESSION N71506
NID g1228218
KEYWORDS EST.
SOURCE human clone=253943 primer=reverse ET library=Morton Fetal Cochlea
vector=pBluescript SK- host-SOLR cells (kanamycin resistant)
Raitel=EcoRI Raitel2=XhoI The cDNA was oligo (dT) primed with an
XhoI restriction enzyme recognition site and an 18 base poly dT
sequence. For the 5' end, the synthesized cDNA termini were
treated with T4 DNA polymerase and EcoRI adaptors were ligated to
the blunt ends. adaptor linker: GAATTCGGCAGCAG.
ORGANISM Homo sapiens
```


Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 362

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source
i..484
/organism="Homo sapiens"
/clone="201842"
/note="human"

BASE COUNT 144 a 87 c 112 g 136 t 5 others
ORIGIN
Query Match 35.4%; Score 17; DB 21; Length 484;
Best Local Similarity 86.4%; Pred. No. 3.42e-04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 281 cgttacaccagcgtgagat 302

||||||| || ||||||| ||

Qy 25 CGTTACACCGGCGCTGAAAT 46

RESULT 11

LOCUS H04977 485 bp mRNA EST 21-JUN-1995
DEFINITION y174a10.s1 Homo sapiens cDNA clone 43636 3' similar to contains Alu
repetitive element;

ACCESSION H04977

NID 9868529

KEYWORDS EST.

SOURCE human clone=43636 library=Soares infant brain lNIB vector=Iafmid BA
host=DH10B (ampicillin resistant) primer=Promega -21m13 Rsite1=Not
I Rsite2=Hind III Whole brain from a 73 days post natal female. 1st
strand cDNA was primed with a Not I - oligo (dT) primer [5'
AACTGAGAAATTCGGCGCCGAGAAATTTTTTTTTTTT 3']; double-stranded
cDNA was ligated to Hind III adaptors (Pharmacia), digested with
Not I and directionally cloned into the Not I and Hind III sites of
the Iafmid BA vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.Fatima
Bonaldo.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 485)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL

COMMENT Unpublished (1995)

GDB: G00-416-177

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 395

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source
i..485
/organism="Homo sapiens"
/clone="43636"
/note="human"

BASE COUNT 93 a 120 c 136 g 132 t 4 others
ORIGIN

Query Match 35.4%; Score 17; DB 8; Length 485;
Best Local Similarity 73.0%; Pred. No. 3.42e-04;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 292 ttccagctgggtgttagttttttatcatcacccag 328

||||| || ||||||| || || || || || || ||

Cp 45 TTTGAGCTCGGCTTGAACGTTTGTCTGCTGCCAG 9

RESULT 12

LOCUS N49145 234 bp mRNA EST 14-FEB-1996

DEFINITION yy84a10.r1 Homo sapiens cDNA clone 280218 5'.

ACCESSION N49145

NID q1190311

KEYWORDS EST.

SOURCE human clone=280218 primer=T7 library=Soares multiple sclerosis
2NHMSP vector=pT73D (Pharmacia) with a modified polylinker
V_TYPE: phagemid host=DH10B (ampicillin resistant) Rsite1=Not I
Rsite2=Eco RI 46 year old male. 1st strand cDNA was primed with a
Not I - oligo (dT) primer
[5'-TGTTACCAATCGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pTT vector (Pharmacia). Library went
through one round of normalization to a Cot = 5. Library
constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4
multiple sclerosis lesions from one patient was kindly provided by
Dr. Kevin G. Becker (NINDS/NIH).

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 234)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL

COMMENT Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 208

Mar 19 08:44

US-08-612-929-55.rst

13

Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

1..234
/organism="Homo sapiens"
/clone="280218"
/note="human"
<1..>234

BASE COUNT 78 a 37 c 57 g 61 t 1 others
ORIGIN

Query Match 33.3%; Score 16; DB 61; Length 234;
Best Local Similarity 83.3%; Pred. No. 7.63e-03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 178 caaacgttacactgcagcagaa 201

|||||

Qy 21 CAACGTTACACCGACCTGAA 44

RESULT 13

LOCUS HUM029G04B 273 bp mRNA EST 26-AUG-1995
DEFINITION Human fetal brain cDNA 5'-end GEN-029G04.

ACCESSION D59416

NTD 9960522

KEYWORDS EST (expressed sequence tag); Human fetal brain;
similar to none (May 29, 1995).

SOURCE Homo sapiens (library: Clontech human fetal brain polyA+ mRNA
(#6535)) cDNA to mRNA.

ORGANISM

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Sarcopterygia; Mammalia; Eutheria; Primates;
Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 273)

AUTHORS Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E.-I., Hirai, Y.,
Maekawa, H., Shin, S. and Nakamura, Y.

TITLE Unpublished(101)

JOURNAL Unpublished (1995)

COMMENT Submitted (30-May-1995) to DDBJ by:

Tsutomu Fujiwara

Otsuka GEN Research Institute

Otsuka Pharmaceutical Co., Ltd

463-10 Kagasuno Kawauchi-cho

Tokushima, Tokushima

771-01

Japan

Phone: 0886-65-2888

Fax : 0886-37-1035.

Location/Qualifiers

source

1..273
/organism="Homo sapiens"
/sequenced_mol="cDNA to mRNA"
/clone_lib="Clontech human fetal brain polyA+ mRNA
(#6535)"

BASE COUNT 68 a 51 c 67 g 62 t 25 others
ORIGIN

Query Match 33.3%; Score 16; DB 46; Length 273;
Best Local Similarity 77.3%; Pred. No. 7.63e-03;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Mar 19 08:44

US-08-612-929-55.rst

14

Db 108 atcybtgtgacgacgacac 129

||||: |||

Qy 4 ATCTACTGGGACGACGACAAAC 25

RESULT 14

LOCUS T94533 296 bp mRNA EST 24-MAR-1995
DEFINITION ye36f07.r1 Homo sapiens cDNA clone 119845 5'.

ACCESSION T94533

NTD 9728021

KEYWORDS EST.

SOURCE

human clone=119845 library=Stratagene lung (#937210)
vector=pBluescript SK- host=SOER cells (kanamycin resistant)
primer=M13RP1 ReiteI=EcoRI ReiteI=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTTTT-3'.

ORGANISM

Homo sapiens
Eucaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1

(bases 1 to 296)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevas, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

WashU-Merck EST Project

Unpublished (1995)

JOURNAL

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 202

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

1..296
/organism="Homo sapiens"
/clone="119845"
/note="human"

BASE COUNT 66 a 75 c 83 g 70 t 2 others
ORIGIN

Query Match 33.3%; Score 16; DB 127; Length 296;
Best Local Similarity 86.4%; Pred. No. 7.63e-03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 34 ggatttctggctcagctgtaa 55

|||||

Cp 48 GGATTTAGGTCGGGTGTAA 27

RESULT 15

LOCUS H14807 312 bp mRNA EST 27-JUN-1995
DEFINITION ym24h12.s1 Homo sapiens cDNA clone 49118 3'.

ACCESSION H14807

NTD 9879627

KEYWORDS EST.

SOURCE

human clone=49118 library=Soares infant brain LNL vector=Lafmid BA

host=DH10B (ampicillin resistant) primer=Promega -21m13 Rsite1=Not
I Reite2=Hind III Whole brain from a 73 days post natal female. 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AACTGGACGATTCGGCGCCGACGAAATTTTTTTTTTTT 3']; double-stranded
cDNA was ligated to Hind III adaptors (Pharmacia), digested with
Not I and directionally cloned into the Not I and Hind III sites of
the Lfamid BA vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.Fatima
Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 312)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

GDB: G00-421-659
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 200
Source: IMAGE Consortium, LIND
This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.lind.gov) for further information.

FEATURES

source

1..312
/organism="Homo sapiens"
/clone="49118"
/note="human"

BASE COUNT 87 a 62 c 72 g 90 t 1 others
ORIGIN

Query Match 33.3%; Score 16; DB 10; Length 312;
Best Local Similarity 83.3%; Pred.No. 7.63e-03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 199 aaaccttacaatccgagactaaaa 222

||||| ||||| ||||| ||||| |||||
QY 22 AAACGTTACAAACCGAGCGCTGAAA 45

Search completed: Wed Mar 19 08:46:41 1997
Job time : 79 secs.

(MI)

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```

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:44:46 1997; MapPar time 12.52 Seconds
334.509 Million cell updates/sec

Tabular output not generated.

```

```

Title:
Description:
Perfect Score:
N.A. Sequence:
Comp:

```

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0: Query 0

Searched: 113505 seqs. 43611913 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database:
n-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22
```

Statistics: Mean 6.056: Variance 3.431: scale 1.765

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	48	100.0	120	14	Q83499	Heavy chain variable	1.12e-19
2	48	100.0	423	14	Q83493	Humanized antibody 3B	1.12e-19
3	33	68.8	91	9	Q51746	Oligonucleotide probe	9.91e-10
4	26	54.2	423	14	Q83492	Chimeric antibody 3B9	2.41e-05
5	26	54.2	483	14	Q83491	Mouse MAb 3B9 heavy c	2.41e-05
6	24	50.0	39	7	Q51787	Mixed oligonucleotide	3.87e-04
7	24	50.0	204	1	N81164	Base substituted E.co	3.87e-04
8	24	50.0	738	12	O70612	IL-6 binding inhibito	3.87e-04

Query Match	45.8%;	Score 22;	DB 19;	Length 360;
Best Local Similarity	75.0%;	Pred. No. 5.82e-03;		

RESULT 13
ID Q11197 standard; DNA; 33 BP.
AC Q11197;
DT 05-JUN-1991 (first entry)
DE Ballast Constituent coding sequence #4.
KW ballast constituent; fusion protein; oligonucleotide library; es.
KW Synthet ic.

FH	Key	Location/Qualifiers
FT	repeat_unit	7..9
FT	*tag_	a
FT	/note=	"can be present 4 to 7 times"
PPN	WO9103550-A.	
PD	21-MAR-1991.	
PPE	28-AUG-1990; U04840.	
PPR	29-AUG-1989; US-399874.	
RPA	(FARR) HOECHST AG.	
RPA	(GEO-) GEN HOSPITAL CORP.	
PPI	Stengelin S, Ulmer W, Habermann P, Uhlmann E, Seed B;	
DR	WFJ; 91-102070/14.	
PT	Prepn. of fusion proteins contg. ballast constituent and protein	
PPT	- giving prods. which are protease resistant or insoluble	
PCS	Claim 12; Page 50; 60pp; English.	
CC	This oligonucleotide is an example of a member of an oligonucleotide	
CC	library encoding ballast constituents. The oligonucleotides are	
CC	inserted into a vector, functionally linked to a regulatory region	
CC	and to a structural gene encoding a desired protein, e.g. proinsulin.	
CC	Host cells transformed with such plasmids produce fusion proteins in	
CC	high yield. The ballast is short and does not disturb the folding of	
CC	the desired protein. The fusion protein is soluble or easily	
CC	solubilised. The oligonucleotide encodes a cleavage site at its 3'	
CC	end which allows easy removal of the ballast constituent.	
SSQ	Sequence	33 BP; 2 A; 10 C; 3 G; 1 T;
Query Match	41.7%;	Score 20; DB 2; Length 33;
Best Local Similarity	27.3%;	Pred. No. 8.14e-02;
Matches	6; Conservative	15; Mismatches 1; Indels 0; Gaps
Ddb	7	dccddccddccddccddccdd 28
Qv	:	: :: :: : :: :: :
	2	ACATCTACTGGCACCACCAA 23

RESULT	ID	Q46603 standard; DNA; 33 BP.
AC	Q46603;	
20-DEC-1993	(first entry)	
Mixed oligonucleotide	f5 encodes ballast constituent.	
Fusion protein; ballast constituent; pro-insulin production;		
recombinant protein production; HMG CoA reductase;		
human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;		
mixed oligonucleotide; ss.		
Synthetic.		
OS	Synthetic.	
Key	Location/Qualifiers	
repeat_unit	7..9	
/*tag= a		
/rpt type= tandem		
/note= "can be repeated 4-8 times"		
repeat_region	7..30	
/*tag= b		
/note= "(DCD)8"		
US5227293-A.		
13-JUL-1993.		
29-AUG-1989; 3998874.		
29-AUG-1989; US-399874.		
23-APR-1992; US-838221.		
(GEHO) GEN HOSPITAL CORP.		
(FAH) HOECHST AG.		
Habermann P, Seed B, Stengelin S, Uhlmann E, Ulmer W;		
WPI; 93-235119/29.		
Fusion proteins for prodn. of e.g. pro-insulin - comprise gene		

Search completed: Wed Mar 19 08:45:02 1997
Job time : 16 secs.

```

PT for desired protein and oligo-nucleotide(s) encoding ballast
PT protein
PS Claim 4; Column 29; 22pp; English.
CC This preferred mixed oligonucleotide encodes a ballast constituent
CC and is inserted between a regulatory region and the structural gene
CC encoding a desired protein. The short ballast component improves
CC protease resistance of the fusion protein while still allowing the
CC desired protein to adopt its correct conformation prior to cleavage
CC of the ballast constituent. Proteins which can be produced as fusion
CC proteins with a ballast region include pro-insulin and HMG CoA
SQ Sequence 33 BP; 1 A; 10 C; 3 G; 1 T;

Query Match 41.7%; Score 20; DB 7; Length 33;
Best Local Similarity 27.3%; Pred. No. 8.14e-02;
Matches 6; Conservative 15; Mismatches 1; Indels 0; Gaps 0;

Db 7 dcdedddcdcdcdcdcdcdcd 28
      :|::||:::||::||::|
QY 2 ACATCTACTGGGACGCAGCAA 23

RESULT 15
ID Q68709 standard; cDNA to mRNA; 366 BP.
AC Q68709;
DT 08-FEB-1995 (first entry)
DE Humanised Mab H-chain coding sequence.
KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;; da.
KK complementarity determining region; CDH; IgC; kappa; IIIB; IIMN; da.
KW Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
PN J06141885-A.
PD 24-MAY-1994.
PF 05-NOV-1992; 322476.
PR 05-NOV-1992; JP-322476.
PP (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
DR WPI; 94-205040/25.

```

Recombinant anti-HIV monoclonal antibody - capable of neutralising strains which can not be neutralised by anti-IIIB and IIIMN antibodies

Disclosure; Page 13; 23pp; Japanese.

The sequences given in Q68709-10 encode the heavy and light chains respectively of the humanised monoclonal antibody (MAB) of the CC invention. The antibody has the ability to neutralise human CC immunodeficiency virus. The antibody is classified as IGC kappa and CC has the sequence RIGPCR or RVGPCR in the principal neutralising CC domain. The antibody may be used to neutralise the clinically CC separate strains which cannot be neutralised by the neutralising CC antibodies against IIIB and IIIMN strains.

Sequence 366 BP; 85 A; 98 C; 84 G; 99 T; 99 SQ

Query Match 41.7%; Score 20; DB 11; Length 366;
Best Local Similarity 72.7%; Pred. No. 8.14e-02;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 154 cacatttattggatgatgacaagcactataaccatctttgaa 197
||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 CACATCTACTGGGACGACGACAAACGTTACACCCGAGCTGAA 44

Search completed: Wed Mar 19 08:45:02 1997
Job time : 16 secs.

Search completed: Wed Mar 19 08:45:02 1997
Job time : 16 secs.



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```
MPPerch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Wed Mar 19 08:43:18 1997; MasPar time 65.65 Seconds
602.210 Million cell updates
Tabular output not generated.
```

```

Title:
Description:
Perfect Score: 48
N.A. Sequence: 1 CACATCTACTGGCAGCAGCG
Comp: GTGTAGATACACCTGTGTGC
>US-08-612-929-55
(1-48) from US08612929.seq

```

Scoring table: TABLE default
Gap 10

Match STN : Phase 0: Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new5
1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI
10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR
Database: genbank94

genbank94

Database:

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7
23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5
30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2
37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLN1 43:PLN2
44:PLN3 45:PLN4 46:PLN5 47:PLN6 48:PLN7 49:PLN8 50:PRI1
51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8
58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1
64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8
71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4
78:VRL5 79:VRL6 80:VRL7 81:VRL8

Database: genbank-new5
82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG
89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL

Database: u-embl46_94
96:part1

Statistics: Mean 7.797; Variance 3.063; scale 2.546

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		ID	Description	Pred. No.
		Match	Length			
1	28	58.3	345.67	MUS1HCVR5	Mouse mRNA for immuno	9.03e-08
2	54.2	286.65	MMU23024	MUS1HCVR5	Mouse mRNA for immuno	3.73e-06
3	26	54.2	286.65	MMU23029	Mus musculus C57BL/6	3.73e-06
4	26	54.2	306.66	MUSB	Mus musculus immunogl	3.73e-06
5	26	54.2	328.66	MUSIGHAEO	Mouse Ig heavy-chain	3.73e-06
6	26	54.2	348.63	MHHCVR4	M.musculus (A.SW) mRN	3.73e-06
7	26	54.2	359.65	MMU23007	Mus musculus CB17 SCI	3.73e-06
8	26	54.2	360.65	MMU22988	Mus musculus CB17 SCI	3.73e-06
9	26	54.2	360.62	MMU22979	Mus musculus CB17 SCI	3.73e-06
10	26	54.2	360.91	MMU22988	Mus musculus CB17 SCI	3.73e-06
11	26	54.2	360.63	MHHCVR3	M.musculus (A.SW) mRN	3.73e-06
12	26	54.2	360.62	MMU22994	Mus musculus CB17 SCI	3.73e-06
13	26	54.2	360.65	MMU22994	Mus musculus CB17 SCI	3.73e-06
14	26	54.2	360.65	MMU22979	Mus musculus CB17 SCI	3.73e-06
15	26	54.2	360.91	MMU22979	Mus musculus CB17 SCI	3.73e-06
16	26	54.2	360.12	MMU22977	Mus musculus CB17 SCI	3.73e-06
17	26	54.2	360.91	MMU22977	Mus musculus CB17 SCI	3.73e-06
18	26	54.2	360.61	MMU22977	Mus musculus CB17 SCI	3.73e-06
19	26	54.2	360.12	MMU22988	Mus musculus CB17 SCI	3.73e-06
20	26	54.2	366.94	MMU22994	Mus musculus CB17 SCI	3.73e-06
21	26	54.2	366.61	MMU22994	Mus musculus CB17 SCI	3.73e-06
22	26	54.2	438.70	S75897	Mouse mRNA for variab	3.73e-06
23	24	50.0	234.66	MUSIGHAHL	Ig VH-IgC heavy chain	1.39e-04
24	24	50.0	265.67	MUSIGHAHL	Mouse Ig heavy-chain	1.39e-04
25	24	50.0	286.65	MMU23021	Mus musculus Ig rearr	1.39e-04
26	24	50.0	318.65	MMU22990	Mus musculus C57BL/6	1.39e-04
27	24	50.0	318.12	MMU22990	Mus musculus CB17 SCI	1.39e-04
28	24	50.0	318.91	MMU22990	Mus musculus CB17 SCI	1.39e-04
29	24	50.0	320.65	MMU22991	Mus musculus CB17 SCI	1.39e-04
30	24	50.0	320.12	MMU22991	Mus musculus CB17 SCI	1.39e-04
31	24	50.0	320.91	MMU22991	Mus musculus CB17 SCI	1.39e-04
32	24	50.0	326.65	MMU22986	Mus musculus CB17 SCI	1.39e-04
33	24	50.0	326.91	MMU22986	Mus musculus CB17 SCI	1.39e-04
34	24	50.0	330.12	MMU22975	Mus musculus CB17 SCI	1.39e-04
35	24	50.0	331.66	MUSIGHASC	Mouse Ig heavy-chain	1.39e-04
36	24	50.0	358.65	MMU23002	Mus musculus CB17 SCI	1.39e-04
37	24	50.0	360.65	MMU23013	Mus musculus CB17 SCI	1.39e-04
38	24	50.0	360.12	MMU22992	Mus musculus CB17 SCI	1.39e-04
39	24	50.0	360.65	MMU23010	Mus musculus CB17 SCI	1.39e-04
40	24	50.0	360.12	MMU22981	Mus musculus CB17 SCI	1.39e-04
41	24	50.0	360.91	MMU22981	Mus musculus CB17 SCI	1.39e-04
42	24	50.0	360.65	MMU22999	Mus musculus CB17 SCI	1.39e-04
43	24	50.0	360.65	MMU22992	Mus musculus CB17 SCI	1.39e-04
44	24	50.0	360.65	MMU23004	Mus musculus CB17 SCI	1.39e-04
45	24	50.0	361.65	MMU23004	Mus musculus CB17 SCI	1.39e-04

ALIGNMENTS

RESULT	1
LOCUS	MUS1HCVR5 345 bp mRNA
DEFINITION	Mouse mRNA for immunoglobulin heavy chain variable region, partial sequence.
ACCESSION	D50394
NID	G804910
KEYWORDS	immunoglobulin heavy chain variable region.
SOURCE	Mus musculus (strain BALB/c) hybridoma producing anti-human procollagenase antibody, cell-line K5E1 cDNA to mRNA

ORGANISM

Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Sarcophrygii; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 345)

AUTHORS

Yamanaka, H.I., Kirii, Y. and Ohmoto, H.

TITLE

An improved phage display antibody cloning system using newly designed PCR primers optimized for Pfu DNA polymerase

JOURNAL

J. Biochem. 117 (6), 1218-1227 (1995)

MEDLINE

96104992

COMMENT

Submitted (21-Apr-1995) to DDBJ by:

Hachiro Yamanaka

New Drug Research Laboratories

Kanebo Ltd.

1-5-90 Tomobuchi-cho Miyakojima-ku

Osaka, Osaka 534

Japan

Phone: 06-921-1281 x3609

Fax: 06-923-3381.

Location/Qualifiers

1..345

/organism="Mus musculus"

/strain="BALB/c"

/sub species="domesticus"

/cell_line="KSE1"

/cell_type="hybridoma producing anti-human procollagenase antibody"

/sequenced_mol="cDNA to mRNA"

1..11

/note="PCR primer"

/product="immunoglobulin heavy chain variable region"

79 a 95 c 80 g 91 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 58.3%; Score 28; DB 67; Length 345;

Matches 36; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 142 cacattactggatgatgacaaagcctataaccatccctgaa 185

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Qy 1 CACATCTACTGGACGACGACAAACGCTTACAAACCGAGCCTGAA 44

RESULT 2

LOCUS

MMU23024 286 bp DNA ROD 06-MAY-1995

DEFINITION

Mus musculus C57BL/6 immunoglobulin heavy chain V region mRNA, clone CB17H-8, partial cds.

ACCESSION

U23024

NID

g780650

KEYWORDS

house mouse.

SOURCE

Mus musculus

ORGANISM

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcophrygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

1 (bases 1 to 286)

Young, D.C. and Kearney, J.F.

AUTHORS

Sequence analysis and antigen binding characteristics of

TITLE

immunoglobulins from SCID Ig⁺ mice

JOURNAL

Int. Immunol. 7 (1995) In press

2 (bases 1 to 286)

AUTHORS

Young, D.C.

TITLE

Direct Submission

JOURNAL

Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

FEATURES

Location/Qualifiers

source

1..286

/clones="CB17H-8"

/strain="C57BL/6"

/organism="Mus musculus"

/sub species="domesticus"

/germline

/tissue_type="Liver"

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/note="7183 Vh gene family"

/codon_start=2

/product="immunoglobulin heavy chain"

/db_xref="PID:g780651"

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BASE COUNT

68 a 77 c 69 g 72 t

ORIGIN

Query Match

54.2%; Score 26; DB 65; Length 286;

Best Local Similarity 79.5%; Pred. No. 3.73e-06;

Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 155 cacattactggatgatgacaaagcctataaccatccctgaa 198

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Qy 1 CACATCTACTGGACGACGACAAACGCTTACAAACCGAGCCTGAA 44

RESULT 3

LOCUS

MMU23019 286 bp DNA ROD 06-MAY-1995

DEFINITION

Mus musculus C57BL/6 immunoglobulin heavy chain V region mRNA, clone CB17H-1, partial cds.

ACCESSION

U23019

NID

g780640

KEYWORDS

house mouse.

SOURCE

Mus musculus

ORGANISM

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcophrygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

1 (bases 1 to 286)

Young, D.C. and Kearney, J.F.

Sequence analysis and antigen binding characteristics of

immunoglobulins from SCID Ig⁺ mice

Int. Immunol. 7 (1995) In press

2 (bases 1 to 286)

Young, D.C.

AUTHORS

Direct Submission

TITLE

Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA

FEATURES

Location/Qualifiers

source

1..286

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/strain="C57BL/6"

/organism="Mus musculus"

/sub species="domesticus"

/germline

Mar 19 08:42

US-08-612-929-55.rge

5

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/db_xref="PID:g780641"
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ORIGIN
Query Match      54.2%; Score 26; DB 65; Length 286;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 155 cacattactgggatgacgaagcgctataaaccatccctgaa 198
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Qy 1 CACATCTACTGGGACGACGACAAACGTTACACCCGAGCCTGAA 44

RESULT 4
LOCUS MUSB 306 bp mRNA ROD 14-MAR-1994
DEFINITION Mus musculus immunoglobulin heavy chain (Igh) mRNA, VDJ4 region,
partial cds.
ACCESSION L22743
NID g348959
KEYWORDS Ig heavy chain; diversity region; immunoglobulin; joining region;
variable region.
SOURCE Mus musculus (strain BALB/cByJ) female adult spleen cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 306)
AUTHORS Sheehan,K.M., Mainville,C.A., Willert,S. and Brodeur,P.H.
TITLE The utilization of individual VH exons in the primary repertoire of
adult BALB/c mice
JOURNAL J. Immunol. 151 (10), 5364-5375 (1993)
MEDLINE 94044761
FEATURES
source
location/Qualifiers
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/strain="BALB/cByJ"
/cell_type="B-lymphocyte"
/dev_stage="adult"
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/sex="female"
/tissue_type="spleen"
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/map="chromosome 12"
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SIKSRLLTISKDTSRNQVFLKITSVDADTATTYCARAWLLRDYMDYWGQGTSTVSS"
BASE COUNT      72 a   80 c   75 g   79 t
ORIGIN
Query Match      54.2%; Score 26; DB 66; Length 306;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
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Mar 19 08:42

US-08-612-929-55.rge

6

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Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 97 cacattactgggatgacgaagcgctataaaccatccctgaa 140
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Qy 1 CACATCTACTGGGACGACGACAAACGTTACACCCGAGCCTGAA 44

RESULT 5
LOCUS MUSIGHAEO 328 bp mRNA ROD 14-NOV-1991
DEFINITION Mouse Ig heavy-chain mRNA V region, partial cds. L2-5D2HV.
ACCESSION M36234
NID g194851
KEYWORDS V-region; immunoglobulin heavy chain; processed gene.
SOURCE Mouse (strain BALB/c), cDNA to mRNA, from hybridoma L2-5D2.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 328)
AUTHORS Kavalier,J., Caton,A.J., Staudt,L.M., Schwartz,D. and Gerhard,W.
TITLE A set of closely related antibodies dominates the primary antibody
response to the antigenic site CB of the A/PR/8/34 influenza virus
hemagglutinin
JOURNAL J. Immunol. 145, 2312-2321 (1990)
MEDLINE 90375932
COMMENT Draft entry and computer-readable sequence for [J. Immunol. (1990)
In press] kindly submitted
by J.Kavaler, 06-JUL-1990.
FEATURES
source
location/Qualifiers
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IYMDDKRYNPSIKSRLLTISKDTSRNQVFLKITSVDADTATTYCARSYGNQGYAMD
YWGQGTG"
BASE COUNT      76 a   85 c   82 g   83 t   2 others
ORIGIN
Query Match      54.2%; Score 26; DB 66; Length 328;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 131 cacattactgggatgacgaagcgctataaaccatccctgaa 174
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Qy 1 CACATCTACTGGGACGACGACAAACGTTACACCCGAGCCTGAA 44

RESULT 6
LOCUS MMHCIVR4 348 bp RNA ROD 23-FEB-1994
DEFINITION M.musculus (A.SW) mRNA for ASWP1 antibody heavy chain variable
region.
ACCESSION X75098
NID g414167
KEYWORDS antibody; variable region; VH region.
SOURCE house mouse.
```


ORGANISM

Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 348)

Monestier, M.

Direct Submission

JOURNAL

Submitted (09-SEP-1993) to the EMBL/GenBank/DBJ databases. M.

Monestier, Center for Molecular Medicine and Immunology, one Bruce

Street, Newark, NJ 07103-2763, USA

2 (bases 1 to 348)

Monestier, M., Iosman, M.J., Novick, K.E. and Aris, J.P.

Molecular analysis of mercury-induced antinuclear antibodies in

H-2S mice

J. Immunol. 152 (2), 667-675 (1994)

94110621

Location/Qualifiers

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KGLGLAHYWDKRYNPSLKSRNQLTISKDTSRNQVFKITSVDATATYYCAQTET

GFDYWGCGTTLTVSS"

BASE COUNT 81 a 95 c 85 g 85 t 2 others

ORIGIN

Query Match 54.2%; Score 26; DB 63; Length 348;

Best Local Similarity 79.5%; Pred. No. 3.73e-06;

Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacattactgggatgatgacaaagcgtataaccatccctgaa 197

||||| ||||||| || ||||| || ||||| |||||

Qy 1 CACATCTACTGGGACGACGACAAAGCTTACACCCGAGCCTGAA 44

RESULT 7

LOCUS MMU23007 359 bp mRNA ROD 26-APR-1995

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,

clone 45-4h, partial cds.

ACCESSION U23007

NID 9780616

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

1 (bases 1 to 359)

REFERENCE

1 (bases 1 to 359)

Monestier, M., Iosman, M.J., Novick, K.E. and Aris, J.P.

Molecular analysis of mercury-induced antinuclear antibodies in

H-2S mice

J. Immunol. 152 (2), 667-675 (1994)

94110621

Location/Qualifiers

AUTHORS

Young, D.C. and Kearney, J.F.

TITLE Sequence analysis and antigen binding characteristics of

immunoglobulins from SCID Ig+ mice

JOURNAL Int. Immunol. 7 (1995) In press

REFERENCE 2 (bases 1 to 359)

AUTHORS Young, D.C.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

FEATURES

source

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/clone="45-4h"

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/cell_type="lymphocyte"

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BASE COUNT 83 a 97 c 87 g 92 t

ORIGIN

Query Match 54.2%; Score 26; DB 65; Length 359;

Best Local Similarity 79.5%; Pred. No. 3.73e-06;

Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 153 cacattactgggatgatgacaaagcgtataaccatccctgaa 196

||||| ||||||| || ||||| || ||||| |||||

Qy 1 CACATCTACTGGGACGACGACAAAGCTTACACCCGAGCCTGAA 44

RESULT 8

LOCUS MMU22988 360 bp mRNA ROD 26-APR-1995

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,

clone 45-23h, partial cds.

ACCESSION U22988

NID q780578

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;

Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

1 (bases 1 to 360)

Young, D.C. and Kearney, J.F.

TITLE Sequence analysis and antigen binding characteristics of

immunoglobulins from SCID Ig+ mice

JOURNAL Int. Immunol. 7 (1995) In press

REFERENCE 2 (bases 1 to 360)

AUTHORS Young, D.C.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

FEATURES

source

1..360

/clone="45-23h"
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KGLEWLAHIYWDGDKRNPISIKSRLTISKDTSRKQVFLKITSVDTADTATYYCARRPL
AITFDYWGQGTTLTVSG"

BASE COUNT 82 a 101 c 87 g 90 t
ORIGIN

Query Match 54.2%; Score 26; DB 65; Length 360;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacattactggatggcagaagcgctataaccctccctgaa 197
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QY 1 CACATCTACTGGGACGACGACAAACGTTACACCCGAGCCTGAA 44

RESULT 9
ID MM22979 standard; RNA; ROD; 360 BP.
AC U22979;
DT 29-APR-1995 (Rel. 43, Created)
DT 09-APR-1996 (Rel. 47, Last updated, Version 2)
DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DE clone 45-12h, partial cds.
KW .
OS Mus musculus (mouse)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-360
RA Young D., Kearney J.F.;
RT "Sequence analysis and antigen binding characteristics of Ig SCID
Ig+ mice";
RL Int. Immunol. 7:807-819(1995).
RN [2]
RP 1-360
RA Young D.C.;

Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.
RL David C. Young, University of Texas Health Science Center, Houston,
RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
CC NCBI gi: 780560
FH Key Location/Qualifiers

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CDS
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Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

K
FT S GLEWLAHIYDDDKRNPISIKSRLTISKDTSRNQVFLKITSVDTADTATYYCARRALG
FT SYFDYWGQGTTLTVSS"
SQ Sequence 360 BP; 84 A; 98 C; 87 G; 91 T; 0 other;

Query Match 54.2%; Score 26; DB 12; Length 360;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacattactggatggcagaagcgctataaccctccctgaa 197
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QY 1 CACATCTACTGGGACGACGACAAACGTTACACCCGAGCCTGAA 44

RESULT 10
LOCUS MMU22988 360 bp mRNA ROD 09-APR-1996
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-23h, partial cds.

ACCESSION U22988
NID g780578
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM

Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.

REFERENCE 1 (bases 1 to 360)
AUTHORS Young,D. and Kearney,J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
Ig+ mice
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543

REFERENCE 2 (bases 1 to 360)
AUTHORS Young,D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
COMMENT NCBI gi: 780578
FEATURES Location/Qualifiers

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CDS

BASE COUNT 82 a 101 c 87 g 90 t
ORIGIN

Query Match 54.2%; Score 26; DB 91; Length 360;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacattactggatggcagaagcgctataaccctccctgaa 197


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QY 1 CACATCTACTGGGACGACGACAAACGTTACAAACCGAGCCTGAA 44
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RESULT 11
LOCUS MMHCVR3 360 bp RNA ROD 23-FEB-1994
DEFINITION M.musculus (A.SW) mRNA for ASWB1 antibody heavy chain variable
region.
ACCESSION X75097
NID 9414165
KEYWORDS antibody; variable region; VH region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Monestier,M.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1993) to the EMBL/GenBank/DBJ databases. M.
Monestier, Center for Molecular Medicine and Immunology, one Bruce
Street, Newark, NJ 07103-2763, USA

REFERENCE
AUTHORS Monestier,M., Losman,M.J., Novick,K.E. and Aris,J.P.
TITLE Molecular analysis of mercury-induced antinuclear antibodies in
H-2S mice
JOURNAL J. Immunol. 152 (2), 667-675 (1994)
MEDLINE 94110621
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source Location/Qualifiers
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BASE COUNT 82 a 95 c 89 g 94 t
ORIGIN

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Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacattactggatgatgacaggcgtataaccatccctgaa 197
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QY 1 CACATCTACTGGGACGACGACAAACGTTACAAACCGAGCCTGAA 44

RESULT 12
ID MM22994 standard; RNA; ROD; 360 BP.
AC U22994;
DT 29-APR-1995 (Rel. 4.3, Created)
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DT 09-APR-1996 (Rel. 47, Last updated, Version 2)
DE Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DE clone 45-27h, partial cds.
KW .
OS Mus musculus (mouse)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-360
RA Young D., Kearney J.F.;
RT "Sequence analysis and antigen binding characteristics of Ig SCID
RT Ig+ mice";
RL Int. Immunol. 7:807-819(1995).
RN [2]
RP 1-360
RA Young D.C.;
RT ;
RL Submitted (17-MAR-1995) to the EMBL/GenBank/DBJ databases.
RL David C. Young, University of Texas Health Science Center, Houston,
RL Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
CC NCBI gi: 780590
FH Key Location/Qualifiers
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FT S
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FT S
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Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacattactggatgatgacaggcgtataaccatccctgaa 197
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QY 1 CACATCTACTGGGACGACGACAAACGTTACAAACCGAGCCTGAA 44

RESULT 13
LOCUS MMU22994 360 bp mRNA ROD 26-APR-1995
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-27h, partial cds.
ACCESSION U22994
NID g780590
KEYWORDS .
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
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REFERENCE 1 (bases 1 to 360)
AUTHORS Young, D.C. and Kearney, J.F.
TITLE Sequence analysis and antigen binding characteristics of immunoglobulin from SCID Ig⁺ mice
JOURNAL Int. Immunol. 7 (1995) In press
REFERENCE 2 (bases 1 to 360)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
FEATURES
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CDS
BASE COUNT 84 a 95 c 87 g 94 t
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Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Db 154 cacattactgggatgacgaagcgctataaccatccctgaa 197
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KGLEWLAHIYDDDKRNPISIKSLRTISKDTSRNQVFLIKITSVDTAUTATYYCARRVL
GSSYFDYWGQGTTLTVSS"
RESULT 14
LOCUS MMU22979 360 bp mRNA ROD 26-APR-1995
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA, clone 45-12h, partial cds.
ACCESSION U22979
NID g780560
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 360)
AUTHORS Young, D.C. and Kearney, J.F.
TITLE Sequence analysis and antigen binding characteristics of immunoglobulin from SCID Ig⁺ mice
JOURNAL Int. Immunol. 7 (1995) In press
REFERENCE 2 (bases 1 to 360)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
FEATURES
Location/Qualifiers

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BASE COUNT 84 a 98 c 87 g 91 t
ORIGIN
Query Match 54.2%; Score 26; DB 65; Length 360;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Db 154 cacattactgggatgacgaagcgctataaccatccctgaa 197
||||| ||||||| || |||||| || |||||| |||||||
Qy 1 CACATCTACTGGGACGACGACAAAGCTTACACCCGAGCCTGAA 44
KGLEWLAHIYDDDKRNPISIKSLRTISKDTSRNQVFLIKITSVDTAUTATYYCARRAL
GSSYFDYWGQGTTLTVSS"
RESULT 15
LOCUS MMU22979 360 bp mRNA ROD 09-APR-1996
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA, clone 45-12h, partial cds.
ACCESSION U22979
NID g780560
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 360)
AUTHORS Young, D. and Kearney, J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID Ig⁺ mice
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
REFERENCE 2 (bases 1 to 360)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
COMMENT NCBI gi: 780560
FEATURES Location/Qualifiers
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/strain="CB17 SCID"
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Mar 19 08:42

US-08-612-929-55 rge

15

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BASE COUNT 84 a 98 c 87 g 91 t
ORIGIN

Query Match 54.2%; Score 26; DB 91; Length 360;
Best Local Similarity 79.5%; Pred. No. 3.73e-06;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 154 cacattactgggatgacaaagcgctataaaccatccctgaa 197

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Qy 1 CACATCTACTGGGACGACGACAAACGTTACACCCCGACCTGAA 44

Search completed: Wed Mar 19 08:44:28 1997
Job time : 70 secs.

WQESREH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Mar 19 08:49:17 1997; MasPar time 52.75 Seconds
275.919 Million cell updates/sec

Tabular output not generated.

Title: >US-08-612-929-56
Description: (1-33) from US08612929.seq
Perfect Score: 33
N.A. Sequence: 1 CGCGAACCGTTTCTACTGCTGACTGACGTT 33
Comp: CGCGTTTGGCAAGATGACCATGACGTCGA

Scoring table:
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
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63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
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87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98
99:EST99
EST-STS-TWO
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114
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125:EST125 126:EST126 127:EST127 128:EST128 129:EST129

Database:

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136:STS8 137:STS9 138:STS10 139:STS11 140:STS12
141:STS13 142:STS14 143:STS15 144:STS16 145:STS17
146:STS18 147:STS19 148:STS20 149:STS21 150:STS22
151:STS23 152:STS24 153:STS25 154:STS26 155:STS27
156:STS28 157:STS29 158:STS30 159:STS31 160:STS32
161:STS33 162:STS34 163:STS35 164:STS36 165:STS37
166:STS38 167:STS39 168:STS40 169:STS41 170:STS42
171:STS43 172:STS44 173:STS45 174:STS46

Statistics: Mean 6.934; Variance 1.401; scale 4.951

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
c 1	16	48.5	382 129	G01101	fruit fly STS Dml786	5.94e-03
c 2	16	48.5	409 29	H77083	17514 Arabidopsis tha	5.94e-03
c 3	16	48.5	1023 170	MM4651	mb50d09.rl Soares mou	5.94e-03
c 4	16	48.5	1023 148	W08465	mb50d09.rl Soares mou	5.94e-03
c 5	15	45.5	183 38	HSC02D012	H. sapiens partial cD	1.02e-01
c 6	15	45.5	224 153	W21175	zb57c09.rl Soares fet	1.02e-01
c 7	15	45.5	224 159	HS175387	zb57c09.rl Soares fet	1.02e-01
c 8	15	45.5	250 16	H31942	EST106521 Rattus sp.	1.02e-01
c 9	15	45.5	270 37	HS17H021	H. sapiens partial cD	1.02e-01
c 10	15	45.5	290 22	H53129	yq84f06.sl Homo sapie	1.02e-01
c 11	15	45.5	299 30	H80521	yu76c03.sl Homo sapie	1.02e-01
c 12	15	45.5	303 3	CELK032CYR	C.elegans cDNA clone	1.02e-01
c 13	15	45.5	318 6	CELK12903R	C.elegans cDNA clone	1.02e-01
c 14	15	45.5	320 81	R36228	yh91c09.sl Homo sapie	1.02e-01
c 15	15	45.5	354 93	R76012	yl22d11.sl Homo sapie	1.02e-01
c 16	15	45.5	357 138	HUMUT147	Human STS UT147.	1.02e-01
c 17	15	45.5	360 5	CELK089AYF	C.elegans cDNA clone	1.02e-01
c 18	15	45.5	409 123	T81859	vd34e02.rl Homo sapie	1.02e-01
c 19	15	45.5	428 49	HUM408F02B	Human fetal brain cDN	1.02e-01
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c 21	15	45.5	437 82	R36669	yh89g06.sl Homo sapie	1.02e-01
c 22	15	45.5	443 172	TC5073	TgESTzy55b04.rl Toxop	1.02e-01
c 23	15	45.5	443 142	N82507	TgESTzy55b04.rl Toxop	1.02e-01
c 24	15	45.5	454 10	H12331	yj11f06.sl Homo sapie	1.02e-01
c 25	15	45.5	455 144	N94475	zb80b01.sl Homo sapie	1.02e-01
c 26	15	45.5	455 162	HS475320	zb80b01.sl Homo sapie	1.02e-01
c 27	15	45.5	513 121	T75965	10743 Arabidopsis tha	1.02e-01
c 28	14	42.4	91 34	H93159	yt93b07.rl Homo sapie	1.53e+00
c 29	14	42.4	184 38	HSC02D022	H. sapiens partial cD	1.53e+00
c 30	14	42.4	261 173	HS238VD10	H. sapiens (D8S1770) D	1.53e+00
c 31	14	42.4	292 102	RICR2383A	Rice cDNA, partial se	1.53e+00
c 32	14	42.4	314 17	H35246	EST111446 Rattus sp.	1.53e+00
c 33	14	42.4	315 136	HS4070TH5	H. sapiens DNA segment	1.53e+00
c 34	14	42.4	342 2	BNAF1556	Brassica campestris (1.53e+00
c 35	14	42.4	349 125	T88344	12040 Arabidopsis tha	1.53e+00
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c 39	14	42.4	440 75	R12213	yf51h11.rl Homo sapie	1.53e+00
c 40	14	42.4	445 54	N24692	yx91e09.sl Homo sapie	1.53e+00
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c 42	14	42.4	463 165	HS740301	za01f12.sl Homo sapie	1.53e+00

43 14 42.4 569 1 ATTS0202 A. thaliana transcrib 1.53e+00
 44 14 42.4 604 56 N32182 yy25c11.s1 Homo sapie 1.53e+00
 45 14 42.4 1359 150 W13169 ma93gil.r1 Soares mou 1.53e+00

ALIGNMENTS

RESULT 1
 LOCUS G01101 382 bp DNA STS 27-FEB-1995
 DEFINITION fruit fly STS Dm1786 clone DS07454 T7.
 ACCESSION G01101
 NID g684505
 KEYWORDS STS sequence; primer; sequence tagged site.
 SOURCE fruit fly vector=PAD105ac11 The P1 library was made by D. Smoller in D. Hartl's lab (see Smoller et al., Chromosoma 100: 487). Chromosomal position was mapped by polytene chromosome in situ hybridization in the Hartl lab (see Hartl et al., PNAS 91: 6824). STS's were generated by sequencing the ends of the Drosophila insert in these P1 clones, by the W. Kimmerly, C. Martin, and M. Palazzolo lab at LBL.

ORGANISM Drosophila melanogaster
 Eucaryotae; Metazoa; Arthropoda; Tracheata; Insecta; Diptera; Brachycera; Cyclorhapha; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 382)
 AUTHORS Rubin, G.
 TITLE Drosophila STS
 JOURNAL Unpublished (1994)
 COMMENT

Contact: Berkeley Drosophila Genome Project

Primer A: GGGAAAGCTGTACAGGAGG

Primer B: CAAGGACATGTACGAGGAC

STS size: 217

PCR Profile:

Annealing: 58 degrees C

PCR Cycles: 32

Protocol:

Template: P1 Library Pools

Primer: 1 uM each

dNTPs: 250 uM each

Taq Poly: 0.05 units/ul

Total Vol: 15 ul

Buffer:

MgCl2: 1.5mM

KCl: 50 mM

Tris-HCl: 50 mM

pH: 8.3

Gelatin: .001 %

The P1 library has been distributed to 16 regional sites. A list of these sites is available from FlyBase, via anonymous ftp to ftp.bio.indiana.edu in the file flybase/allied-data/genome-projects/1bl/1BL.doc.

FEATURES
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 /note="fruit fly"

STS 28..244

primer_bind 28..47

primer_bind complement(225..244)

BASE COUNT 94 a 77 c 117 g 91 t 3 others

ORIGIN

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 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 244 gtcgaagtaccagtagctacataa 263

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Cp 30 GTCGAAGTAGCTACCTAGAAAA 11

RESULT 2

LOCUS H77083 409 bp mRNA EST 07-NOV-1995

DEFINITION 17514 Arabidopsis thaliana cDNA clone 203C1977.

ACCESSION H77083

NID g1054334

KEYWORDS EST.

SOURCE thale cress clone=203C1977 primer=T7 dye primer library=Lambda-PRL2 strain=var columbia vector=Lambda Zip-Lox Reitel=Sal Reitel=Not Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRL's Lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA.

ORGANISM Arabidopsis thaliana

Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 409)

AUTHORS

Newman, T., de Bruijn, F. J., Green, P., Keegstra, K., Kende, H.,

McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomasow, M.,

Retzel, E. and Somerville, C.

Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)

Contact: Thomas Newman

MSU-DOE Plant Research Laboratory

Michigan State University

MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.

Lansing, MI

Tel: 517-353-0854

Fax: 517-353-9168

Email: 22313tcn@lbnm.cl.msu.edu.

FEATURES

Location/Qualifiers

1..409

/organism="Arabidopsis thaliana"

/clone="203C1977"

/strain="var columbia"

/note="thale cress"

BASE COUNT

107 a 92 c 86 g 108 t 16 others

ORIGIN

Query Match 48.5%; Score 16; DB 29; Length 409;
 Best Local Similarity 86.4%; Pred. No. 5.94e-03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 152 gaatccctttttctctgtact 173

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Qy 4 GAAACCGTTTCTACTGTACT 25

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 183)
AUTHORS Genexpress.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-1995) to the EMBL/GenBank/DBJ databases.
Genethon, B.P. 60, 91002 Evry Cedex France and Genetique
Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801
Villejuif Cedex France.E-mail: genexpress@genethon.fr
REFERENCE 2 (bases 1 to 183)
AUTHORS Genexpress.
TITLE The Genexpress cDNA program
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 183)
AUTHORS Auffray,C., Behar,G., Bois,F., Boucher,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: Integrated molecular analysis of the human genome and its
expression
JOURNAL C.R. Acad. Sci., III, Sci. Vie 318, 263-272 (1995)
COMMENT Cloning method: total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA
vector;
Sequencing method: single read, full automatic;
Primer: (-21)/M13 universal;
cDNA sequence complementary to mRNA (3' end)
Stretch removed: removed at sequence 5' end
Normalization method: Bento Soares, P.N.A.S in press;
Genexpress_library_id: C;
Genexpress_sequence_id: alc-02d01.
FEATURES
source
1..183
/organism="Homo sapiens"
/clone_lib="normalized infant brain cDNA from B.Soaers,
Psychiatry Dept. Columbia University USA"
/sex="female"
/tissue_type="total brain"
/dev_stage="3 months old"
/isolates="muscular atrophy patient"
BASE COUNT 64 a 25 c 31 g 54 t 9 others
ORIGIN
Query Match 45.5%; Score 15; DB 38; Length 183;
Best Local Similarity 88.9%; Pred. No. 1.02e-01;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 116 ttctactggtacttcac 133
|||||
Qy 13 TTCTACTGGTACTTCGAC 30
RESULT 6
LOCUS W21175 224 bp mRNA EST 06-MAY-1996
DEFINITION zb57c09.r1 Soares fetal lung NBHL19W Homo sapiens cDNA clone 307696
5' similar to gb:M88458 ER LUMEN PROTEIN RETAINING RECEPTOR 2
(HUMAN);.
ACCESSION W21175
NID g1298226

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 224)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawking,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.RECA+ET
High quality sequence stop: 211.
NCBI gi: 1298226
Location/Qualifiers
1..224
/organism="Homo sapiens"
/notes="Organ: lung; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
15'-TGTTACCAATCTCAAGTGGAGGCGCGCAATTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Patima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBHL19W."
/clone="307696"
/clone_lib="Soares fetal lung NBHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
BASE COUNT 59 a 53 c 49 g 63 t
ORIGIN
Query Match 45.5%; Score 15; DB 153; Length 224;
Best Local Similarity 82.6%; Pred. No. 1.02e-01;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 142 aaaccattcttactgtgacttc 164
|||||
Qy 5 AAACCGTTTTCTACTGTCTTC 27
RESULT 7
ID HSI75387 standard; RNA; EST; 224 BP.
AC W21175;
DT 08-MAY-1996 (Rel. 47, Created)
DT 08-MAY-1996 (Rel. 47, Last updated, Version 1)

DE z657c09.r1 Soares fetal lung NBHL19W Homo sapiens cDNA clone 307696
DE 5' similar to gb:M89458 ER LUMEN PROTEIN RETAINING RECEPTOR 2
DE (HUMAN);.
KW EST.
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RN [1]
RP 1-224
RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
RA Trevaskis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;
RT "The WashU-Merck EST Project";
RL Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu This clone is available royalty-free through
CC LNU ; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: mob.REGA+ET High quality sequence
CC stop: 211. NCBI gi: 1298226
FH Key
FH Location/Qualifiers
FH source
FT 1..224
FT /organism="Homo sapiens"
FT /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
FT modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
FT strand cDNA was primed with a Not I - oligo(dT) primer
FT [5'-TGTTACCAATCTCAAGTCGAGCGCGCAATTTTTTTTTT-3'],
FT double-stranded cDNA was size selected, ligated to Eco RI
FT adapters (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified pT7T3 vector
FT (Pharmacia). Library went through one round of
FT normalization to a Cot = 5. Library constructed by Bento
FT Soares and M.Fatima Bonaldo. This library was constructed
FT from the same fetus as the fetal heart library, Soares
FT fetal heart NBHL19W."
FT /clone="307696"
FT /clone.lib="Soares fetal lung NBHL19W"
FT /dev_stage="19 weeks"
FT /lab_host="DH10B (ampicillin resistant)"
FT <1..>224
FT mRNA
SQ Sequence 224 BP; 59 A; 53 C; 49 G; 63 T; 0 other;

Query Match 45.5%; Score 15; DB 159; Length 224;
Best Local Similarity 82.6%; Pred. No. 1.02e-01;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 142 aaaccattcttactgtgacttc 164
||||| | ||||| | |||||
QY 5 AAACGGTTTCTACTGGTACTTC 27

RESULT 8
LOCUS H31942 250 bp mRNA EST 08-SEP-1995
DEFINITION EST106521 Rattus sp. cDNA 3' end.
ACCESSION H31942
NID g977359
KEYWORDS EST.
SOURCE rat primer-M13 - 21 library-Rat PC-12 cells, untreated
vector=pBluescript SK- Rsite=EcoRI Rsite2=XhoI poly(A) + RNA was
purified from untreated PC12 cells cultured for 9 days. cDNA was
constructed using an oligo-dT primer and directionally cloned using

the Lambda ZAP II Vector Kit by Stratagene.
ORGANISM Rattus sp.
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha;
Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 250)
AUTHORS Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A.,
Fuldner, R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D.,
Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
TITLE Comparative expressed sequence tag analysis of differential gene
expression profiles in PC-12 cells before and after nerve growth
factor treatment
JOURNAL Proc. Natl. Acad. Sci. USA 92, 8303-8307 (1995)
COMMENT Other ESTs: EST106522
Contact: Lee NH
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: nhlee@tigr.org
For clone availability please contact the TIGR Database
(tcbinfo@db.tigr.org).
FEATURES
source
1..250
/organism="Rattus sp."
/note="rat"
mRNA
BASE COUNT 72 a 58 c 42 g 75 t 3 others
ORIGIN
Query Match 45.5%; Score 15; DB 16; Length 250;
Best Local Similarity 80.0%; Pred. No. 1.02e-01;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 116 cgtttctagtgtactttaagtt 140
||||| | ||||| | |||||
QY 9 CGTTTCTACTGTTACTTCGACGTT 33

RESULT 9
LOCUS HSA17H021 270 bp RNA EST 04-JUN-1993
DEFINITION H. sapiens partial cDNA sequence; clone 17H02; strand (-), single
read.
ACCESSION Z13017
NID g24384
KEYWORDS partial cDNA sequence; transcribed sequence fragment.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 270)
AUTHORS Genexpress.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-1992) Genethon, B.P. 60, 91002 Evry Cedex France
and Genetique Moleculaire et Biologie du developpement, CNRS UPR420
B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr
REFERENCE 2 (bases 1 to 270)
AUTHORS Genexpress.
TITLE The Genexpress cDNA program
JOURNAL Unpublished
COMMENT cloning vector is pBluescript SK(+);
Genexpress library reference is A.
full automatic
IMPORTANT: Computer analyses of the total data set derived from

this library indicate a significant proportion of sequences of yeast and bacterial origin. Please contact us if you identify such an entry.

FEATURES

source Location/Qualifiers
1..270
/organism="Homo sapiens"
/cell_line="T Lymphoblastoid cell line ATCC#CCL119"
/clone_lib="CLONTECH cDNA library CCRF-CEM, cat# HL 1063g"
BASE COUNT 54 a 57 c 55 g 94 t 10 others
ORIGIN

Query Match 45.5%; Score 15; DB 37; Length 270;
Best Local Similarity 94.1%; Pred. No. 1.02e-01;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 41 ttctactggaactcg 57
|||||||
Qy 12 TTCTACTGCTACTTCG 28

RESULT 10

LOCUS H53129 290 bp mRNA EST 20-SEP-1995
DEFINITION yq94f06.s1 Homo sapiens cDNA clone 202499 3' similar to gb:M64925
55 KD ERYTHROCYTE MEMBRANE PROTEIN (HUMAN);

ACCESSION H53129
NID 9933276
KEYWORDS EST.

SOURCE human clone=202499 primer=Promega -21ml3 library=Soares fetal liver
spleen INFUS vector=pf7T3D (Pharmacia) with a modified polylinker
host=DHI10B (ampicillin resistant) Reitel-Pac I Reite2=Eco RI Liver
and spleen from a 20 week-post conception male fetus. 1st strand
cDNA was primed with a Pac I - oligo(dT) primer [5'
AACTGAGAAATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 290)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality.

FEATURES

source Location/Qualifiers
1..290
/organism="Homo sapiens"
/clone="202499"
/note="human"
mRNA 72 a 61 c 62 g 64 t 31 others
ORIGIN

Query Match 45.5%; Score 15; DB 22; Length 290;
Best Local Similarity 72.0%; Pred. No. 1.02e-01;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 84 aagttncagtnaaaacqcttnc 108
|||||
Cp 26 AAGTACCAGTAGAAGCGTTTCG 2

RESULT 11

LOCUS H80521 299 bp mRNA EST 09-NOV-1995
DEFINITION yu76c03.s1 Homo sapiens cDNA clone 239716 3' similar to gb:M64925
55 KD ERYTHROCYTE MEMBRANE PROTEIN (HUMAN);

ACCESSION H80521

NID g1058610

KEYWORDS EST.

SOURCE human clone=239716 primer=Promega -21ml3 library=Soares fetal liver
spleen INFUS vector=pf7T3D (Pharmacia) with a modified polylinker
host=DHI10B (ampicillin resistant) Reitel-Pac I Reite2=Eco RI Liver
and spleen from a 20 week-post conception male fetus. 1st strand
cDNA was primed with a Pac I - oligo(dT) primer [5'
AACTGAGAAATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

Homo sapiens

ORGANISM
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 299)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence stops: 175

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

FEATURES Location/Qualifiers

source 1..299

/organism="Homo sapiens"

/clone="239716"

Mar 19 08:49

US-08-612-929-56.rst

13

NID
mRNA
BASE COUNT 81 a 62 c 61 g 68 t 27 others
ORIGIN
/note="human"
Query Match 45.5%; Score 15; DB 30; Length 299;
Best Local Similarity 76.0%; Pred. No. 1.02e-01;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 92 aagttgcagtnaaacgcttttc 116
||||| ||||| ||||| ||||| |||||
Cp 26 AAGTACCAGTAGAARACGGTTGCC 2

RESULT 12
LOCUS CEIK032CYR 303 bp mRNA EST 06-AUG-1994
DEFINITION C.elegans cDNA clone yk32c11 : 3' end, single read.
ACCESSION D33521
NID g524450
KEYWORDS EST (expressed sequence tag).
SOURCE Caenorhabditis elegans (strain CB1489 him-8(e1489)) (Library: Yuji Kohara unpublished cDNA) Hermaphrodite, male varied whole animal cDNA to mRNA.

ORGANISM
Caenorhabditis elegans
Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae.

REFERENCE 1 (bases 1 to 303)
AUTHORS Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and Tabara, H.
TITLE Toward an expression map of the C.elegans genome
JOURNAL Unpublished (1994)
COMMENT Submitted (1-Jul-1994) to DDBJ by: Yuji Kohara
National Institute of Genetics
Gene Library Lab
Yata 1111, Mishima
Shizuoka 411
Phone: 0559-75-0771
Fax: 0559-75-6240
Email: ykoha@dbj.nig.ac.jp.

FEATURES
source
Location/Qualifiers
1..303
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/dev_stage="varied"
/sequenced_mol="cDNA to mRNA"
/sex="Hermaphrodite, male"
/tissue_type="whole animal"
/clone_lib="Yuji Kohara unpublished cDNA"

BASE COUNT 94 a 71 c 36 g 92 t 10 others
ORIGIN

Query Match 45.5%; Score 15; DB 3; Length 303;
Best Local Similarity 88.9%; Pred. No. 1.02e-01;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 225 gtttctcgtggtcttc 242
||||||| ||||| |||||
Qy 10 GTTTCTACTGGTACTC 27

RESULT 13
LOCUS CEIK129D3R 318 bp mRNA EST 12-DEC-1995
DEFINITION C.elegans cDNA clone yk129d3 : 3' end, single read.
ACCESSION D64997

Mar 19 08:49

US-08-612-929-56.rst

14

NID g1117437
KEYWORDS EST (expressed sequence tag).
SOURCE Caenorhabditis elegans (strain CB1489 him-8(e1489)), (Library: Yuji Kohara unpublished cDNA) Hermaphrodite, male varied whole animal cDNA to mRNA.

ORGANISM
Caenorhabditis elegans
Eukaryota; Mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Caenorhabditis.

REFERENCE 1 (bases 1 to 318)
AUTHORS Kohara, Y., Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and Nishigaki, A.
TITLE Toward an expression map of the C.elegans genome
JOURNAL Unpublished (1995)
COMMENT Submitted (23-Aug-1995) to DDBJ by: Yuji Kohara
Gene Library Lab.
National Institute of Genetics
Yata 1111, Mishima Shizuoka 411 Japan
Phone: 0559-81-6854
Fax : 0559-81-6855
Email: ykoha@dbj.nig.ac.jp.

FEATURES
source
Location/Qualifiers
1..318
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/dev_stage="varied"
/sequenced_mol="cDNA to mRNA"
/sex="Hermaphrodite, male"
/tissue_type="whole animal"
/clone_lib="Yuji Kohara unpublished cDNA"

BASE COUNT 129 a 58 c 57 g 73 t 1 others
ORIGIN

Query Match 45.5%; Score 15; DB 6; Length 318;
Best Local Similarity 82.6%; Pred. No. 1.02e-01;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 104 tcaaaagtaccagtggaaacctgt 126
||||| ||||| ||||| ||||| |||||
Cp 29 TCGAAGTACCAGTAGAARACGGT 7

RESULT 14
LOCUS R36228 320 bp mRNA EST 02-MAY-1995
DEFINITION yh91c09.s1 Homo sapiens cDNA clone 1371104 3'.
ACCESSION R36228
NID g793129
KEYWORDS EST.
SOURCE human clone=1371104 library=Soares placenta Nb2HP vector=p7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=Promega -21m13 Reitel=Not I Reite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGATTTCGGCGCGAGGAATTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM
Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 320)

Mar 19 08:49

US-08-612-929-56.rst

15

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterson, R., Williamson, A., Wohldmann, P. and Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 272
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source
1..320
/organism="Homo sapiens"
/clone="137104"
/note="human"

BASE COUNT 90 a 45 c 77 g 107 t 1 others

ORIGIN

Query Match 45.5%; Score 15; DB 81; Length 320;
Best Local Similarity 82.6%; Pred. No. 1.02e-01;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 108 gaagtaacatttgaaactgttt 130
||||| || | ||||| |||||

Cp 27 GAAGTACCAGTAGAAGCGTTT 5

RESULT 15

LOCUS R76012 354 bp mRNA EST 06-JUN-1995

DEFINITION Y122d11.s1 Homo sapiens cDNA clone 158997 3'.

ACCESSION R76012

NTID q850694

KEYWORDS EST.

SOURCE
human clone=158997 library=Soares breast 2NBH8et vector=ptT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=Promega -2lm13 Rsite1=Not I Rsite2=Eco RI Adult female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

TITLE

The WashU-Merck EST Project

Mar 19 08:49

US-08-612-929-56.rst

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JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 118
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source
1..354
/organism="Homo sapiens"
/clone="158997"
/note="human"

BASE COUNT 103 a 80 c 99 g 59 t 13 others

ORIGIN

Query Match 45.5%; Score 15; DB 93; Length 354;
Best Local Similarity 79.2%; Pred. No. 1.02e-01;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 305 gaagacaagtgganaacgggttc 328
|||| | ||| | ||||| |||

Cp 27 GAAGTACCAGTAGAAGCGTTTC 4

Search completed: Wed Mar 19 08:50:38 1997
Job time : 81 secs.

OS Synthetic.
PN EP-571911-A.
PD 01-DEC-1993.
PF 24-MAY-1993; 108325.
PR 26-MAY-1992; US-889651.
PA (BECT) BECTON DICKINSON CO.
PI Shank DD, Spears PA;
DR WPI; 93-378844/48.
PT New oligo:nucleotide probes specific for Mycobacteria - used for
PT detection and amplification of Mycobacteria nucleic acid in
PT samples
PS Claim 3; Page 14; 23pp; English.
CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
CC (Q51735). It hybridized to all spp. of mycobacteria tested, but
CC cross reacted to a few non-mycobacterial spp. The probe may
CC be useful as an initial screen for mycobacterial infection.
CC See also Q51735-45 and Q51747-59.
SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 63.6%; Score 21; DB 9; Length 91;
Best Local Similarity 0.0%; Pred. No. 2.06e-02;
Matches 0; Conservative 26; Mismatches 5; Indels 0; Gaps 0;

Db 18 vhhvhhvhhvhhvhhvhhvhhvhhv 48
QY 1 CGCGAACCCTTTTCTACTGCTACTTCGACG 31

RESULT 5

ID Q51746 standard; cDNA; 91 BP.
AC Q51746;
DE 31-MAY-1994 (first entry)
DT Oligonucleotide probe MK14-A
KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
KW ss.
OS Synthetic.
PN EP-571911-A.
PD 01-DEC-1993.
PF 24-MAY-1993; 108325.
PR 26-MAY-1992; US-889651.
PA (BECT) BECTON DICKINSON CO.
PI Shank DD, Spears PA;
DR WPI; 93-378844/48.
PT New oligo:nucleotide probes specific for Mycobacteria - used for
PT detection and amplification of Mycobacteria nucleic acid in
PT samples
PS Claim 3; Page 14; 23pp; English.
CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
CC (Q51735). It hybridized to all spp. of mycobacteria tested, but
CC cross reacted to a few non-mycobacterial spp. The probe may
CC be useful as an initial screen for mycobacterial infection.
CC See also Q51735-45 and Q51747-59.
SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 63.6%; Score 21; DB 9; Length 91;
Best Local Similarity 0.0%; Pred. No. 2.06e-02;
Matches 0; Conservative 27; Mismatches 6; Indels 0; Gaps 0;

Db 28 vhhvhhvhhvhhvhhvhhvhhvhhv 60
CP 33 AACGTCGAGTACCACTAGAAAACGGTTCCG 1

RESULT 6
ID Q83492 standard; cDNA; 423 BP.
AC Q83492;
DT 20-SEP-1995 (first entry)
DE Chimeric antibody 3B9 heavy chain.
KW Chimeric antibody; antibody engineering; monoclonal antibody;
KW MAb; interleukin-4; IL-4; allergy; ds.
OS Homo sapiens; Mus sp.
FH Key Location/Qualifiers
FT CDS 1..423
FT /tag= a
FT sig_peptide 1..57
FT /tag= b
FT mat_peptide 58..423
FT /tag= c
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
DR WPI; 95-123387/16.
DR P-PSDB; R70191.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mAbs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.3; 97pp; English.
CC A human/mouse chimeric antibody heavy chain variable region was
CC constructed (given in R70191) that contained the mouse anti-human
CC IL-4 MAb 3B9 variable region including 3 CDRs (R70198-200) and a
CC human antibody signal peptide (R70193). The construct was used
CC for humanized antibody production.
SQ Sequence 423 BP; 87 A; 115 C; 110 G; 111 T;

Query Match 63.6%; Score 21; DB 14; Length 423;
Best Local Similarity 86.2%; Pred. No. 2.06e-02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 361 gagactgtgtctactgtacttcgatgt 389
QY 4 GAACCGTTTTCTACTGCTACTTCGACGT 32

RESULT 7
ID Q83491 standard; cDNA; 483 BP.
AC Q83491;
DT 20-SEP-1995 (first entry)
DE Mouse MAb 3B9 heavy chain.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 64..483
FT /tag= a
FT sig_peptide 64..120
FT /tag= b
FT mat_peptide 121..483
FT /tag= c
PN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.

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US-08-612-929-56.mg

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PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR P-PSDB; R70190.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Fig.2; 97pp; English.
 CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 CC chains were cloned into pCEM7f+ and transformed into E. coli
 CC DH5-alpha. The clones were sequenced (Q83490-91), and used for
 CC antibody engineering.
 SQ Sequence 483 BP; 108 A; 130 C; 124 G; 121 T;

Query Match 63.6%; Score 21; DB 14; Length 483;
 Best Local Similarity 86.2%; Pred. No. 2.06e-02;
 Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 421 gagactgttctactgtactgtactgtatgt 449

QY 4 GAAACCGTTTCTACTGGTACTTCGACGT 32

RESULT 8

ID Q11195 standard; DNA; 36 BP.
 AC Q11195;
 DT 05-JUN-1991 (first entry)
 DE Ballast Constituent coding sequence #2.
 KW Ballast constituent; fusion protein; oligonucleotide library; ss.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT repeat_unit 7..9
 FT /tag= a
 FT /note= "can be present 4 to 8 times"
 PN W09103550-A.
 PD 21-MAR-1991.
 PF 28-AUG-1990; U04840.
 PR 29-AUG-1989; US-399874.
 PA (FARH) HOECHST AG.
 PA (GEHO-) GEN HOSPITAL CORP.
 PI Stengel S, Ulmer W, Habermann P, Uhlmann E, Seed B;
 DR WPI; 91-102070/14.
 PT Prepn. of fusion proteins contg. ballast constituent and protein
 PT - giving prods. which are protease resistant or insoluble
 PS Claim 11; Page 50; 60pp; English.
 CC This oligonucleotide is an example of a member of an oligonucleotide
 CC library encoding ballast constituents. The oligonucleotides are
 CC inserted into a vector, functionally linked to a regulatory region
 CC and to a structural gene encoding a desired protein, e.g. proinsulin.
 CC Host cells transformed with such plasmids produce fusion proteins in
 CC high yield. The ballast is short and does not disturb the folding of
 CC the desired protein. The fusion protein is soluble or easily
 CC solubilised. The oligonucleotide encodes a cleavage site at its 3'
 CC end which allows easy removal of the ballast constituent.
 CC See also Q11194 and Q11196-Q11202.
 SQ Sequence 36 BP; 1 A; 11 C; 3 G; 1 T;

Query Match 60.6%; Score 20; DB 2; Length 36;
 Best Local Similarity 26.7%; Pred. No. 7.30e-02;
 Matches 8; Conservative 17; Mismatches 5; Indels 0; Gaps 0;

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Db 4 gwcddcdcdcdcdcdcdcdcdcdcdcdcd 33
 QY 2 GCGAAACCGTTTCTACTGGTACTTCGACG 31

RESULT 9

ID Q51785 standard; DNA; 30 BP.
 AC Q51785;
 DT 20-DEC-1993 (first entry)
 DE Mixed oligonucleotide #17 encodes ballast constituent.
 KW Fusion protein; ballast constituent; pro-insulin production;
 KW recombinant protein production; HMG CoA reductase;
 KW human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;
 KW mixed oligonucleotide; ss.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT repeat_unit 7..9
 FT /tag= a
 FT /rpt_type= tandem
 FT /note= "can be repeated 3-6 times"
 FT repeat_region 7..24
 FT /tag= b
 FT /note= "(DCD)6"
 PN US5227293-A.
 PD 13-JUL-1993.
 PF 29-AUG-1989; 399874.
 PR 29-AUG-1989; US-399874.
 PR 23-APR-1992; US-838221.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARH) HOECHST AG.
 PI Habermann P, Seed B, Stengel S, Uhlmann E, Ulmer W;
 DR WPI; 93-235119/29.
 PT Fusion proteins for prodn. of e.g. pro-insulin - comprise gene
 PT for desired protein and oligo-nucleotide (s) encoding ballast
 PT protein
 PS Claim 6; Column 30; 22pp; English.
 CC This preferred mixed oligonucleotide encodes a ballast constituent
 CC and is inserted between a regulatory region and the structural gene
 CC encoding pro-insulin. The short ballast component improves protease
 CC resistance of the fusion protein while still allowing the desired
 CC protein to adopt its correct conformation prior to cleavage of the
 CC ballast constituent.
 SQ Sequence 30 BP; 2 A; 9 C; 4 G; 2 T;

Query Match 57.6%; Score 19; DB 7; Length 30;
 Best Local Similarity 34.8%; Pred. No. 2.54e-01;
 Matches 8; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

Db 5 cddcdcdcdcdcdcdcdcdcdcdcdcdacg 27

QY 9 CGTTTCTACTGGTACTTCGACG 31

RESULT 10

ID Q11201 standard; DNA; 30 BP.
 AC Q11201;
 DT 05-JUN-1991 (first entry)
 DE Proinsulin Ballast Constituent-coding sequence #4.
 KW ballast constituent; fusion protein; oligonucleotide library;
 KW proinsulin; ss.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT repeat_unit 7..9


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FT /tag= a
FT /note= "can be present 3 to 6 times"
PN W09103550-A.
PD 21-MAR-1991.
PF 28-AUG-1990; U04840.
PR 29-AUG-1989; US-399874.
PA (FARH ) HOECHST AG.
PA (GEO-) GEN HOSPITAL CORP.
PI Stengelin S, Ulmer W, Habermann P, Uhlmann E, Seed B;
DR WPI; 91-102070/14.
PT Prepn. of fusion proteins contg. ballast constituent and protein
PT - giving prods. which are protease resistant or insoluble
PS Claim 13; Page 51; 60pp; English.
CC This oligonucleotide is an example of a member of an oligonucleotide
CC library encoding ballast constituents. The oligonucleotides are
CC inserted into a vector, functionally linked to a regulatory region
CC and to the proinsulin structural gene. Host cells transformed with
CC such plasmids produce proinsulin-ballast fusion proteins in
CC high yield. The ballast is short and does not disturb the folding of
CC the proinsulin. The fusion protein is soluble or easily
CC solubilised. The oligonucleotide encodes a cleavage site at its 3'
CC end which allows easy removal of the ballast constituent.
CC See also Q11194-Q11200 and Q11202.
SQ Sequence 30 BP; 2 A; 9 C; 4 G; 2 T;

Query Match 57.6%; Score 19; DB 2; Length 30;
Best Local Similarity 34.8%; Pred. No. 2.54e-01;
Matches 8; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

Db 5 cddcdcdcdcdcdcdcdcdcdacg 27
|:::|:::|:::|:::|:::|
QY 9 CGTTTCTACTGCTACTTCGACG 31

RESULT 11
ID Q11197 standard; DNA; 33 BP.
AC Q11197;
DT 05-JUN-1991 (first entry)
DE Ballast Constituent coding sequence #4.
KW Ballast constituent; fusion protein; oligonucleotide library; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT repeat_unit 7..9
FT /tag= a
FT /note= "can be present 4 to 7 times"
PN W09103550-A.
PD 21-MAR-1991.
PF 28-AUG-1990; U04840.
PR 29-AUG-1989; US-399874.
PA (FARH ) HOECHST AG.
PA (GEO-) GEN HOSPITAL CORP.
PI Stengelin S, Ulmer W, Habermann P, Uhlmann E, Seed B;
DR WPI; 91-102070/14.
PT Prepn. of fusion proteins contg. ballast constituent and protein
PT - giving prods. which are protease resistant or insoluble
PS Claim 12; Page 50; 60pp; English.
CC This oligonucleotide is an example of a member of an oligonucleotide
CC library encoding ballast constituents. The oligonucleotides are
CC inserted into a vector, functionally linked to a regulatory region
CC and to a structural gene encoding a desired protein, e.g. proinsulin.
CC Host cells transformed with such plasmids produce fusion proteins in
CC high yield. The ballast is short and does not disturb the folding of
CC the desired protein. The fusion protein is soluble or easily
CC solubilised. The oligonucleotide encodes a cleavage site at its 3'
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CC end which allows easy removal of the ballast constituent.
CC See also Q11194-6 and Q11198-Q11202.
SQ Sequence 33 BP; 2 A; 10 C; 3 G; 1 T;

Query Match 57.6%; Score 19; DB 2; Length 33;
Best Local Similarity 26.1%; Pred. No. 2.54e-01;
Matches 6; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

Db 8 cddcdcdcdcdcdcdcdcdcdcd 30
|:::|:::|:::|:::|:::|
QY 9 CGTTTCTACTGCTACTTCGACG 31

RESULT 12
ID Q46603 standard; DNA; 33 BP.
AC Q46603;
DT 20-DEC-1993 (first entry)
DE Mixed oligonucleotide #5 encodes ballast constituent.
KW Fusion protein; ballast constituent; pro-insulin production;
KW recombinant protein production; HMG CoA reductase;
KW human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;
KW mixed oligonucleotide; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT repeat_unit 7..9
FT /tag= a
FT /rpt_type= tandem
FT /note= "can be repeated 4-8 times"
FT repeat_region 7..30
FT /tag= b
FT /note= "(DCD)8"
PN US5227293-A.
PD 13-JUL-1993.
PF 29-AUG-1989; 399874.
PR 29-AUG-1989; US-399874.
PR 23-APR-1992; US-838221.
PA (GEO ) GEN HOSPITAL CORP.
PA (FARH ) HOECHST AG.
PI Habermann P, Seed B, Stengelin S, Uhlmann E, Ulmer W;
DR WPI; 93-235119/29.
PT Fusion proteins for prodn. of e.g. pro-insulin - comprise gene
PT for desired protein and oligo-nucleotide(s) encoding ballast
PT protein
PS Claim 4; Column 29; 22pp; English.
CC This preferred mixed oligonucleotide encodes a ballast constituent
CC and is inserted between a regulatory region and the structural gene
CC encoding a desired protein. The short ballast component improves
CC protease resistance of the fusion protein while still allowing the
CC desired protein to adopt its correct conformation prior to cleavage
CC of the ballast constituent. Proteins which can be produced as fusion
CC proteins with a ballast region include pro-insulin and HMG CoA
CC reductase.
SQ Sequence 33 BP; 1 A; 10 C; 3 G; 1 T;

Query Match 57.6%; Score 19; DB 7; Length 33;
Best Local Similarity 26.1%; Pred. No. 2.54e-01;
Matches 6; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

Db 8 cddcdcdcdcdcdcdcdcdcdcd 30
|:::|:::|:::|:::|:::|
QY 9 CGTTTCTACTGCTACTTCGACG 31

RESULT 13
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ID Q46605 standard; DNA; 48 BP.
 AC Q46605;
 DT 20-DEC-1993 (first entry)
 DE Mixed oligonucleotide (9a) encodes ballast constituent.
 KW Fusion protein; ballast constituent; monkey pro-insulin;
 KW recombinant protein production; HMG CoA reductase;
 KW human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;
 KW mixed oligonucleotide; ss.
 OS Synthetic.
 PN U55227293-A.
 PD 13-JUL-1993.
 PF 29-AUG-1989; 399874.
 PR 29-AUG-1989; US-399874.
 PR 23-APR-1992; US-838221.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARH) HOECHST AG.
 PI Habermann P, Seed B, Stengelin S, Uhlmann E, Ulmer W;
 PI WPI; 93-235119/29.
 DR Fusion proteins for prodn. of e.g. pro-insulin - comprise gene
 PT for desired protein and oligo-nucleotide(s) encoding ballast
 PT protein
 PS Example 1; Column 7; 22pp; English.
 CC Mixed oligonucleotide (9) (Q46604) encodes a ballast constituent
 CC and forms part of a fusion gene with the monkey pro-insulin gene;
 CC the double-stranded ballast constituent insert was prepared from
 CC the synthetic mixed oligonucleotide (9a) (Q46605) which was filled
 CC in with Klenow polymerase and cut with MluI and Nco. The genebank
 CC pINT4x contains the resulting plasmid population. After transforming
 CC E.coli WS3110 with the genebank, one clone (pINT41) was found to
 CC produce, in relatively large quantities, a protein containing an
 CC insulin constituent. The exact sequence of the pINT41 ballast
 CC constituent is given in Q51798.
 SQ Sequence 48 BP; 3 A; 9 C; 16 G; 7 T;

Query Match 57.6%; Score 19; DB 7; Length 48;
 Best Local Similarity 34.8%; Pred. No. 2.54e-01;
 Matches 8; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

Db 5 cgtghghghghghghghghg 27
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 Cp 31 CGTCGAGTACCAGTAGAAACG 9

RESULT 14
 ID Q46602 standard; DNA; 30 BP.
 AC Q46602;
 DT 20-DEC-1993 (first entry)
 DE Mixed oligonucleotide #4 encodes ballast constituent.
 KW Fusion protein; ballast constituent; pro-insulin production;
 KW recombinant protein production; HMG CoA reductase;
 KW human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;
 KW mixed oligonucleotide; ss.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT repeat unit 7..9
 FT /*tag= a
 FT /rpt_type= tandem
 FT /note= "can be repeated 4-8 times"
 FT repeat region 7..27
 FT /*tag= b
 FT /note= "(DCD) 7"
 PN U55227293-A.
 PD 13-JUL-1993.
 PF 29-AUG-1989; 399874.

PR 29-AUG-1989; US-399874.
 PR 23-APR-1992; US-838221.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARH) HOECHST AG.
 PI Habermann P, Seed B, Stengelin S, Uhlmann E, Ulmer W;
 DR WPI; 93-235119/29.
 PT Fusion proteins for prodn. of e.g. pro-insulin - comprise gene
 PT for desired protein and oligo-nucleotide(s) encoding ballast
 PT protein
 PS Claim 4; Column 29; 22pp; English.
 CC This preferred mixed oligonucleotide encodes a ballast constituent
 CC and is inserted between a regulatory region and the structural gene
 CC encoding a desired protein. The short ballast component improves
 CC protease resistance of the fusion protein while still allowing the
 CC desired protein to adopt its correct conformation prior to cleavage
 CC of the ballast constituent. Proteins which can be produced as fusion
 CC proteins with a ballast region include pro-insulin and HMG CoA
 CC reductase.
 SQ Sequence 30 BP; 1 A; 9 C; 3 G; 1 T;

Query Match 54.5%; Score 18; DB 7; Length 30;
 Best Local Similarity 25.0%; Pred. No. 8.62e-01;
 Matches 5; Conservative 14; Mismatches 1; Indels 0; Gaps 0;

Db 6 wdcddcdcdcdcdcdcdcd 25
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 QY 13 TTCTACTGGTACTTCGCGT 32

RESULT 15
 ID T12830 standard; cDNA; 363 BP.
 AC T12830;
 DT 10-OCT-1996 (first entry)
 DE Switched VL region kappa-body fragment hZCE-CSVL.
 KW Variable region; hZCE-CSVL; in vitro; in vivo;
 KW CDR switched variable light chain region; kappa-body fragment;
 KW diagnosis; therapy; naked antibody; radioimmunotherapy;
 KW radioimmunodiagnostics; radioimmunometric assays; ELISA;
 KW immunohistochemical; complementarity determining region; ss.
 OS Synthetic.
 PN W09606625-A1.
 PD 07-MAR-1996.
 PF 25-AUG-1995; U10791.
 PR 26-AUG-1994; US-296625.
 PA (ELIL) LILLY & CO ELI.
 PI Ill CR, Ludwig JR, Rathnachalam R;
 DR WPI; 96-160137/16.
 PT Recombinant antibody comprising CDR-switched light chain variable
 PT region - having VL domain framework and VH domain CDRs, useful in
 PT radioimmunotherapy, ELISA assays, etc.
 PS Example 11; Page 105; 162pp; English.
 CC The present sequence encodes the CDR switched light chain variable
 CC (VL) region (CSVL) kappa-body fragment, hZCE-CSVL. A CSVL comprises
 CC at least 1 VL region with 3 CDR, where 1 or more of the CDR is
 CC derived from the corresponding CDR of a heavy chain variable (VH)
 CC region of 1 (donor) Ab, and 4 framework (FW) regions where 1 or more
 CC of the regions is derived from the corresponding FW region(s) from
 CC the VL region of the same or different (acceptor) Ab.
 CC The CSVL Ab, or kappa-body fragment can be used in vitro and
 CC in vivo diagnostic and therapeutic applications, including naked Ab
 CC therapy, radioimmunotherapy (i.e. when fused to a chelating peptide
 CC incorporating Yttrium-90 as the therapeutic radioion), in vivo
 CC radioimmunodiagnostics, in vitro radioimmunometric assays, ELISA
 CC and immunohistochemical applications.

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SQ Sequence 363 BP; 74 A; 138 C; 86 G; 65 T;

Query Match 54.5%; Score 18; DB 22; Length 363;
Best Local Similarity 100.0%; Pred. No. 8.62e-01;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 315 ctactgggtacttcgacgt 332

|||||

Qy 15 CTACTGGGTACTTCGACGT 32

Search completed: Wed Mar 19 08:48:57 1997
Job time : 18 secs.

REFERENCE
AUTHORS
TITLE
The genes encoding the biotin carboxyl carrier protein and biotin carboxylase subunits of *Bacillus subtilis* acetyl coenzyme A carboxylase, the first enzyme of fatty acid synthesis
J. Bacteriol. 177 (23), 7003-7006 (1995)
96074336
2 (bases 1 to 1993)
Gornicki, P., Scappino, L.A. and Haselkorn, R.
Genes for two subunits of acetyl coenzyme A carboxylase of *Anabaena* sp. strain PCC 7120: biotin carboxylase and biotin carboxyl carrier protein
J. Bacteriol. 175 (16), 5268-5272 (1993)
93352435
3 (sites)
Norman, E., De Smet, K.A., Stoker, N.G., Ratledge, C., Wheeler, P.R. and Dale, J.W.
Lipid synthesis in mycobacteria: characterization of the biotin carboxyl carrier protein genes from *Mycobacterium leprae* and *M. tuberculosis*
J. Bacteriol. 176 (9), 2525-2531 (1994)
94222829
4 (bases 1 to 1993)
Marini, P.
Direct Submission
Submitted (13-SEP-1995) Patricia E. Marini, Prombie -Universidad De Rosario, Microbiologia, Suipacha 531, Rosario, Santa Fe, Argentina, 2000
Location/Qualifiers
1..1993
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FEATURES
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RBS

CDS

RBS

CDS

BASE COUNT 654 a 400 c 480 g 459 t
ORIGIN
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Best Local Similarity 88.0%; Pred. No. 6.64e-01;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 505 cgttgaagtattagtagaaacggt 529
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Cp 31 CGTCGAGTACCACTAGAGAAACGGT 7
RESULT 2
LOCUS S67978 53 bp mRNA ROD 15-MAR-1994
DEFINITION Ig VH81X-Ig heavy chain VDJ region [mice, BALB/c, liver, mRNA
Partial, 53 nt].
ACCESSION S67978
NID 9460843
KEYWORDS
SOURCE mice liver BALB/c.
ORGANISM Mus sp.
Unclassified.
REFERENCE 1 (bases 1 to 53)
AUTHORS Chukwocha, R.U. and Feeney, A.J.
TITLE Role of homology-directed recombination: predominantly productive
rearrangements of Vh81X in newborns but not in adults
JOURNAL Mol. Immunol. 30 (16), 1473-1479 (1993)
MEDLINE 94049838
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 142175] from the original journal article.
This sequence comes from Fig. 3.
Location/Qualifiers
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/translation="ARFSMTHTVTPSTGTSMS"
BASE COUNT 12 a 16 c 11 g 14 t
ORIGIN

FEATURES
source

CDS

BASE COUNT 12 a 16 c 11 g 14 t
ORIGIN

Query Match 54.5%; Score 18; DB 70; Length 53;
Best Local Similarity 95.0%; Pred. No. 2.93e+00;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 33 ttctactgttacttgatgt 52

||||| ||||| ||||| ||||| |||||
QY 13 TTCTACTGGTACTTCGACGT 32

RESULT 3
LOCUS HSB7G3D12 321 bp DNA PRI 24-JUL-1995
DEFINITION H.sapiens B7-g3D12 gene for immunoglobulin heavy chain variable
region.
ACCESSION X87022
NID g1052632
KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;
joining region; variable region.
SOURCE human.
ORGANISM Homo sapiens


```

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Sarcophrygii; Mammalia; Eutheria; Primates;
Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 321)
AUTHORS
Brezinschek, H.P.
TITLE
Direct Submission
JOURNAL
Submitted (05-MAY-1995) to the EMBL/GenBank/DBJ databases.
Brezinschek H.P., Department of Internal Medicine, Harold C.
Simmons Arthritis Research Center, University of Texas Southwestern
Medical Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8884, USA
2 (bases 1 to 321)
REFERENCE
Brezinschek, H.P., Brezinschek, R.I. and Lipsky, P.E.
AUTHORS
Analysis of the heavy chain repertoire of human peripheral B cells
using single-cell polymerase chain reaction
JOURNAL
J. Immunol. 155 (1), 190-202 (1995)
MEDLINE
95325588
FEATURES
source
Location/Qualifiers
1..321
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/tissue_type="blood"
/cell_type="B lymphocyte"
/cell_line="single B lymphocyte"
/rearranged
/chromosome="14"
V_region
1..321
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/note="VH3 family, 3-49RE"
BASE COUNT
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ORIGIN

Query Match 54.5%; Score 18; DB 52; Length 321;
Best Local Similarity 100.0%; Pred. No. 2.93e+00;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 294 ttctactggtactctga 311
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QY 12 TTCTACTGGTACTTCTGA 29

RESULT 4
LOCUS MUSIHC 414 bp mRNA ROD 05-MAY-1995
DEFINITION Mus musculus immunoglobulin heavy chain mRNA, 5' end of cds.
ACCESSION L41877
NID g798802
KEYWORDS immunoglobulin heavy chain.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
ORGANISM Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Wyomorpha; Muridae; Murinae.
REFERENCE
1 (bases 1 to 414)
AUTHORS Asakura, K., Miller, D.J., Foglia, R.J., Pease, L.R. and Rodriguez, M.
TITLE Oligodendrocyte-specific O1, O4, and HNK-1 monoclonal antibodies
are encoded by germ-line immunoglobulin genes
JOURNAL DNA (1995) In press
FEATURES
source
Location/Qualifiers
1..414
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
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/sequenced_mol="cDNA to mRNA"
1..>414
/codon_start=1
CDS
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/product="immunoglobulin heavy chain"
BASE COUNT
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ORIGIN

Query Match 54.5%; Score 18; DB 67; Length 414;
Best Local Similarity 95.0%; Pred. No. 2.93e+00;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 361 ttctactggtactctgagt 380
|||||
QY 13 TTCTACTGGTACTTTCGACGT 32

RESULT 5
LOCUS ANABCLSA 2169 bp DNA BCT 06-JUL-1993
DEFINITION Anabaena sp. ribulose 1,5-bisphosphate carboxylase/oxygenase large
subunit (rbcL) gene, complete cds; ribulose 1,5-bisphosphate
carboxylase/oxygenase small subunit (rbcS) gene, complete cds.
ACCESSION L02520
NID q142081
KEYWORDS RUBISCO; large subunit; rbcL gene; rbcS gene;
ribulose 1,5-bisphosphate carboxylase/oxygenase; small subunit.
SOURCE Anabaena sp. (strain PCC 7120) (library: PCC7120) DNA.
ORGANISM Prokaryota; Gracilicutes; Oxysphobacteria; Cyanobacteria;
Nostocales; Nostocaceae.
REFERENCE
1 (bases 1 to 2169)
AUTHORS Curtis, S.E. and Haselkorn, R.
TITLE Isolation and sequence of the gene for the large subunit of
ribulose-1,5-bisphosphate carboxylase from the cyanobacterium
Anabaena 7120
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80, 1835-1839 (1983)
REFERENCE
2 (bases 1 to 2169)
AUTHORS Nierzwiki-Bauer, S.A., Curtis, S.E. and Haselkorn, R.
TITLE Cotranscription of genes encoding the small and large subunits of
ribulose-1,5-bisphosphate carboxylase in the cyanobacterium
Anabaena 7120
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81, 5961-5965 (1984)
MEDLINE 85014888
REFERENCE
3 (bases 1 to 2169)
AUTHORS Larimer, F.W. and Soper, T.S.
TITLE Overproduction of Anabaena PCC7120 ribulose-bisphosphate
carboxylase/oxygenase in Escherichia coli
JOURNAL Gene 126, 85-92 (1993)
MEDLINE 93231541
FEATURES
Location/Qualifiers
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/strain="PCC 7120"
/sequenced_mol="DNA"
/tissue_lib="PCC7120"
23..28
-35_signal
/gene="rbcL"
/note="tac promoter"
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	/gene="rbcL"										
	/note="tac promoter"										
RBS	84...89										
	/gene="rbcL"										
	/evidence=experimental										
CDS	100...1530										
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	/function="catalytic subunit"										
	/evidence=experimental										
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	1553..1882										
	/gene="rbcS"										
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	/EC_number="4.1.1.39"										
	/codon_start=1										
	/function="structural subunit"										
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	/citation={2}										
	/transl_table=11										
	/product="ribulose 1,5-bisphosphate carboxylase/oxygenase small subunit"										
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BASE COUNT	600 a 512 c 459 g 598 t										
ORIGIN											
	Query Match 54.5%; Score 18; DB 16; Length 2169;										
	Best Local Similarity 90.9%; Pred. No. 2.93e+00;										
	Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;										
Db	282 gtccttactggtacttgacg 303										
Qy	10 GTTCTTACTGCTTCTGCAG 31										
RESULT	6										
LOCUS	ANABRCLSB 2285 bp DNA BCT 06-JUL-1993										
DEFINITION	Anabaena sp. ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, complete cds; ribulose 1,5-bisphosphate carboxylase/oxygenase small subunit (rbcS) gene, complete cds.										
ACCESSION	U02521										
NID	g142084										
KEYWORDS	RUBISCO; large subunit; rbcL gene; rbcS gene;										
	ribulose 1,5-bisphosphate carboxylase/oxygenase; small subunit.										
SOURCE	Anabaena sp. (strain PCC 7120) (library: PCC7120) DNA.										

ORGANISM	source
Anabaena sp.	Proc. Natl. Acad. Sci. U.S.A. 80, 1835-1839 (1983)
Prokaryotae; Gracilicutes; Oxyphotobacteria; Cyanobacteria; Nostocales; Nostocaceae.	
1 (bases 1 to 2285)	
Curtis, S.E. and Haselkorn, R.	
Isolation and sequence of the gene for the large subunit of ribulose-1,5-bisphosphate carboxylase from the cyanobacterium Anabaena 7120	
2 (bases 1 to 2285)	
Nierzwicki-Bauer, S.A., Curtis, S.E. and Haselkorn, R.	
Cotranscription of genes encoding the small and large subunits of ribulose-1,5-bisphosphate carboxylase in the cyanobacterium Anabaena 7120	
Proc. Natl. Acad. Sci. U.S.A. 81, 5961-5965 (1984)	
85014888	
3 (bases 1 to 2285)	
Larimer, F.W. and Soper, T.S.	
Overproduction of Anabaena PCC7120 ribulose-bisphosphate carboxylase/oxygenase in Escherichia coli	
Gene 126, 85-92 (1993)	
93231541	
Location/Qualifiers	
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45..50	
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84..89	
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104..433	
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446..1876	
/gene="rbcL"	
/standard_name="LSU"	
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/citation={1}	
/transl_table=11	
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large subunit"
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AYPLDIFEGSITNVLTYIVGNVFVKALRALRLIEDIRFPVAYIKTFQGPFGICQIYER
DKLNKGRPLLCCTIKPKLGLSANNYGRAVYECIRGGDLFTKDDENINSAPFORWRDR
FLFVADAITKAQAGTETKRGHYINVTAPTCEEMIKRAEYAKELKQP IIMHDYLTAGFT
ANNTLAWCRDNGLLIHRAMHAVIDROKNHGIHFRVLAKALRLSGGDHIHTGTWVG
KLEGCRTIMGEVDLLRENYVEQDKSRGIYFTQDWASIPGWAVASGGIHWHPALV
EIFGDDVILQFGGTLGHPGNARGATANRVALEACYQARNEGRLAREGNDVIREAA
KWSPELAVACELWKEIKFEFAMDTV"
BASE COUNT      637 a   558 c   516 g   574 t
ORIGIN
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Query Match      54.5%; Score 18; DB 16; Length 2285;
Best Local Similarity 90.9%; Pred. No. 2.93e+00;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 628 gtcttctactgtacttgagc 649
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Qy 10 GTTTTCTACTGCTACTTCGACG 31
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```
RESULT 7
LOCUS ANABCLSC 2695 bp DNA BCT 06-JUL-1993
DEFINITION Anabaena sp. ribulose 1,5-bisphosphate carboxylase/oxygenase large
subunit (rbcl) gene, complete cds; ribulose 1,5-bisphosphate
carboxylase/oxygenase small subunit (rbcs) gene, complete cds;
(rbcs) gene, complete cds.
ACCESSION L02522
NID g142087
KEYWORDS RUBISCO; large subunit; rbcl gene; rbcS gene;
ribulose 1,5-bisphosphate carboxylase/oxygenase; small subunit.
SOURCE Anabaena sp. (strain PCC 7120) (library: PCC7120) DNA.
ORGANISM Anabaena sp.
Prokaryotes; Gracillicutes; Oxyphotobacteria; Cyanobacteria;
Nostocales; Nostocaceae.
REFERENCE 1 (bases 1 to 2695)
AUTHORS Curtis, S.E. and Haselkorn, R.
TITLE Isolation and sequence of the gene for the large subunit of
ribulose-1,5-bisphosphate carboxylase from the cyanobacterium
Anabaena 7120
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80, 1835-1839 (1983)
REFERENCE 2 (bases 1 to 2695)
AUTHORS Nierzwickl-Bauer, S.A., Curtis, S.E. and Haselkorn, R.
TITLE Cotranscription of genes encoding the small and large subunits of
ribulose-1,5-bisphosphate carboxylase in the cyanobacterium
Anabaena 7120
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81, 5961-5965 (1984)
MEDLINE 85014888
REFERENCE 3 (bases 1 to 2695)
AUTHORS Larimer, F.W. and Soper, T.S.
TITLE Overproduction of Anabaena PCC7120 ribulose-bisphosphate
carboxylase/oxygenase in Escherichia coli
JOURNAL Gene 126, 85-92 (1993)
MEDLINE 93231541
FEATURES Location/Qualifiers
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/strain="PCC 7120"
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/tissue_lib="PCC7120"
23..28
/gene="rbcl"
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45..50 /gene="rbcl"
/note="tac promoter"
84..89 /gene="rbcl"
/evidence=experimental
100..1530 /gene="rbcl"
/standard_name="LSU"
/EC_number="4.1.1.39"
/codon_start=1
/function="catalytic subunit"
/evidence=experimental
/transl_table=11
/product="ribulose 1,5-bisphosphate carboxylase/oxygenase
large subunit"
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DKLNKGRPLLCCTIKPKLGLSANNYGRAVYECIRGGDLFTKDDENINSAPFORWRDR
FLFVADAITKAQAGTETKRGHYINVTAPTCEEMIKRAEYAKELKQP IIMHDYLTAGFT
ANNTLAWCRDNGLLIHRAMHAVIDROKNHGIHFRVLAKALRLSGGDHIHTGTWVG
KLEGCRTIMGEVDLLRENYVEQDKSRGIYFTQDWASIPGWAVASGGIHWHPALV
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2079..2408
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/evidence=experimental
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VHKPSRY"
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BASE COUNT      770 a   628 c   570 g   727 t
ORIGIN
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Query Match      54.5%; Score 18; DB 16; Length 2695;
Best Local Similarity 90.9%; Pred. No. 2.93e+00;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 282 gtcttctactgtacttgagc 303
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```
Qy 10 GTTTTCTACTGCTACTTCGACG 31
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RESULT	LOCUS	3429 bp	DNA	BCT	14-SEP-1992
DEFINITION	Anabaena sp. (clone pAM600)	rbcL & rbcS genes encoding both ribulose-1,5-bisphosphate carboxylase subunits, complete cds.			
ACCESSION	J01540				
NID	g142104				
KEYWORDS	carboxylase; ribulose biphosphate carboxylase.				
SOURCE	Anabaena sp. (library: PCC 7120) DNA.				
ORGANISM	Anabaena sp.				
	Prokaryotae; Gracilicutes; Oxyphotobacteria; Cyanobacteria; Nostocales; Nostocaceae.				
REFERENCE	1 (bases 511 to 2363)				
AUTHORS	Curtis, S.E. and Haselkorn, R.				
TITLE	Isolation and sequence of the gene for the large subunit of ribulose-1,5-bisphosphate carboxylase from the cyanobacterium Anabaena 7120				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 80, 1835-1839 (1983)				
REFERENCE	2 (bases 1 to 720; 2055 to 3429)				
AUTHORS	Nierzwick-Bauer, S.A., Curtis, S.E. and Haselkorn, R.				
TITLE	Cotranscription of genes encoding the small and large subunits of ribulose-1,5-bisphosphate carboxylase in the cyanobacterium Anabaena 7120				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 81, 5961-5965 (1984)				
MEDLINE	85014888				
REFERENCE	3 (bases 1 to 720)				
AUTHORS	Nierzwick-Bauer, S.A., Curtis, S.E. and Haselkorn, R.				
TITLE	Cotranscription of genes encoding the small and large subunits of ribulose-1,5-bisphosphate carboxylase in the cyanobacterium Anabaena 7120; Correction				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 82, 1568-1568 (1985)				
COMMENT	rbcL [2] was formerly designated rbcA [1]. The two genes appear to be cotranscribed, beginning with the mRNA start given in the FEATURES TABLE and ending with a potential termination site (hairpin and poly-T, bases 3061-3092) downstream of the rbcS stop codon [1].				
	revision 474 505	aagaa...22 bp...aaaag in [3]; ag in [2]			
	revision 564 595	ctaaa...22 bp...gtcgc in [1], [3]; cc in [2]			
	revision 655 686	gtgag...22 bp...tttga in [1], [3]; ga in [2].			
FEATURES	Location/Qualifiers				
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	/note="contains the rbcL and rbcS genes"				
	721..2151				
	/gene="rbc"				
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	/transl_table=11				
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mRNA					
CDS					

CDS	KLEGGRTMGVDLIRENYVEQDKRGIFYFTQDWSLSPGMWVASGGTWHVHPALP EIFGDDFVLAQGGGTGLCHPGWNGARGATNRVVALEACVQARNEGNIAREGNDVITREAA KWSPELAVACELWKEIKEFEFAMDTV" 2700...3029 /gene="ribulose-1,5-bisphosphate carboxylase small subunit (rbcS)" /codon_start=1 /transl_table=11 /db_xref="PID:g142106" /translation="MOTLPPKRRYETLSYLPPLTDVIEKQVQVILSQGYTPAVERNEF VSEPTLYMTLWKLPLFGAKTSREVLAEVQSCRQYPGHYIRVVGFNDIKQQLILSI VHKPSRY"			
BASE COUNT	1046 a	730 c	721 g	932 t
ORIGIN	79 bp upstream of HinfI site.			
Query Match	54.58; Score 18; DB 16; Length 3429;			
Best Local Similarity	90.9%; Pred. No. 2.93e+00;			
Matches	20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Db	903 gtcttctactgttacttgagc 924 Qy 10 GTTTCTACTGCTACTTCGACG 31			
RESULT	9			
LOCUS	PVTAT4G 4546 bp DNA INV 05-MAY-1995			
DEFINITION	P.vulgata alpha-tubulin-4 gene.			
ACCESSION	X77618			
NID	9454314			
KEYWORDS	alpha-tubulin #4; alpha-tubulin gene.			
SOURCE	common limpet.			
ORGANISM	Patella vulgata Eukaryota; Animalia; Eumetazoa; Mollusca; Gastropoda; Prosobranchia; Archaeogastropoda; Patelliidae. 1 (bases 1 to 4546) Damen,W.G., van Grunsven,L.A. and van Loon,A.E. Transcriptional regulation of tubulin gene expression in differentiating trochoblasts during early development of Patella vulgata Development 120 (10), 2835-2845 (1994) 95331123 2 (bases 1 to 4546) Damen,W.G.M. Direct Submission Submitted (09-FEB-1994) to the EMBL/GenBank/DBJ databases. W.G.M. Damen, Utrecht University, Dept of Experimental Zoology, Padualaan 8, 3584 CH Utrecht, NETHERLANDS Location/Qualifiers source 1..4546 /organism="Patella vulgata" /clone_lib="lambda EMBL3A genomic library" TATA_signal 1127..1134 /gene="alpha tubulin-4" join(1157..1258,1618..>2970) /gene="alpha tubulin-4" /product="alpha tubulin" 1157..1258 /number=1 /product="alpha tubulin" join(1256..1258,1618..2973) /gene="alpha tubulin-4" /codon_start=1 /product="alpha tubulin"			
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
source				
TATA_signal				
mRNA				
exon				
CDS				

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YARGHYTVYGRKIIDLVDRIRKLDQCTGACGLIFHSFGGTSGSGSSLMERLSVD
YCKSKLEAFIYPAPOISTAVVEP YNSILTTHTTLEHSDCAFMVDNEAIYDTCRRNLD
IERPTYNNRLRLGQIVSSITASIRFDGALNVDLTQEQNNLVPYPRIFHEFLATYAPVI
SAKAYVHQLTVAEITNACFEFANQVMDPRHGKYMSCMLYRGDVPVKNVAAIAT
IKTKRTIOFQWPCFTGKGVINQYPTTVVPGGDLAKVRQVCMLSNTTAIAEAWARLD
HKFDLMYAKRAFYHWYVCGMEGEESEAREDLAALKDYEEVGVDSVEGEEGEEGEE
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Intron 1259..1617
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exon 1618..>2970
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/gene="alpha tubulin-4"
polyA_signal 3369..3399
/gene="alpha tubulin-4"
polyA_signal 3436..3442
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BASE COUNT 1430 a 875 c 903 g 1338 t
ORIGIN

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Best Local Similarity 80.0%; Pred. No. 2.93e+00;
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Db 4043 gcgaactgtttctgtgggtatttcaacg 4072
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Qy 2 CGGAACCGTTTTCTACTGCTACTTCGACG 31

RESULT 10
LOCUS SPU23729 44913 bp DNA PLN 12-APR-1995
DEFINITION Schizosaccharomyces pombe cosmid 855, complete sequence.
ACCESSION U23729
NID g763539
KEYWORDS
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
Eukaryotae; mitochondrial eukaryotes; eukaryote crown group;
Metazoa/Eumycota group; Eumycota; Ascomycotina; Archaeascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.

REFERENCE 1 (bases 1 to 44913)
AUTHORS CSLH,Advanced Genome Sequencing Course.
TITLE Sequence of a 44.9 kb cosmid insert determined during a two week course

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 44913)
AUTHORS McCombie,W.R.

TITLE Direct Submission
JOURNAL Submitted (28-MAR-1995) W. Richard McCombie, Cold Spring Harbor
Labs, 1 Bungtown Road, Cold Spring Harbor, NY 11724

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/organism="Schizosaccharomyces pombe"
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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 11577 gaattaccagtagtaaacggtt 11598
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Cp 27 GAAGTACCAGTAGAAGCGGTT 6

RESULT 11
LOCUS BACJH642 282700 bp DNA BCT 02-MAY-1996
DEFINITION Bacillus subtilis DNA.
ACCESSION D84432

NID g1303696
KEYWORDS
LybA; SpoVAF; SpoVAE; SpoVAD; SpoVAC; SpoVAB; SpoVAA; SpoIIAC;
spoIIAB; spoIIAA; DacF; YqkQ; YqkN; YqkM; YqkL; SpoIIM; YqkK;
YqkJ; YqkI; AnaB; AnaA; AnaR; YqkH; YqkG; YqkE; YqkD; YqkC;
YqkB; YqkA; YqJY; YqJX; YqJW; YqJV; YqJU; YqJT; YqJS; YqJR;
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YqJF; YqJE; YqJD; YqJC; YqJB; YqJN; YqIZ; YqIV; YqIX; YqIW; BarD;
Bmr; BmrB; BmrB; BmrB; BmrB; YqIV; YqIU; YqIT; YqIS; YqIR;
YqIQ; YqIP; YqIO; YqIN; YqIM; YqIL; YqIK; YqIU; YqII; YqIH; YqIG;
Spo0A; SpoIIVB; RecN; AhrC; YqIF; YqIE; YqID; YqIC; YqIB; YqIA;
YqBZ; YqNV; YqNX; YqNW; SpoIIAH; SpoIIAG; SpoIIAF; SpoIIAE;
SpoIIAD; SpoIIAC; SpoIIIB; SpoIIIAA; YqHV; YqHU; YqHT; YqHS;
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Cdd; DgKA; YqFG; YqFI; YqFE; YqFD; YqFC; YqFB; YqFA; YqE2; YqE1;
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YqEL; YqEK; YqEJ; YqEI; Arod; YqEH; YqEG; YqEF; YqED; YqEC;
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YrkS; YrkR; YrkP; YrkQ; YrkK; YrkN; YrkL; YrkM; YrkK; YrkJ; YrkI;
YrkH; YrkG; YrkF; YrkE; YrkD; YrkC; YrkB; YrkA; Yrk; BltR; Blt; Bld.
Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA.
Bacillus subtilis

ORGANISM

Eubacteria; Firmicutes; Low G+C gram-positive bacteria;
Bacillaceae; Bacillus.

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (16-APR-1996) to the DDBJ/EMBL/GenBank databases. Yasuo Kobayashi, Tokyo University of Agriculture and Technology, Applied Biological Science, 3-5-8 Saiwai-cho, Fuchu, Tokyo 183, Japan (E-mail:ykobaya@cc.tuat.ac.jp, Tel:81-423-67-5706, Fax:81-423-67-5715)

REFERENCE

AUTHORS

2 (bases 1 to 282700)
Kobayashi,Y., Mizuno,M., Masuda,S., Takemaru,K., Hosono,S., Sato,T.
and Takeuchi,M.

TITLE

Systematic sequencing of the 283 Kb region of the Bacillus subtilis genome containing the skin element

JOURNAL

COMMENT

FEATURES

source

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/strain="JH642(trpC2 PheA1)"
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GIRMPFFFAALITAAVTSVFLIKESLSTEERHQLSSHTKSNF IKOLKRSIHPVVF
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RBS

CDS

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2757..3578
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RBS

RBS

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RBS

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Mar 19 08:46

US-08-612-929-56.rge

21

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Best Local Similarity 87.5%; Pred. No. 2.93e+00;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 187816 cgttgaagtattagtagaaacgg 187839
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Cp 31 CGTCGAAGTACCAGTACAAAACGG 8

RESULT 13
LOCUS S60819 54 bp DNA ROD 07-JUL-1993
DEFINITION VH7183=immunoglobulin heavy chain V-D-J region (clone FL12,
non-functional rearrangement) [mice, BALB/c, large bone marrow
pre-B cells, Genomic, 54 nt].
ACCESSION S60819
NID g300379
KEYWORDS .
SOURCE mice BALB/c large bone marrow pre-B cells.
ORGANISM Mus sp.
Unclassified.
REFERENCE 1 (bases 1 to 54)
AUTHORS Huetz,F., Carlsson,L., Tornberg,U.C. and Holmberg,D.
TITLE V-region directed selection in differentiating B lymphocytes
JOURNAL EMBO J. 12 (5), 1819-1826 (1993)
MEDLINE 93259123
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibseq 131677] from the original journal article.
This sequence comes from Fig. 4.
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/organism="Mus sp."
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Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 14 TCTACTGGTACTTCGCGT 32

RESULT 14
LOCUS MUSIGHUHAJ 214 bp DNA ROD 10-SEP-1991
DEFINITION Mouse Ig rearranged heavy-chain gene V-D-J region, isolate 12SP12.
ACCESSION M73852
NID g197806
KEYWORDS D-region; J-region; V-region; immunoglobulin heavy chain;
rearranged gene.
SOURCE Mus musculus adult spleen DNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 214)
AUTHORS Decker,D.J., Boyle,N.E. and Klinman,N.R.
TITLE Predominance of nonproductive rearrangements of V-H81X gene
segments evidences a dependence of B cell clonal maturation on the
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Mar 19 08:46

US-08-612-929-56.rge

22

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structure of nascent H chains
J. Immunol. 147, 1406-1411 (1991)
MEDLINE 91332457
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Best Local Similarity 94.7%; Pred. No. 1.24e+01;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 192 tctactgtacttcgatgt 210
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Qy 14 TCTACTGGTACTTCGCGT 32

RESULT 15
LOCUS MUSIGHUHP 229 bp DNA ROD 10-SEP-1991
DEFINITION Mouse Ig rearranged heavy-chain gene V-D-J region, isolate 12SP18.
ACCESSION M73858
NID g197812
KEYWORDS D-region; J-region; V-region; immunoglobulin heavy chain;
rearranged gene.
SOURCE Mus musculus adult spleen DNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 229)
AUTHORS Decker,D.J., Boyle,N.E. and Klinman,N.R.
TITLE Predominance of nonproductive rearrangements of V-H81X gene
segments evidences a dependence of B cell clonal maturation on the
structure of nascent H chains
J. Immunol. 147, 1406-1411 (1991)
MEDLINE 91332457
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Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 200 gtctctactgtacttcgatgt 222
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Qy 10 GTTTTCTACTGGTACTTCGCGT 32

Search completed: Wed Mar 19 08:48:20 1997
Job time : 74 secs.
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Mar 18 10:13

US-08-612-929-24.fsp

3

Qy 2 IYWDKRYNPSIKS 16
:|||||:|||||

RESULT 2

ID HV2B HUMAN STANDARD; PRT; 125 AA.
AC P01817;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-II REGION (MCE).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 81118242.
RA GERBER-JENSON B., KAZIN A., KEHOE J.M., SCHEFFEL C., ERICKSON B.W.,
RA LITMAN G.W.;
RL J. IMMUNOL. 126:1212-1216(1981).
CC -/- THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM CRYOIMMUNOGLOBULIN.
DR PIR; A02092; MHUMC.
DR HSSP; P01772; IFGV.
KW IMMUNOGLOBULIN V REGION.
FT MOD_RES 1 1
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 13783 MW; 7F897793 CRC32;

Query Match 71.9%; Score 92; DB 4; Length 125;
Best Local Similarity 73.3%; Pred. No. 6.06e-06;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 53 inwdddkrypslrs 67
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Qy 2 IYWDKRYNPSIKS 16

RESULT 3

ID HV2B HUMAN STANDARD; PRT; 120 AA.
AC P01815;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-II REGION (COR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 70258837.
RA PRESS E.M., HOGG N.M.;
RL BIOCHEM. J. 117:641-660(1970).
CC -/- THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.
DR PIR; A02089; GIHUCO.
DR HSSP; P01789; 2FGW.
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT MOD_RES 1 1
FT DISULFID 22 94
FT CARBOHYD 62 62
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13226 MW; D690F656 CRC32;

Query Match 53.9%; Score 69; DB 4; Length 120;
Best Local Similarity 62.5%; Pred. No. 1.47e-01;

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Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 52 ridwdddkryntslet 67

Qy 1 HIYWDKRYNPSIKS 16
:|||||:|||||

RESULT 4

ID YJFC ECOLI STANDARD; PRT; 387 AA.
AC P33222;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 45.0 KD PROTEIN IN VAC-AIDB INTERGENIC REGION (0387).
GN YJFC.
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE; 95334362.
RA BURLAND V.D., PLUNKETT G. III, SOFIA H.J., DANIELS D.L.,
RA BLATTNER F.R.;
RL NUCLEIC ACIDS RES. 23:2105-2119(1995).
RN [2]
RP SEQUENCE OF 208-387 FROM N.A.
RC STRAIN=K12;
RX MEDLINE; 95050217.
RA LANDINI P., HAJEC L.I., VOLKERT M.R.;
RL J. BACTERIOL. 176:6583-6589(1994).
CC -/- SIMILARITY: STRONG, TO THE N-TERMINAL OF E.COLI GSP AND TO E.COLI
CC YGIC.
DR EMBL; U14003; G537027; -.
DR EMBL; L20915; G304861; -.
DR ECOGENE; EG11812; YJFC.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 387 AA; 45019 MW; 358B5D1B CRC32;

Query Match 52.3%; Score 67; DB 10; Length 387;
Best Local Similarity 42.9%; Pred. No. 3.28e-01;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 30 iywdestayzftlr 43

Qy 2 IYWDKRYNPSIK 15
:||||:|:|:

RESULT 5

ID HV2H HUMAN STANDARD; PRT; 147 AA.
AC P04438;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-II REGION (SESS).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84298107.
RA TAKAHASHI N., NOMA T., HONJO T.;
RL PROC. NATL. ACAD. SCI. U.S.A. 81:5194-5198(1984).
DR PIR; A02090; G2HUUS.

[illegible]

FT	CARBOHYD	313	313	POTENTIAL.
FT	CARBOHYD	377	377	POTENTIAL.
FT	CARBOHYD	434	434	POTENTIAL.
FT	CONFLICT	422	422	F -> V (IN REF. 2).
SQ	SEQUENCE	560 AA; 63818 MW; 44D98FDE CRC32;		
Query Match 49.2%; Score 63; DB 5; Length 560;				
Best Local Similarity 28.6%; Pred.No. 1.57e+00;				
Matches 4; Conservative 6; Mismatches 4; Indels 0; Gaps 0;				
Db	317 fwisekefntemkt	330		
Qy	3 YWDDKRYNPSIKS	16		
RESULT 7				
ID	NDDB_RAT	STANDARD;	PRT;	204 AA.
AC	P06300;			
DT	01-JAN-1988 (REL. 06, CREATED)			
DT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)			
DT	01-AUG-1990 (REL. 15, LAST ANNOTATION UPDATE)			
DE	BETA-NEOENDORPHIN-DYNORPHIN PRECURSOR (PROENKEPHALIN B PRECURSOR)			
DE	(FRAGMENT).			
OS	RATTUS NORVEGICUS (RAT).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=HYPOTHALAMUS;			
RX	MEDLINE; 85216680.			
RA	CIVELLI O., DOUGLASS J., GOLDSTEIN A., HERBERT E.;			
RA	PROC. NATL. ACAD. SCI. U.S.A. 82:4291-4295(1985).			
DR	EMBL; M10088; G204040; --.			
DR	PIR; A01480; DFRTF.			
KW	OPIOID PEPTIDE; NEUROTRANSMITTER; HYPOTHALAMUS; NEUROPEPTIDE;			
KW	ENDORPHIN; CLEAVAGE ON PAIR OF BASIC RESIDUES.			
FT	NON_TER	1		
FT	PEPTIDE	122	130	ALPHA-NEOENDORPHIN.
FT	PEPTIDE	122	126	LEU-ENKEPHALIN 1.
FT	PEPTIDE	158	174	DYNORPHIN A.
FT	PEPTIDE	158	162	LEU-ENKEPHALIN 2.
FT	PEPTIDE	177	204	DYNORPHIN B.
FT	PEPTIDE	177	181	LEU-ENKEPHALIN 3.
SQ	SEQUENCE	204 AA; 23386 MW; 3B451063 CRC32;		
Query Match 48.4%; Score 62; DB 6; Length 204;				
Best Local Similarity 50.0%; Pred.No. 2.31e+00;				
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;				
Db	171 wdnqkrygfflr	182		
Qy	4 WDDDKRYNPSIK	15		
RESULT 8				
ID	NDDB_HUMAN	STANDARD;	PRT;	254 AA.
AC	P01213;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)			
DE	BETA-NEOENDORPHIN-DYNORPHIN PRECURSOR (PROENKEPHALIN B PRECURSOR).			
GN	PDYN.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			

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Best Local Similarity 50.0%; Pred. No. 2.31e+00;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 222 wdnkryggflr 233
||:|||||
Qy 4 WDDDKRYNPSIK 15

RESULT 10

ID GLRI HUMAN STANDARD; PRT; 906 AA.
AC P42261;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GLUTAMATE RECEPTOR 1 PRECURSOR (GLUR-1) (GLUR-A) (GLUR-K1) (GLUTAMATE RECEPTOR, IONOTROPIC, AMPA 1).
GN GRIAL OR GLUR1 OR GLUH1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92159065.
RA SUN W., FERRER-MONTIEL A.V., SCHINDER A.F., MCPHERSON J.P.,
RA EVANS G.A., MONTAL M.,
RA PROC. NATL. ACAD. SCI. U.S.A. 89:1443-1447 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HIPPOCAMPUS;
RX MEDLINE; 92329975.
RA POTIER M.C., SPILLANTINI M.G., CARTER N.P.;
RL DNA SEQ. 2:211-218 (1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91352027.
RA PUCKETT C., GOMEZ C.M., KORENBERG J.R., TUNG H., MEIER T.J.,
RA CHEN X.N., HOOD L.E.;
RL PROC. NATL. ACAD. SCI. U.S.A. 88:7557-7561 (1991).
CC -!- FUNCTION: L-GLUTAMATE ACTS AS AN EXCITATORY NEUROTRANSMITTER AT MANY SYNAPSES IN THE CENTRAL NERVOUS SYSTEM. THE POSTSYNAPTIC ACTIONS OF GLU ARE MEDIATED BY A VARIETY OF RECEPTORS THAT ARE NAMED ACCORDING TO THEIR SELECTIVE AGONISTS.
CC -!- THIS RECEPTOR BINDS AMPA (QUISQUALATE) > GLUTAMATE > KAINATE.
CC -!- ALTERNATIVE PRODUCTS: THIS RECEPTOR EXISTS IN TWO VERSIONS (FLOP, SHOWN HERE) AND FLIP, WHICH DIFFER IN A REGION IN FRONT OF TM4.
CC THE TWO FORMS ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN BRAIN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; M81886; G179442; -.
DR EMBL; X58633; G414893; -.
DR EMBL; M64752; G183281; -.
DR MIM; 138248; 11TH EDITION.
KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 906 GLUTAMATE RECEPTOR A.
FT DOMAIN 19 536 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 537 557 POTENTIAL.
FT TRANSMEM 585 605 POTENTIAL.
FT TRANSMEM 618 638 POTENTIAL.
FT TRANSMEM 806 826 POTENTIAL.
FT VARSPLIC 758 758 N -> G (IN FLIP).

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OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84068211.
RA HORIKAWA S., TAKAI T., TOYOSATO M., TAKAHASHI H., NODA M.,
RA KAKIDANI H., KUBO T., HIROSE T., INAYAMA S., HAYASHIDA H., MIYATA T.,
RA NUMA S.;
RL NATURE 306:611-614 (1983).
DR EMBL; X02536; -; NOT ANNOTATED CDS.
DR EMBL; K02267; -; NOT ANNOTATED CDS.
DR EMBL; K02268; G182105; -.
DR EMBL; X00176; G182105; JOINED.
DR EMBL; X00176; G31155; -.
DR PIR; A01478; DFHU.
DR MIM; 131340; 11TH EDITION.
KW OPIOID PEPTIDE; NEUROTRANSMITTER; HYPOTHALAMUS; NEUROPEPTIDE;
KW ENDORPHIN; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
FT SIGNAL 1 20
FT PEPTIDE 175 183 BETA-NEOENDORPHIN.
FT PEPTIDE 207 223 DYNORPHIN.
FT PEPTIDE 226 230 LEO-ENKEPHALIN.
FT PEPTIDE 226 238 RIMORPHIN.
FT PEPTIDE 226 254 LEUMORPHIN.
SQ SEQUENCE 254 AA; 28385 MW; 49A11156 CRC32;

Query Match 48.4%; Score 62; DB 6; Length 254;
Best Local Similarity 50.0%; Pred. No. 2.31e+00;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 220 wdnkryggflr 231
||:|||||
Qy 4 WDDDKRYNPSIK 15

RESULT 9

ID NDB PIG STANDARD; PRT; 256 AA.
AC P01214;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE BETA-NEOENDORPHIN-DYNORPHIN PRECURSOR (PROENKEPHALIN B PRECURSOR).
OS SUS SCROFA (PIC).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOTHALAMUS;
RX MEDLINE; 82220112.
RA KAKIDANI H., FURUTANI Y., TAKAHASHI H., NODA M., MORIMOTO Y.,
RA HIROSE T., ASAI M., INAYAMA S., NAKANISHI S., NUMA S.;
RL NATURE 298:245-249 (1982).
DR EMBL; V01362; G1944; -.
DR PIR; A01479; DFPG.
KW OPIOID PEPTIDE; NEUROTRANSMITTER; HYPOTHALAMUS; NEUROPEPTIDE;
KW ENDORPHIN; CLEAVAGE ON PAIR OF BASIC RESIDUES; SIGNAL.
FT SIGNAL 1 20
FT PEPTIDE 175 183 BETA-NEOENDORPHIN.
FT PEPTIDE 209 225 DYNORPHIN.
FT PEPTIDE 228 232 LEO-ENKEPHALIN.
FT VARIANT 147 147 G -> E.
FT VARIANT 197 197 R -> G.
SQ SEQUENCE 256 AA; 28616 MW; 9427FFC4 CRC32;

Query Match 48.4%; Score 62; DB 6; Length 256;

FT VARSPLIC 768 768 N -> S (IN FLIP).
FT VARSPLIC 772 772 L -> V (IN FLIP).
FT VARSPLIC 778 778 N -> S (IN FLIP).
FT VARSPLIC 790 793 GCGD -> KDSG (IN FLIP).
FT CONFLICT 345 345 R -> A (IN REF. 2).
FT CONFLICT 375 375 S -> G (IN REF. 2 AND 3).
FT CONFLICT 863 863 S -> SA (IN REF. 3).
FT CONFLICT 865 867 AGA -> TAP (IN REF. 3).
SQ SEQUENCE 906 AA; 101536 MW; 703BEF31 CRC32;

Query Match 47.7%; DB 4; Length 906;
Best Local Similarity 36.4%; Pred. No. 3.36e+00;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 381 yneddkfvpa 391
||:| :| :|
Qy 3 YWDDKRYNPS 13

RESULT 11
ID GLRI MOUSE STANDARD; PRT; 907 AA.
AC P23818;
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GLUTAMATE RECEPTOR 1 PRECURSOR (GLUR-1) (GLUR-A) (GLUR-K1).
GN GR1AL OR GLUR1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91032147.
RA SAKIMURA K., BUJO H., KUSHIYA E., ARAKI K., YAMAZAKI M.,
RA MEGURO H., WARASHINA A., NUMA S., MISHINA M.;
RL FEBS LETT. 272:73-80(1990).
CC -|- FUNCTION: L-GLUTAMATE ACTS AS AN EXCITATORY NEUROTRANSMITTER AT
CC MANY SYNAPSES IN THE CENTRAL NERVOUS SYSTEM. THE POSTSYNAPTIC
CC ACTIONS OF GLU ARE MEDIATED BY A VARIETY OF RECEPTORS THAT ARE
CC NAMED ACCORDING TO THEIR SELECTIVE AGONISTS.
CC -|- THIS RECEPTOR BINDS AMPA (QUISQUALATE) > GLUTAMATE > KAINATE.
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -|- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; X57497; G51080; -.
DR PIR; S12874; S12874.
KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
KW TRANSMEMBRANE.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 907 GLUTAMATE RECEPTOR 1.
FT DOMAIN 19 538 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 539 558 POTENTIAL.
FT TRANSEM 585 603 POTENTIAL.
FT TRANSEM 614 632 POTENTIAL.
FT TRANSEM 806 826 POTENTIAL.
FT CARBOHYD 63 63 POTENTIAL.
FT CARBOHYD 249 249 POTENTIAL.
FT CARBOHYD 257 257 POTENTIAL.
FT CARBOHYD 363 363 POTENTIAL.
FT CARBOHYD 401 401 POTENTIAL.
FT CARBOHYD 406 406 POTENTIAL.
SQ SEQUENCE 907 AA; 101569 MW; D94C24A9 CRC32;

Query Match 47.7%; DB 4; Length 907;
Best Local Similarity 36.4%; Pred. No. 3.36e+00;

Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 381 yneddkfvpa 391
||:| :| :|
Qy 3 YWDDKRYNPS 13

RESULT 12
ID GLRI RAT STANDARD; PRT; 907 AA.
AC P19490;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GLUTAMATE RECEPTOR 1 PRECURSOR (GLUR-1) (GLUR-A) (GLUR-K1).
GN GR1AL OR GLUR1.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=BRAIN;
RX MEDLINE; 90341779.
RA KEINANEN K., WISDEN W., SOMMER B., WERNER P., HERB A., VERDOORN T.A.,
RA SAKMANN B., SEEBURG P.H.;
RL SCIENCE 249:556-560(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90081835.
RA HOLLMANN M., O'SHEA-GREENFIELD A., ROGERS S.W., HEINEMANN S.;
RL NATURE 342:643-648(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90371298.
RA BOULTER J., HOLLMANN M., O'SHEA-GREENFIELD A., HARTLEY M., DENERIS E.,
RA MARON C., HEINEMANN S.;
RL SCIENCE 249:1033-1037(1990).
RN [4]
RP VARIANTS FLIP/FLIP.
RX MEDLINE; 91019421.
RA SOMMER B., KEINANEN K., VERDOORN T.A., WISDEN W., BURNASHEV N.,
RA HERB A., KOEHLER M., TAKAGI T., SAKMANN B., SEEBURG P.H.;
RL SCIENCE 249:1580-1585(1990).
CC -|- FUNCTION: L-GLUTAMATE ACTS AS AN EXCITATORY NEUROTRANSMITTER AT
CC MANY SYNAPSES IN THE CENTRAL NERVOUS SYSTEM. THE POSTSYNAPTIC
CC ACTIONS OF GLU ARE MEDIATED BY A VARIETY OF RECEPTORS THAT ARE
CC NAMED ACCORDING TO THEIR SELECTIVE AGONISTS.
CC -|- THIS RECEPTOR BINDS AMPA(QUISQUALATE) > GLUTAMATE > KAINATE.
CC -|- ALTERNATIVE PRODUCTS: THIS RECEPTOR EXISTS IN TWO VERSIONS (FLOP,
CC SHOWN HERE) AND FLIP, WHICH DIFFER IN A REGION IN FRONT OF TM4.
CC THE TWO FORMS ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME
CC GENE.
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -|- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; M36418; G204394; -.
DR EMBL; X17184; G55529; -.
DR EMBL; M38060; G202868; -.
DR PIR; S07059; ACRTK1.
DR PIR; A40170; A40170.
KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
KW TRANSMEMBRANE; ALTERNATIVE SPLICING.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 907 GLUTAMATE RECEPTOR 1.
FT DOMAIN 19 538 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 539 558 POTENTIAL.

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FT TRANSEM 585 603 POTENTIAL.
 FT TRANSEM 614 632 POTENTIAL.
 FT TRANSEM 806 826 POTENTIAL.
 FT CARBOHYD 63 63 POTENTIAL.
 FT CARBOHYD 249 249 POTENTIAL.
 FT CARBOHYD 257 257 POTENTIAL.
 FT CARBOHYD 363 363 POTENTIAL.
 FT CARBOHYD 401 401 POTENTIAL.
 FT CARBOHYD 406 406 POTENTIAL.
 FT VARSPLIC 758 758 N -> G (IN FLIP).
 FT VARSPLIC 768 768 N -> S (IN FLIP).
 FT VARSPLIC 772 772 L -> V (IN FLIP).
 FT VARSPLIC 778 778 N -> S (IN FLIP).
 FT VARSPLIC 789 793 TGGGD -> SKDSC (IN FLIP).
 FT CONFLICT 698 698 L -> R (IN REF. 2 AND 3).
 FT CONFLICT 710 710 T -> S (IN REF. 2 AND 3).
 SQ SEQUENCE 907 AA; 101647 MW; 97B0B2F8 CRC32;

Query Match 47.7%; Score 61; DB 4; Length 907;
 Best Local Similarity 36.4%; Pred. No. 3.36e+00;
 Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 381 ymnedkfcpa 391
 ||::||::||
 Qy 3 YMDDDKRYNS 13

RESULT 13

ID Y16E_BPT4 STANDARD; PRT; 70 AA.
 AC P22977;
 DT 01-AUG-1991 (REL. 19, CREATED)
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION.
 GN Y16E OR MOTA.-2 OR ASIA.5.
 OS BACTERIOPHAGE T4.
 OC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; MYOVIRIDAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91141300.
 RA UZAN M., BRODY E., FAVRE R.;
 RL MOL. MICROBIOL. 4:1487-1495(1990).
 DR EMBL; 248569; G695452; -.
 DR PIR; JVO103; JVO103.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 70 AA; 8461 MW; 8DA7F78B CRC32;

Query Match 46.9%; Score 60; DB 10; Length 70;
 Best Local Similarity 50.0%; Pred. No. 4.89e+00;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 52 ywdenqky 59
 ||::||
 Qy 3 YMDDDKRY 10

RESULT 14

ID RK28_TOBAC STANDARD; PRT; 151 AA.
 AC P30956;
 DT 01-JUL-1993 (REL. 26, CREATED)
 DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE 50S RIBOSOMAL PROTEIN L28 CHLOROPLAST PRECURSOR (CL28).
 GN RPL28.

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OS NICOTIANA TABACUM (COMMON TOBACCO).
 OC EUKARYOTA; PLANTA; EMERYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
 OC SOLANALES; SOLANACEAE.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 75-95.
 RC STRAIN=CV. BRIGHT YELLOW 4; TISSUE=LEAF;
 RX MEDLINE; 92371638.
 RA YOKOI F., SUGIURA M.;
 RL FEBS LETT. 308:258-260(1992).
 CC -/- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
 DR EMBL; X68078; G20016; -.
 DR PIR; S24123; R5NT28.
 KW RIBOSOMAL PROTEIN; TRANSIT PEPTIDE; CHLOROPLAST.
 FT TRANSIT 1 74 CHLOROPLAST.
 FT CHAIN 75 151 50S RIBOSOMAL PROTEIN L28.
 SQ SEQUENCE 151 AA; 16697 MW; B68E598A CRC32;

Query Match 46.9%; Score 60; DB 7; Length 151;
 Best Local Similarity 50.0%; Pred. No. 4.89e+00;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 110 riwweagkry 119
 :||:|
 Qy 1 HIYMDDDKRY 10

RESULT 15

ID CRP_MOUSE STANDARD; PRT; 225 AA.
 AC P14847;
 DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE C-REACTIVE PROTEIN PRECURSOR.
 GN CRP.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89050112.
 RA OHNISHI S., MAEDA S., NISHICUCHI S., ARAO T., SHIMADA K.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 156:814-822(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA/J; TISSUE=LIVER;
 RX MEDLINE; 90179719.
 RA WHITEHEAD A.S., ZAHEDI K., RITS M., MORTENSEN R.F., LELIAS J.M.;
 RL BIOCHEM. J. 266:283-290(1990).
 CC -/- FUNCTION: CRP DISPLAYS SEVERAL FUNCTIONS ASSOCIATED WITH HOST
 CC DEFENSE: IT PROMOTES AGGLUTINATION, BACTERIAL CAPSULAR SWELLING,
 CC PHAGOCYTOSIS, & COMPLEMENT FIXATION THROUGH ITS CALCIUM-DEPENDENT
 CC BINDING TO PHOSPHORYLCHOLINE.
 CC -/- INDUCTION: THE CONCENTRATION OF CRP IN PLASMA INCREASES GREATLY
 CC DURING ACUTE PHASE RESPONSE TO TISSUE INJURY OR INFLAMMATION.
 CC -/- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -/- SIMILARITY: BELONGS TO THE FAMILY OF PENTAXINS.
 DR EMBL; X13588; G295904; -.
 DR EMBL; X17496; G50564; -.
 DR PIR; A31583; A31583.
 DR PIR; S08286; S08286.
 DR HSSP; P02743; ISAC.
 DR PROSITE; PS00289; PENTAXIN.
 KW ACUTE PHASE; PLASMA; CALCIUM; PENTAXIN; SIGNAL.

13

US-08-612-929-24.rsp

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FT SIGNAL 1 19
FT CHAIN 20 225
FT DOMAIN 20 225
FT DISULFID 55 116
FT CONFLICT 134 134
SQ SEQUENCE 225 AA; 25361 MB; 3C57F01C CRC32;

C-REACTIVE PROTEIN.
PENTAXIN.
BY SIMILARITY.
A -> P (IN REF. 2).

Query Match 46.9%; Score 60; DB 2; Length 225;
Best Local Similarity 55.6%; Pred. No. 4.89e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 84 ifwnkdqy 92
l:l: ||:|
Qy 2 IYWDDKRY 10

Search completed: Tue Mar 18 10:14:46 1997
Job time : 6 secs.

(TM)

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```

protein - protein database search, using Smith-Waterman algorithm
MPsrch_pp
Run on: Tue Mar 18 10:15:04 1997; MasPar time 3.17 Seconds
129.657 Million cell updates/sec

```

```

Title:
Description: (1-16) from US08612929.pep
Perfect Score: 128
Sequence: 1 HIYDDDKRNP SLK 16

```

Scoring table: PAM 150
Gap 15

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database: pir48
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unann10
14:unrev
```

Statistics: Mean 27.523; Variance 52.762; scale 0.522

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		ID	Description	Pred. No.
		Match	Length			
1	128	100.0	122	5	S11740	Ig heavy chain precu 1.52e-10
2	117	91.4	107	12	A49442	Ig heavy chain v reg 1.46e-08
3	115	89.8	141	11	S26936	Ig heavy chain v reg 3.30e-08
4	115	89.8	138	5	S31513	Ig heavy chain - hum 3.30e-08
5	112	87.5	119	5	S18555	Ig heavy chain - hum 1.12e-07
6	109	85.2	124	5	A49002	rheumatoid factor he 3.75e-07
7	105	82.0	121	2	GIHUNE	Ig heavy chain V-II 1.85e-06
8	100	78.1	113	5	S26455	Ig heavy chain v reg 1.33e-05
9	92	71.9	125	2	MHHJWC	Ig heavy chain V-II 2.92e-04
10	92	71.9	143	5	P01174	Ig heavy chain precu 2.92e-04
11	86	67.2	103	5	B25913	Ig heavy chain precu 2.78e-03
12	86	67.2	116	12	S26328	Ig heavy chain v reg 2.78e-03

3

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```

RESULT 2
ENTRY A49442 #type fragment
TITLE Ig heavy chain V region (50.1) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995
ACCESSIONS A49442
REFERENCE A49442
#authors Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.;
Roguska, M.; Hincapié, L.M.; Simmerman, H.K.B.; Profy,
A.T.; Wilson, I.A.
#journal Proteins (1992) 14:499-508
#title Crystallization, sequence, and preliminary crystallographic
data for an antipeptide Fab 50.1 and peptide complexes with
the principal neutralizing determinant of HIV-1 gp120.
#accession A49442
#status preliminary; not compared with conceptual translation
#molecule_type DNA
#residues 1-107 #label STU
SUMMARY #length 107 #checksum 9363

Query Match 91.4%; Score 117; DB 12; Length 107;
Best Local Similarity 87.5%; Pred. No. 1.46e-08;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 44 hlfddgdkrypslks 59
|||||:|||||:|||||
Qy 1 HIYDDDKRYNPSLKS 16

```

```

RESULT 3
ENTRY S26936 #type fragment
TITLE Ig heavy chain V region (DP-76) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change
17-Nov-1995
ACCESSIONS S26936
REFERENCE S26885
#authors Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.;
Winter, G.
#journal J. Mol. Biol. (1992) 227:776-798
#title The repertoire of human germline V(H) sequences reveals about
fifty groups of V(H) segments with different hypervariable
loops.
#accession S26936
#status preliminary
#molecule_type DNA
#residues 1-41 #label TOM
#cross-references EMBL:Z14072
#note the nucleotide sequence was submitted to the EMBL Data
Library, July 1992
#note neither amino acid nor nucleotide sequence is given
SUMMARY #length 41 #checksum 7016

Query Match 89.8%; Score 115; DB 11; Length 41;
Best Local Similarity 93.3%; Pred. No. 3.30e-08;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 23 iywdddkrypslks 37
|||||:|||||:|||||
Qy 2 IYDDDKRYNPSLKS 16

```

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4

```

RESULT 4
ENTRY S31513 #type complete
TITLE Ig heavy chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
12-Apr-1995
ACCESSIONS S31513
REFERENCE S31509
#authors Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
#submission Submitted to the EMBL Data Library, December 1992
#description Dominance of clonotypic patterns and variable gene usage of
anti-DNA autoantibodies from patient with lupus.
#accession S31513
#status preliminary
#molecule_type mRNA
#residues 1-138 #label CHA
#cross-references EMBL:X69861
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 138 #molecular-weight 15115 #checksum 3666

Query Match 89.8%; Score 115; DB 5; Length 138;
Best Local Similarity 93.3%; Pred. No. 3.30e-08;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 68 iywdddkrypslks 82
|||||:|||||:|||||
Qy 2 IYDDDKRYNPSLKS 16

RESULT 5
ENTRY S18555 #type complete
TITLE Ig heavy chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Apr-1995
ACCESSIONS S18555
REFERENCE S18551
#authors Shin, E.K.; Mateuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.;
Yokoyama, K.; Soeda, E.; Honjo, T.
#journal EMBO J. (1991) 10:3641-3645
#title Physical map of the 3' region of the human immunoglobulin
heavy chain locus: clustering of antibody-related
variable segments in one haplotype.
#cross-references WUID:92037524
#accession S18555
#status preliminary
#molecule_type DNA
#residues 1-119 #label SHI
#cross-references EMBL:X62111
GENETICS 16/1
#introns
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 119 #molecular-weight 13230 #checksum 1886

Query Match 87.5%; Score 112; DB 5; Length 119;
Best Local Similarity 86.7%; Pred. No. 1.12e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 72 iywdddkrypslks 86
|||||:|||||:|||||
Qy 2 IYDDDKRYNPSLKS 16

RESULT 6

```


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5

ENTRY A49002 #type fragment
 TITLE rheumatoid factor heavy chain variable domain, RF H chain V domain-anti-IgM heavy chain variable domain - human (fragment)
 ORGANISM #formal name Homo sapiens #common name man
 DATE 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 22-Apr-1995
 ACCESSIONS A49002
 REFERENCE A49002
 #authors Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.; Fu, S.M.
 #journal Arthritis Rheum. (1992) 35:900-904
 #title A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene segments.
 #cross-references M01D:92352481
 #accession A49002
 #status preliminary
 #molecule_type mRNA
 #residues 1-124 #label STU
 #cross-references NCBIN:110261; NCBIP:110262
 #experimental_source EVB-transformed lymphoblastoid cell line SSH23
 #note sequence extracted from NCB1 backbone
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 SUMMARY #length 124 #checksum 3208

Query Match 85.24; Score 109; DB 5; Length 124;
 Best Local Similarity 80.04; Pred. No. 3.75e-07;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 53 iywddrryeps1ks 67
 |||:||||:||||
 Qy 2 IYWDDDKRYNPS1KS 16

RESULT 7
 ENTRY GLHUE #type complete
 TITLE Ig heavy chain V-II region (He) - human
 ORGANISM #formal name Homo sapiens #common name man
 DATE #sequence_revision 07-May-1981 #text_change 16-Feb-1996
 ACCESSIONS A02093
 REFERENCE A02093
 #authors Cunningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman, G.M.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1969) 64:997-1003
 #title Subgroups of amino acid sequences in the variable regions of immunoglobulin heavy chains.
 #cross-references M01D:70114712
 #accession A02093
 #molecule_type protein
 #residues 1-121 #label CUN
 COMMENT This gamma-1 chain was isolated from a myeloma protein.
 GENETICS
 #gene GDB:IGHV8
 #map_position 14q32.33
 #cross-references GDB:C00-128-528
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 FEATURE 1
 #modified site blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental
 #length 121 #molecular-weight 13483 #checksum 9601

Summary
 Query Match 82.04; Score 105; DB 2; Length 121;
 Best Local Similarity 80.04; Pred. No. 1.85e-06;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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6

Db 54 lywdddkrfeps1ks 68
 :|||||:|||||
 Qy 2 IYWDDDKRYNPS1KS 16
 RESULT 8
 ENTRY S26465 #type complete
 TITLE Ig heavy chain V region - mouse
 ORGANISM #formal name Mus musculus #common name house mouse
 DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 12-Apr-1995
 ACCESSIONS S26465
 REFERENCE S26459
 #authors Kavalier, J.
 #submission submitted to the EMBL Data Library, April 1991
 #accession S26465
 #status preliminary
 #molecule_type mRNA
 #residues 1-113 #label KAV
 #cross-references EMBL:X59115
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 SUMMARY #length 113 #molecular-weight 12508 #checksum 2993

Query Match 78.18; Score 100; DB 5; Length 113;
 Best Local Similarity 87.5%; Pred. No. 1.33e-05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 43 hiwdddkyynps1ks 58
 |||:||||:|||||
 Qy 1 HIWDDDKRYNPS1KS 16

RESULT 9
 ENTRY MHHUMC #type complete
 TITLE Ig heavy chain V-II region (McE) - human
 ORGANISM #formal name Homo sapiens #common name man
 DATE 14-Nov-1983 #sequence_revision 22-Nov-1983 #text_change 16-Feb-1996
 ACCESSIONS A02092
 REFERENCE A02092
 #authors Gerber-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.; Erickson, B.W.; Litman, G.W.
 #journal J. Immunol. (1981) 126:1212-1216
 #title Molecular basis for the temperature-dependent insolubility of cryoglobulins. X. The amino acid sequence of the heavy chain variable region of McE.
 #cross-references M01D:81118242
 #accession A02092
 #molecule_type protein
 #residues 1-125 #label GER
 #note this chain was derived from a monoclonal IgM cryoimmunoglobulin

GENETICS
 #gene GDB:IGHV8
 #map_position 14q32.33
 #cross-references GDB:G00-128-528
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS pyrrolidone carboxylic acid
 FEATURE 1
 #modified site pyrrolidone carboxylic acid (Gln) #status experimental
 #length 125 #molecular-weight 13783 #checksum 9697

Summary
 Query Match 82.04; Score 105; DB 2; Length 121;
 Best Local Similarity 80.04; Pred. No. 1.85e-06;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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7

Query Match 71.9%; Score 92; DB 2; Length 125;
 Best Local Similarity 73.3%; Pred. No. 2.92e-04;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 53 inwdddkrynpals 67
 |||||:||||:|
 Qy 2 IYWDKRYNPALS 16

RESULT 10
 ENTRY PT0174 #type fragment
 TITLE Ig heavy chain precursor V region (Idb5.7) - mouse (fragment)
 ORGANISM #formal name Mus musculus #common name house mouse
 DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 12-Apr-1995

ACCESSIONS PT0174
 REFERENCE PT0174
 #authors Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.
 #journal Mol. Immunol. (1991) 28:505-515
 #title Specificity and variable region cDNA sequence of an isogeneic monoclonal antidiotype to an anti-alpha (1-6) dextran.
 #cross-references M01D:9128738
 #accession PT0174
 ##molecule_type mRNA
 ##residues 1-143 ##label PER
 ##experimental_source strain BALB/c
 ##comment Idb5.7 is an antibody to anti-alpha (1-6) dextran.
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 SUMMARY #length 143 #checksum 3660

Query Match 71.9%; Score 92; DB 5; Length 143;
 Best Local Similarity 81.3%; Pred. No. 2.92e-04;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 71 hiswdddkrynpals 86
 |||||:|||||
 Qy 1 HIYWDKRYNPALS 16

RESULT 11
 ENTRY B25913 #type fragment
 TITLE Ig heavy chain precursor V region (BFL23) - mouse (fragment)
 ORGANISM #formal name Mus musculus #common name house mouse
 DATE 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 30-Sep-1993

ACCESSIONS B25913
 REFERENCE A94148
 #authors Lawler, A.M.; Lin, P.-S.; Gearhart, P.J.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:2454-2458
 #title Adult B-cell repertoire is biased toward two heavy-chain variable-region genes that rearrange frequently in fetal pre-B cells
 #cross-references M01D:87175692
 #accession B25913
 ##molecule_type DNA
 ##residues 1-103 ##label LAM
 ##note the authors translated the codon TGT for residue 11 as Ser
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 SUMMARY #length 103 #checksum 957

Query Match 67.2%; Score 86; DB 5; Length 103;
 Best Local Similarity 68.8%; Pred. No. 2.78e-03;

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8

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 56 hilwdddkrynpals 71
 |||||:|||||
 Qy 1 HIYWDKRYNPALS 16

RESULT 12
 ENTRY S26328 #type complete
 TITLE Ig heavy chain V region - mouse
 ORGANISM #formal name Mus musculus #common name house mouse
 DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995

ACCESSIONS S26328
 REFERENCE S26309
 #authors Stark, S.E.; Caton, A.J.
 #journal J. Exp. Med. (1991) 174:613-624
 #title Antibodies that are specific for a single amino acid interchange in a protein epitope use structurally distinct variable regions.
 #accession S26328
 ##status preliminary
 ##molecule_type mRNA
 ##residues 1-116 ##label STA
 ##cross-references EMBL:X59198
 SUMMARY #length 116 #molecular-weight 12895 #checksum 8145

Query Match 67.2%; Score 86; DB 12; Length 116;
 Best Local Similarity 68.8%; Pred. No. 2.78e-03;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 48 hilwdddkrynpals 63
 |||||:|||||
 Qy 1 HIYWDKRYNPALS 16

RESULT 13
 ENTRY S09959 #type fragment
 TITLE Ig heavy chain V-D-J region (31-90) - mouse (fragment)
 ORGANISM #formal name Mus musculus #common name house mouse
 DATE 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Mar-1993

ACCESSIONS S09959
 REFERENCE S09955
 #authors Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatón, J.C.; Izui, S.
 #journal Eur. J. Immunol. (1990) 20:771-777
 #title Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies from autoimmune NZB mice.
 #cross-references M01D:90269328
 #accession S09959
 ##molecule_type mRNA
 ##residues 1-121 ##label REI
 ##cross-references EMBL:X51847
 SUMMARY #length 121 #checksum 7852

Query Match 60.2%; Score 77; DB 12; Length 121;
 Best Local Similarity 62.5%; Pred. No. 7.28e-02;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 52 niwdddkrynpals 67
 |||||:|||||
 Qy 1 HIYWDKRYNPALS 16

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```

RESULT 14
ENTRY S26922 #type fragment
TITLE Ig heavy chain V region (DP-26) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
10-Nov-1995
ACCESSIONS S26922
REFERENCE S26895
#authors Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.;
Winter, G.
#journal J. Mol. Biol. (1992) 227:776-798
#title The repertoire of human germline V(H) sequences reveals about
fifty groups of V(H) segments with different hypervariable
loops.
#accession S26922
##status preliminary
##molecule_type DNA
##residues 1-96 ##label TOM
##cross-references EMBL:212328
SUMMARY #length 96 #checksum 8878

Query Match 59.4%; Score 76; DB 11; Length 96;
Best Local Similarity 56.3%; Pred. No. 1.04e-01;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 52 hifendekystalks 67
QY 1 HIYDDDKRYNPSLKS 16
II:::II:::II:::

RESULT 15
ENTRY S46461 #type complete
TITLE Ig heavy chain V region (VAC-3) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
26-May-1995
ACCESSIONS S46461
REFERENCE S46460
#authors Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.;
Carter, N.P.; Buluwela, L.; Winter, G.; Rabbitts, T.H.
#journal Nature Genet. (1994) 7:162-168
#title A map of the human immunoglobulin V(H) locus completed by
analysis of the telomeric region of chromosome 14q.
#accession S46461
##status preliminary
##molecule_type DNA
##residues 1-78 ##label COO
##cross-references EMBL:227502
SUMMARY #length 78 #molecular-weight 8788 #checksum 5329

Query Match 57.8%; Score 74; DB 11; Length 78;
Best Local Similarity 62.5%; Pred. No. 2.09e-01;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 43 ridwdddkfystalkt 58
QY 1 HIYDDDKRYNPSLKS 16
:II:::II:::II:::

```

Search completed: Tue Mar 18 10:15:15 1997
Job time : 11 secs.

protein - protein database search, using Smith-Waterman algorithm

```
Run on: Tue Mar 18 10:15:33 1997; MasPar time 1.99 Seconds
82.665 Million cell updates
```

Tabular output not generated.

```
>US-08-612-929-24
Title:
Description: (1-16) from US08612929.peg
Perfect Score: 128
Sequence: 1 HIYDDDKRYNPISKS 16
```

Scoring table: PAM 150
Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database: a-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
```

Statistics: Mean 20.200; Variance 65.991; scale 0.306

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description	SUMMARIES	
								Pred. No.
1	128	100.0	16	13	R70199	MAB 3B9 heavy chain C	1.07e-06	
2	128	100.0	140	13	R70190	Mouse MAB 3B9 heavy c	1.07e-06	
3	128	100.0	141	13	R70191	Chimeric antibody 3B9	1.07e-06	
4	128	100.0	141	13	R70192	Humanized antibody 3B	1.07e-06	
5	121	94.5	16	10	R54105	Humanised anti-HIV MA	6.87e-06	
6	121	94.5	122	11	R54101	Humanised MAB H-chain	6.87e-06	
7	121	94.5	122	10	R54110	Humanised anti-HIV MA	6.87e-06	
8	121	94.5	246	11	R58612	IL-6 binding inhibito	6.87e-06	
9	115	89.8	139	8	R38315	Sequence of the VH of	3.34e-05	
10	112	87.5	119	12	R62999	Human immunoglobulin	7.32e-05	
11	110	85.9	120	17	R88109	Murine anti-Protein C	1.23e-04	
12	110	85.9	139	17	R88107	Murine anti-Protein C	1.23e-04	

SUMMARIES

Best Available Copy

ALIGNMENTS

RESULT 1

ID R70199 standard; Protein; 16 AA.

AC	R/0199;
DT	20-SEP-1995 (first entry)

DE MAb 3B9 heavy chain CDR.

KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; CDR;

complementarity determining region.

OS Mus sp.
PN W09507301-A

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.
PT Gross MS. Holmes SD. Sylveste

DR WPI; 95-123387/16.

pt Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic condition

PS Disclosure; Page 31, 31pp, English
CC Spleen cells from mice immunized wi

CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only CC clones 389 and 390 were positive. cDNA clones of the 389 light and heavy

CC chains were cloned into pGEM7f+ and transformed into *E. coli*

CC DH5- α . A heavy chain cDNA clone was sequenced (Q83491) that

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US-08-612-929-24.rag

3

CC encoded the protein given in R70190. 3 CDRs (R70198-200) were
 CC identified.
 SQ Sequence 16 AA;

Query Match 100.0%; DB 13; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.07e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 hiywdkrynpelks 16
 |||
 Qy 1 HIYWDKRYNPSLKS 16

RESULT 2

ID R70190 standard; Protein; 140 AA.

AC R70190;

DT 20-SEP-1995 (first entry)

DE Mouse MAb 3B9 heavy chain.

KW Chimeric antibody; humanized antibody; antibody engineering;

KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.

OS Mus sp.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig_peptide

FT Region 50..56

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 71..86

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 119..129

FT /label= CDR

FT /note= "complementarity determining region"

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WFI; 95-123387/16.

DR N-PSDB; Q83491.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Fig.2; 97pp; English.

CC Spleen cells from mice immunized with human IL-4 were used to prepare

CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only

CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy

CC chains were cloned into pCEW7f+ and transformed into E. coli

CC DH5-alpha. The clones were sequenced (Q83490-91), and used for

CC antibody engineering.

SQ Sequence 140 AA;

Query Match

Best Local Similarity 100.0%; DB 13; Length 140;

Pred. No. 1.07e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 71 hiywdkrynpelks 86

|||||

Qy 1 HIYWDKRYNPSLKS 16

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RESULT 3

ID R70191 standard; Protein; 141 AA.

AC R70191;

DT 20-SEP-1995 (first entry)

DE Chimeric antibody 3B9 heavy chain.

KW Chimeric antibody; antibody engineering; monoclonal antibody;

KW MAb; interleukin-4; IL-4; allergy.

OS Homo sapiens; Mus sp.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig_peptide

FT Region 51..57

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 72..87

FT /label= CDR

FT /note= "complementarity determining region"

FT Peptide 120..130

FT /label= CDR

FT /note= "complementarity determining region"

PN W09507301-A.

PD 16-MAR-1995.

PF 07-SEP-1994; U10308.

PR 07-SEP-1993; US-117366.

PR 14-OCT-1993; US-136783.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WFI; 95-123387/16.

DR N-PSDB; Q83492.

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Fig.3; 97pp; English.

CC A human/mouse chimeric antibody heavy chain variable region was

CC constructed (given in R70191) that contained the mouse anti-human

CC IL-4 MAb 3B9 variable region including 3 CDRs (R70198-200) and a

CC human antibody signal peptide (R70193). The construct was used

CC for humanized antibody production.

SQ Sequence 141 AA;

Query Match

Best Local Similarity 100.0%; DB 13; Length 141;

Pred. No. 1.07e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 72 hiywdkrynpelks 87

|||||

Qy 1 HIYWDKRYNPSLKS 16

RESULT 4

ID R70192 standard; Protein; 141 AA.

AC R70192;

DT 20-SEP-1995 (first entry)

DE Humanized antibody 3B9 heavy chain.

KW Humanized antibody; antibody engineering; monoclonal antibody;

KW MAb; interleukin-4; IL-4; allergy.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig_peptide

FT Region 51..57

FT /label= CDR

FT /note= "complementarity determining region"

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FT Region 72..87
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT Region 120..130
 FT /label= CDR
 FT /note= "complementarity determining region"
 PN W09507301-A.
 PD 16-MAR-1995.
 PF 07-SEP-1994; U10308.
 PR 07-SEP-1993; US-117366.
 PR 14-OCT-1993; US-136783.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Gross MS, Holmes SD, Sylvester DR;
 DR WPI; 95-123387/16.
 DR N-PSDB; Q83493.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS Disclosure; Fig. 4; 97pp; English.
 CC A humanized antibody heavy chain variable region and signal
 CC sequence is given in R70192. The signal sequence is also
 CC provided in R70193. The CDR sequences of the construct are
 CC identical to the native CDRs of mouse anti-human IL-4 MAb
 CC 389 (R70198-200).
 SQ Sequence 141 AA;

Query Match 100.0%; Score 128; DB 13; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.07e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 72 hiywdkdkrynpnlks 87
 |||||
 QY 1 HIYWDKDKRYNPNSLKS 16

RESULT 5
 ID R54105 standard; Protein; 16 AA.
 AC R54105;
 DT 08-FEB-1995 (first entry)
 DE Humanised anti-HIV MAB fragment #3.
 KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
 KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN;
 KW polymerase chain reaction; primer; amplify; PCR.
 OS Synthetic.
 PN J06141885-A.
 PD 24-MAY-1994.
 PF 05-NOV-1992; 322476.
 PR 05-NOV-1992; JP-322476.
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 DR WPI; 94-205040/25.
 PT Recombinant anti-HIV monoclonal antibody - capable of
 PT neutralising strains which can not be neutralised by anti-IIIB
 PS Disclosure; Page 14; 23pp; Japanese.
 CC The sequences given in R54103-11 are fragments of the heavy and light
 CC chains of the humanised monoclonal antibody (MAB) of the invention.
 CC The antibody has the ability to neutralise human immunodeficiency
 CC virus. The antibody is classified as IgG kappa and has the
 CC sequence RIGPCR or RVGPGR in the principal neutralising domain.
 CC The antibody may be used to neutralise the clinically
 CC separate strains which cannot be neutralised by the neutralising
 CC antibodies against IIIB and IIIMN strains.
 SQ Sequence 16 AA;

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Query Match 94.5%; Score 121; DB 10; Length 16;
 Best Local Similarity 93.8%; Pred. No. 6.87e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 hiywdkdkrynpnlks 16
 |||||
 QY 1 HIYWDKDKRYNPNSLKS 16

RESULT 6
 ID R54101 standard; Protein; 122 AA.
 AC R54101;
 DT 08-FEB-1995 (first entry)
 DE Humanised MAB H-chain.
 KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
 KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN.
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 31..37
 FT /label= CDR1
 FT Region 52..67
 FT /label= CDR2
 FT Region 100..111
 FT /label= CDR3
 PN J06141885-A.
 PD 24-MAY-1994.
 PF 05-NOV-1992; 322476.
 PR 05-NOV-1992; JP-322476.
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 DR WPI; 94-205040/25.
 DR N-PSDB; Q68709.
 PT Recombinant anti-HIV monoclonal antibody - capable of
 PT neutralising strains which can not be neutralised by anti-IIIB
 PT and IIIMN antibodies
 PS Disclosure; Page 13; 23pp; Japanese.
 CC The sequences given in R54101-02 represent the heavy and light chains
 CC respectively of the humanised monoclonal antibody (MAB) of the
 CC invention. The antibody has the ability to neutralise human
 CC immunodeficiency virus. The antibody is classified as IgG kappa and
 CC has the sequence RIGPCR or RVGPGR in the principal neutralising
 CC domain. The antibody may be used to neutralise the clinically
 CC separate strains which cannot be neutralised by the neutralising
 CC antibodies against IIIB and IIIMN strains.
 SQ Sequence 122 AA;

Query Match 94.5%; Score 121; DB 11; Length 122;
 Best Local Similarity 93.8%; Pred. No. 6.87e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 52 hiywdkdkrynpnlks 67
 |||||
 QY 1 HIYWDKDKRYNPNSLKS 16

RESULT 7
 ID R54110 standard; Protein; 122 AA.
 AC R54110;
 DT 08-FEB-1995 (first entry)
 DE Humanised anti-HIV MAB fragment #8.
 KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
 KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN;
 KW polymerase chain reaction; primer; amplify; PCR.

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Qy 1 HIYDDDKRYNPSLKS 16

RESULT 9
 ID R38315 standard; Protein; 139 AA.
 AC R38315;
 DT 04-DEC-1993 (first entry)
 DE Sequence of the VH of antibody B17X2
 KW Variable heavy antibody chain; human subgroup 4 germline.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 50..56
 FT /label= CDR1
 FT Region 71..86
 FT /label= CDR2
 FT Region 119..126
 FT /label= CDR3
 PN W09312231-A.
 PD 24-JUN-1993.
 PF 13-DEC-1991; MO-AU0583.
 PR 13-DEC-1991; MO-AU0583.
 PA (DMC) DOW CHEM AUSTRALIA LTD.
 PI Johnson KS, Mezes PS, Richard RA;
 DR WPI; 93-214173/26.
 N-PSDB; Q45597.
 DT New composite antibody binding to tumour associated TAG-72
 PT antigen - includes light chain variable region from human
 PT subgroup 4 germline gene, useful, opt. as conjugate, for
 PT diagnosis or treatment of cancer
 PS Disclosure; Figure 4; 150pp; English.
 CC Cell line B17X2 expresses an antibody utilising a variable light
 CC chain encoded by a gene derived from Hum4 VL and a variable heavy
 CC chain which makes a stable VL and VH combination.
 SQ Sequence 139 AA;

Query Match 89.8%; Score 115; DB 8; Length 139;
 Best Local Similarity 93.3%; Pred. No. 3.34e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 72 iywdddkrypslks 86
 |||||:|||||
 Qy 2 IYDDDKRYNPSLKS 16

RESULT 10
 ID R66299 standard; Protein; 119 AA.
 AC R66299;
 DT 07-AUG-1995 (first entry)
 DE Human immunoglobulin variable heavy chain #5.
 KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pUB81; E.coli; mammalian.
 OS Homo sapiens.
 PN W09426895-A.
 PD 24-NOV-1994.
 PF 10-MAY-1993; J00603.
 PR 10-MAY-1993; MO-J00603.
 PA (NLSB) JAPAN TOBRACCO INC.
 PI Honjo T, Matsuda F;
 DR WPI; 95-006791/01.
 DT DNA fragment comprising human immunoglobulin Vh genes - for the
 PT production of human immunoglobulin in mammalian hosts
 PS Disclosure; Page 36-37; 130pp; Japanese.
 CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain

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OS Synthetic.
 PN J06141885-A.
 PD 24-MAY-1994.
 PF 05-NOV-1992; 322476.
 PR 05-NOV-1992; JP-322476.
 PA (KAGA) ZH KAGAKU & KESSSEI RYOHO KENKYUSHO.
 DR WPI; 94-205040/25.
 PT Recombinant anti-HIV monoclonal antibody - capable of
 PT neutralising strains which can not be neutralised by anti-IIIB
 PT and IIIMN antibodies
 PS Disclosure; Page 14; 23pp; Japanese.
 CC The sequences given in R34103-11 are fragments of the heavy and light
 CC chains of the humanised monoclonal antibody (MAb) of the invention.
 CC The antibody has the ability to neutralise human immunodeficiency
 CC virus. The antibody is classified as IgG kappa and has the
 CC sequence RIGPCR or RVGPCR in the principal neutralising domain.
 CC The antibody may be used to neutralise the clinically
 CC separate strains which cannot be neutralised by the neutralising
 CC antibodies against IIIB and IIIMN strains.
 SQ Sequence 122 AA;

Query Match 94.5%; Score 121; DB 10; Length 122;
 Best Local Similarity 93.8%; Pred. No. 6.87e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 52 hiywdkrypslks 67
 |||||:|||||
 Qy 1 HIYDDDKRYNPSLKS 16

RESULT 8
 ID R58612 standard; Protein; 246 AA.
 AC R58612;
 DT 28-APR-1995 (first entry)
 DE IL-6 binding inhibitor.
 KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
 KW septic shock; multiple myeloma; ss.
 OS Homo sapiens.
 PN EP-617126-A.
 PD 28-SEP-1994.
 PF 16-FEB-1994; 102346.
 PR 17-FEB-1993; JP-028173.
 PA (AJIN) AJINOMOTO KK.
 PI Hamuro J, Nakazawa H, Shimamura T;
 DR WPI; 94-295777/37.
 N-PSDB; Q70612.
 DT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to
 PT its receptor - useful for treating autoimmune disease induced
 PT or aggravated by IL-6
 PS Claim 5; Page 18; 26pp; English.
 CC Q70612 codes for human interleukin-6 binding inhibitor, the
 CC polypeptide described in R58612. This polypeptide inhibits the
 CC binding of human IL-6 to its receptor, and can therefore be
 CC useful in the treatment of a variety of autoimmune diseases;
 CC specifically in the treatment of rheumatoid arthritis, septic
 CC shock due to bacterial infection and multiple myeloma.
 SQ Sequence 246 AA;

Query Match 94.5%; Score 121; DB 11; Length 246;
 Best Local Similarity 93.8%; Pred. No. 6.87e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 174 hiywdkrypslks 189
 |||||:|||||

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CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using primers Q78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with TaqI restriction enzyme. The fragments were separated by gel electrophoresis and 35-45 kb fractions were collected. The fragments were ligated with ClaI-digested cosmid vector pUB81. The ligation products were in vitro packed and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts.

SQ Sequence 119 AA;

Query Match 87.5%; Score 112; DB 12; Length 119;
Best Local Similarity 86.7%; Pred. No. 7.32e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 72 iywdddkrynpvls 86

|||||:|||||:|||||

QY 2 IYWDDDKRYNPSLKS 16

RESULT 11

ID R88109 standard; peptide; 120 AA.
AC R88109;
DT 25-JUL-1996 (first entry)
DE Murine anti-Protein C MAB HPC-4 VH gamma mature peptide.
KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
KW zymogen; cleavage; mouse; humanised antibody; variable region;
KW light chain; inhibition; anticoagulant; coagulation; tumour.
OS Mus musculus.
PN W09534652-A1.
PD 21-DEC-1995.
PF 09-JUN-1995; U07372.
PR 10-JUN-1994; US-259321.
PA (OKLA-) OKLAHOMA MED RES FOUND.
PI Emon CT, Rezaie A;
DR WPI; 96-049681/05.
DR N-PSDB; T09300.
PT Calcium-binding monoclonal antibody immunoreactive with Protein C -
PT inhibits Protein C anticoagulant activation by
PT thrombin-thrombomodulin, e.g. for treating tumours
PS Claim 2; Page 29; 41pp; English.

CC This is the amino acid sequence of the mature peptide from the murine anti-protein C monoclonal antibody HPC-4 heavy chain variable region. CC HPC-4 recognises the activation peptide region (R88106) of the heavy chain of protein C, a vitamin K-dependent plasma protein zymogen. CC Protein C is converted to activated protein C (APC) by cleavage between the Arg-Leu amino acid contained within the activation peptide sequence. CC HPC-4 prevents protein C activation to APC by binding to this region. CC The DNA sequences encoding the variable regions of the heavy and light chains of the antibody (T09299-302) were used to construct humanised antibodies using the PCR primers T09303-9. The humanised antibodies are useful as inhibitors of coagulation and can be used for the treatment of tumours by inhibiting the anticoagulant activity of APC by preventing conversion of protein C to APC.

SQ Sequence 120 AA;

Query Match 85.9%; Score 110; DB 17; Length 120;
Best Local Similarity 87.5%; Pred. No. 1.23e-04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 52 hiwdddkrynpvls 67

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QY 1 HIWDDDKRYNPSLKS 16

RESULT 12

ID R88107 standard; Protein; 139 AA.
AC R88107;
DT 25-JUL-1996 (first entry)
DE Murine anti-Protein C MAB HPC-4 VH gamma protein.
KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
KW zymogen; cleavage; mouse; humanised antibody; variable region;
KW light chain; inhibition; anticoagulant; coagulation; tumour.
OS Mus musculus.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /note= "signal peptide"

FT Peptide 20..139

FT /note= "mature peptide"

PN W09534652-A1.

PD 21-DEC-1995.

PF 09-JUN-1995; U07372.

PR 10-JUN-1994; US-259321.

PA (OKLA-) OKLAHOMA MED RES FOUND.

PI Emon CT, Rezaie A;

DR WPI; 96-049681/05.

DR N-PSDB; T09299.

PT Calcium-binding monoclonal antibody immunoreactive with Protein C -

PT inhibits Protein C anticoagulant activation by

PT thrombin-thrombomodulin, e.g. for treating tumours

PS Claim 2; Page 29; 41pp; English.

CC This is the amino acid sequence of the heavy chain variable region from

CC the murine anti-protein C monoclonal antibody HPC-4 which recognises

CC the activation peptide region (R88106) of the heavy chain of protein C,

CC a vitamin K-dependent plasma protein zymogen. Protein C is converted to

CC activated protein C (APC) by cleavage between the Arg-Leu amino acid

CC contained within the activation peptide sequence. HPC-4 prevents protein

CC C activation to APC by binding to this region. The DNA sequences encoding

CC the variable regions of the heavy and light chains of the antibody

CC (T09299-302) were used to construct humanised antibodies using the PCR

CC primers T09303-9. The humanised antibodies are useful as inhibitors of

CC coagulation and can be used for the treatment of tumours by inhibiting

CC the anticoagulant activity of APC by preventing conversion of protein C

CC to APC.

SQ Sequence 139 AA;

Query Match 85.9%; Score 110; DB 17; Length 139;
Best Local Similarity 87.5%; Pred. No. 1.23e-04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 71 hiwdddkrynpvls 86

|||||:|||||:|||||

QY 1 HIWDDDKRYNPSLKS 16

RESULT 13

ID R54092 standard; Protein; 143 AA.
AC R54092;
DT 29-DEC-1994 (first entry)
DE Sequence of mouse VH showing the sequences of recombinant
DE anti-FHV-1 antibody CDRs 1, 2 and 3.
KW Feline herpes virus; FHV-1; monoclonal antibody; CDR;
KW complementarity determining region.
OS Mus musculus.

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FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= leader
 FT Region 20..47
 FT /label= FR1
 FT Region 48..56
 FT /label= CDR1
 FT Region 57..70
 FT /label= FR2
 FT Region 71..86
 FT /label= CDR2
 FT Region 87..118
 FT /label= FR3
 FT Region 119..132
 FT /label= CDR3
 FT Region 133..143
 FT /label= FR4
 PN W09412661-A.
 PD 09-JUN-1994.
 PR 25-NOV-1993; J01724.
 PR 28-NOV-1992; JP-341255.
 PA (KAGA) CEMO SERO THERAPEUTIC RES INST.
 PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;
 DR WPI; 94-200288/24.
 DR N-PSDB; Q64166.
 PT Feline monoclonal antibody and recombinant antibodies specific
 PT for FHV-1 - for detection, treatment and prevention of FHV-1
 PT infection.
 PS Disclosure; Page 17-18; 53pp; Japanese.
 CC The inventors claim a monoclonal antibody against feline herpes
 CC virus (FHV-1). They also claim a recombinant antibody against FHV-1
 CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
 CC used in the detection, treatment and prevention of FHV-1. The
 CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
 CC antibody are given in R54092. The sequences of the CDRs in the VL of
 CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR
 CC sequences are claimed.
 SQ Sequence 143 AA;
 Query Match 81.3%; Score 104; DB 10; Length 143;
 Best Local Similarity 81.3%; Pred. No. 5.84e-04;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 71 hiwdddkvynpalks 86
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 Qy 1 HIYDDDKRYNPSLKS 16

RESULT 14
 ID R7213 standard; Peptide; 16 AA.
 AC R7213;
 DT 23-AUG-1995 (first entry)
 DE Mouse anti-human IL-6 Ab H chain V region CDR2.
 KW Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;
 KW interleukin; antibody; hybridoma; CDR; framework; constant region;
 KW heavy chain; disorder; antigenicity.
 OS Synthetic.
 PN W09428159-A.
 PD 08-DEC-1994.
 PF 30-MAY-1994; J00859.
 PR 31-MAY-1993; JP-129787.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PA (CHUS) CHUGAI PHARM CO LTD.
 PI Hirata Y, Sato K, Tsuchiya M;

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DR WPI; 95-022828/03.
 PT Antibody against IL-6 - useful for the therapy and treatment of
 PT IL-6 related disorders.
 PS Claim 8; Page 65; 82pp; Japanese.
 CC The sequence of the mouse anti-human interleukin-6 (IL-6) antibody heavy
 CC chain variable region complementarity determining region (CDR) 2. This
 CC sequence and that of CDR1 and 3 (R77212+4) were used in conjunction with
 CC the framework regions 1-4 (R77215-8) to construct a chimaeric antibody
 CC against human interleukin-6 (IL-6). The vectors 075914-7 express
 CC constructs encoding fragments of a chimaeric antibody to the human IL-6
 CC comprising (a) a light chain with (i) a variable region containing 3 CDR
 CC (R77201-3) inserted into several framework regions (FR) (r77204-7) and
 CC (ii) a human light chain constant region and (b) a heavy chain with (i) a
 CC variable region containing 3 CDR (R77212-4) inserted into FR (r77215-8)
 CC and (ii) a human light chain constant region. The FR of the light chain
 CC may be mouse derived (Q75888) or from the human antibody REI. The heavy
 CC chain FR may also be mouse derived (Q75889) or from the human antibody
 CC DAW. The antibodies can be used in the treatment of IL-6 related
 CC disorders. The antibodies are useful as they have low antigenicity due
 CC to the use of human derived sequences and low antigenicity mouse derived
 CC sequences.
 SQ Sequence 16 AA;

Query Match 71.9%; Score 92; DB 12; Length 16;
 Best Local Similarity 68.8%; Pred. No. 1.25e-02;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Db 1 hiwdddkvynpalkg 16
 || ||| ||||| ||||
 Qy 1 HIYDDDKRYNPSLKS 16

RESULT 15
 ID R67658 standard; Protein; 139 AA.
 AC R67658;
 DT 23-AUG-1995 (first entry)
 DE Anti-human IL-6 chimaeric Ab H chain V region in HEL-RVH-SK2a.
 KW Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;
 KW interleukin; antibody; hybridoma; CDR; framework; constant region;
 KW heavy chain; disorder; antigenicity.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Domain 1..19
 FT /label= signal peptide
 FT Domain 20..49
 FT /label= Framework region 1
 FT Domain 50..56
 FT /label= CDR1
 FT Domain 57..70
 FT /label= Framework region 2
 FT Domain 71..86
 FT /label= CDR2
 FT Domain 87..118
 FT /label= Framework region 3
 FT Domain 119..128
 FT /label= CDR3
 FT Domain 129..139
 FT /label= Framework region 4
 PN W09428159-A.
 PD 08-DEC-1994.
 PF 30-MAY-1994; J00859.
 PR 31-MAY-1993; JP-129787.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PA (CHUS) CHUGAI PHARM CO LTD.

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PI Hirata Y, Sato K, Tauchiya M;
 DR WPI; 95-022828/03.
 DR N-PSDB; Q75916.
 PT Antibody against IL-6 - useful for the therapy and treatment of
 PT IL-6 related disorders.
 PS Claim 21; Page 60-61; 82pp; Japanese.
 CC The sequence of the heavy chain variable region of a chimaeric antibody
 CC against human interleukin-6 (IL-6). The sequence is found on the plasmid
 CC HEL-RVH-SK2a. This vector and vectors Q75914, -5 and -7 express
 CC constructs encoding fragments of a chimaeric antibody to the human IL-6
 CC comprising (a) a light chain with (i) a variable region containing 3
 CC complementarity determining regions (CDR) (R77201-3) inserted into
 CC several framework regions (FR) (r77204-7) and (ii) a human light chain
 CC constant region and (b) a heavy chain with (i) a variable region
 CC containing 3 CDR (R77212-4) inserted into an FR (r77215-8) and (ii) a
 CC human light chain constant region. The CDR region are derived from the
 CC mouse anti-human IL-6 antibody SK2. The FR of the light chain may be
 CC mouse derived (Q75888) or from the human antibody REI. The heavy chain FR
 CC may also be mouse derived (Q75889) or from the human antibody DAM. The
 CC antibodies can be used in the treatment of IL-6 related disorders. The
 CC antibodies are useful as they have low antigenicity due to the use of
 CC human derived sequences and low antigenicity mouse derived sequences.
 SQ Sequence 139 AA;

Query Match 71.9%; Score 92; DB 13; Length 139;
 Best Local Similarity 68.8%; Pred. No. 1.25e-02;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 71 hlwnddkynpalkg 86
 ||:|||||:|:
 QY 1 HIYWDKRYNPSLKS 16

Search completed: Tue Mar 18 10:15:44 1997
 Job time : 11 secs.

(R/L)

Handwriting practice lines for the letter 'L' in uppercase and lowercase, showing stroke order and direction.

Release 2.1D John F. Collins, Biocomputing Research Unit.
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protein - protein database search, using Smith-Waterman algorithm

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Run on: Tue Mar 18 10:16:02 1997; MasPar time 1.99 Seconds
102.353 Million cell updates/sec
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Tabular output not generated.

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Title: >US-08-612-929-26
Description: (1-11) from US08612929.pep
Perfect Score: 104
Sequence: 1 RETVFYWFYDV 11

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Scoring table: PAM 150
Gap 15

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot33
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10

Statistics: Mean 27.173; Variance 49.515; scale 0.549

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	71	68.3	284	2	COX3_LEITA	CYTOCHROME C OXIDASE	1.86e-01
2	71	68.3	368	10	YHDX_ECOLI	HYPOTHETICAL 40.4 KD	1.86e-01
3	66	63.5	117	4	HV13_MOUSE	IG HEAVY CHAIN V REGI	1.09e+00
4	66	63.5	122	4	HV21_MOUSE	IG HEAVY CHAIN V REGI	1.09e+00
5	66	63.5	123	4	HV19_MOUSE	IG HEAVY CHAIN V REGI	1.09e+00
6	66	63.5	123	4	HV18_MOUSE	IG HEAVY CHAIN V REGI	1.09e+00
7	66	63.5	123	4	HV23_MOUSE	IG HEAVY CHAIN V REGI	1.09e+00
8	66	63.5	123	4	HV24_MOUSE	IG HEAVY CHAIN V REGI	1.09e+00
9	66	63.5	189	1	APD_RAT	APOLIPOPROTEIN D PREC	1.09e+00
10	66	63.5	570	7	PUTX_EMENI	PROLINE-SPECIFIC PERM	1.09e+00
11	65	62.5	482	6	NF31_NAEFO	VIROLENCE-RELATED PRO	1.54e+00
12	64	61.5	49	10	YZ0A_BACSU	HYPOTHETICAL PROTEIN	2.17e+00
13	64	61.5	508	10	YB9Y_YEAST	PUTATIVE SERINE CARBO	2.17e+00

Query Match 68.3%; Score 71; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

RESULT	1				
ID	COX3 LEITA	STANDARD;	PRT;	284 AA.	
AC	P14546;				
DT	01-JAN-1990	(REL. 13, CREATED)			
DT	01-JAN-1990	(REL. 13, LAST SEQUENCE UPDATE)			
DT	01-OCT-1994	(REL. 30, LAST ANNOTATION UPDATE)			
DE	CYTCHROME C OXIDASE POLYPEPTIDE III	(EC 1.9.3.1).			
DE	LEISHMANIA TARENTOLAE	(SAUROLEISHMANIA TARENTOLAE).			
OG	MITOCHONDRION.				
OC	EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; KINETOPLASTIDA;				
OC	TRYPANOSOMATIDAE.				
RN	{1}				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 85079995.				
RA	DE LA CRUZ V.F., NECKELMANN N., SIMPSON L.;				
RL	J. BIOL. CHEM. 259:15136-15147 (1984).				
CC	-I- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + 0(2) = 2 H(2)O +				
CC	4 FERRICYTOCHROME C.				
CC	-I- FUNCTION: SUBUNIT I, II, AND III FORM THE FUNCTIONAL CORE OF				
CC	THE ENZYME COMPLEX.				
DR	PR; G22848; G22848.				
DR	OXIDOREDUCTASE; MITOCHONDRION; TRANSMEMBRANE; KINETOPLAST.				
KW	SEQUENCE 284 AA; 34151 MW; 3C38259C CRC32;				

Query Match 68.3%; Score 71; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 135 vfywvf 140
 QY 4 VFYWVF 9

RESULT 2

ID YHDX ECOLI STANDARD; PRT; 368 AA.
 AC P45767;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 40.4 KD PROTEIN IN ACRF-RRND INTERGENIC REGION (0368A).
 GN YHDX.
 OS ESCHERICHIA COLI.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RA PLUNKETT G. III;
 RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -/- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM FOR AN AMINO ACID; PROBABLY RESPONSIBLE FOR THE
 CC TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
 CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 CC (POTENTIAL).
 CC -/- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
 CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE HISMQ
 CC SUBFAMILY.
 DR ENBL; U18997; G606210; --.
 DR ECOGENE; EGI2835; YHDX.
 DR PROSITE; P500402; BPD TRANSP INN MEMBR.
 KW HYPOTHETICAL PROTEIN; TRANSPORT; AMINO-ACID TRANSPORT; TRANSMEMBRANE;
 KW INNER MEMBRANE.
 SQ SEQUENCE 368 AA; 40395 MW; 6CD2B39D CRC32;

Query Match 68.3%; Score 71; DB 10; Length 368;
 Best Local Similarity 62.5%; Pred. No. 1.86e-01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 146 iffwyfav 153
 QY 4 VFYWFYDV 11

RESULT 3

ID HV13 MOUSE STANDARD; PRT; 117 AA.
 AC P01757;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (3558).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 80078170.
 RA SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;
 RL NATURE 283:35-40(1980).
 CC -/- THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN
 CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN
 CC THE D AND J SEGMENTS.
 CC -/- THIS PROTEIN BINDS DEXTRAN.

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DR PIR; A26242; MHMSJ5.
 DR HSSP; P01789; 2FCM.
 KW IMMUNOGLOBULIN V REGION.
 FT DISULFID 22 96 BY SIMILARITY.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 13024 MW; E7548A05 CRC32;

Query Match 63.5%; Score 66; DB 4; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.09e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 101 ywyfadv 106
 QY 6 WYFEDV 11

RESULT 4

ID HV21 MOUSE STANDARD; PRT; 122 AA.
 AC P01790;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (MS11).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 81054880.
 RA ROBINSON E.A., APPELLA E.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 77:4909-4913(1980).
 CC -/- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHO-
 CC RYLCHOLINE.
 DR PIR; A02070; AVMS75.
 DR HSSP; P01789; IMCP.
 KW IMMUNOGLOBULIN V REGION.
 FT NON TER 122 122
 SQ SEQUENCE 122 AA; 13652 MW; 4E68C805 CRC32;

Query Match 63.5%; Score 66; DB 4; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.09e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 106 ywyfadv 111
 QY 6 WYFEDV 11

RESULT 5

ID HV19 MOUSE STANDARD; PRT; 123 AA.
 AC P01788;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (H8).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RA BARSTAD P.;
 RL THESIS (1975), CALIFORNIA INSTITUTE OF TECHNOLOGY, U.S.A.
 CC -/- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHO-
 CC RYLCHOLINE.

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DR PIR; A02070; AVMS5.
 DR HSP; P01789; IMCP.
 KW IMMUNOGLOBULIN V REGION.
 FT NON TER 123 123
 SQ SEQUENCE 123 AA; 13805 MW; 705319F1 CRC32;

Query Match 63.5%; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred. No. 1.09e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywyfdv 112
 |||||
 QY 6 YWYFDV 11

RESULT 6

ID HV18 MOUSE STANDARD; PRT; 123 AA.
 AC P01787;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGIONS (TEPC 15, S107, HPCM1, HPCM2, AND HPCM3).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE (TEPC 15).
 RX MEDLINE; 7622762.
 RA RUDIKOFF S., POTTER M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 73:2109-2112(1976).
 [2]
 RP SEQUENCE FROM N.A. (H107).
 RX MEDLINE; 8019926.
 RA EARLY P., HUANG H., DAVIS M., CALAME K., HOOD L.;
 RL CELL 19:981-992(1980).
 [3]
 RP SEQUENCE (S107).
 RX MEDLINE; 76110488.
 RA RUDIKOFF S., BARSTAD P., POTTER M., HOOD L.;
 RL UNPUBLISHED RESULTS, CITED BY:
 RL HOOD L., CAMPBELL J.H., ELGIN S.C.R.;
 RL ANNU. REV. GENET. 9:305-353(1975).
 [4]
 RP SEQUENCE (HPCM1; HPCM2 AND HPCM3).
 RX MEDLINE; 81197602.
 RA GEARHART P.J., JOHNSON N.D., DOUGLAS R., HOOD L.;
 RL NATURE 291:29-34(1981).
 CC -1- ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.
 CC -1- THESE CHAINS WERE ISOLATED FROM MYELOMA AND HYBRIDOMA PROTEINS
 CC THAT BIND PHOSPHORYLCHOLINE.
 DR PIR; A02070; AVMS5.
 DR HSP; P01789; IMCP.
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.
 FT NON TER 123 123
 SQ SEQUENCE 123 AA; 13777 MW; B4F3A2A3 CRC32;

Query Match 63.5%; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred. No. 1.09e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywyfdv 112
 |||||
 QY 6 YWYFDV 11

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RESULT 7
 ID HV23 MOUSE STANDARD; PRT; 123 AA.
 AC P01792;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (HPCG8).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 81197602.
 RA GEARHART P.J., JOHNSON N.D., DOUGLAS R., HOOD L.;
 RL NATURE 291:29-34(1981).
 CC -1- THIS CHAIN WAS ISOLATED FROM HYBRIDOMA PROTEIN THAT BINDS PHOSPHO-
 CC RYLCHOLINE.
 DR PIR; A02070; AVMS5.
 DR HSP; P01789; IMCP.
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.
 FT NON TER 123 123
 SQ SEQUENCE 123 AA; 13879 MW; C4AFD9D0 CRC32;

Query Match 63.5%; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred. No. 1.09e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywyfdv 112
 |||||
 QY 6 YWYFDV 11

RESULT 8
 ID HV24 MOUSE STANDARD; PRT; 123 AA.
 AC P01793;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (HPCG13).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 81197602.
 RA GEARHART P.J., JOHNSON N.D., DOUGLAS R., HOOD L.;
 RL NATURE 291:29-34(1981).
 CC -1- THIS CHAIN WAS ISOLATED FROM HYBRIDOMA PROTEIN THAT BINDS PHOSPHO-
 CC RYLCHOLINE.
 DR PIR; A02070; AVMS5.
 DR HSP; P01789; IMCP.
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.
 FT NON TER 123 123
 SQ SEQUENCE 123 AA; 13808 MW; 23034AB8 CRC32;

Query Match 63.5%; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred. No. 1.09e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywyfdv 112
 |||||
 QY 6 YWYFDV 11

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CC PERMEASES.
 DR PIR; S04547; S04547.
 DR PROSITE; PS00218; AMINO ACID PERMEASE.
 KW TRANSPORT; AMINO-ACID TRANSPORT; TRANSMEMBRANE; GLYCOPROTEIN.
 FT DOMAIN 1 44 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 45 64 POTENTIAL.
 FT TRANSMEM 65 115 POTENTIAL.
 FT TRANSMEM 121 160 POTENTIAL.
 FT TRANSMEM 163 211 POTENTIAL.
 FT TRANSMEM 283 310 POTENTIAL.
 FT TRANSMEM 318 343 POTENTIAL.
 FT TRANSMEM 384 414 POTENTIAL.
 FT TRANSMEM 415 442 POTENTIAL.
 FT TRANSMEM 473 499 POTENTIAL.
 FT TRANSMEM 500 525 POTENTIAL.
 FT DOMAIN 526 570 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 380 380 POTENTIAL.
 FT CARBOHYD 402 402 POTENTIAL.
 FT CARBOHYD 416 416 POTENTIAL.
 SQ SEQUENCE 570 AA; 63101 MW; 25935669 CRC32;

Query Match 63.5%; Score 66; DB 7; Length 570;
 Best Local Similarity 50.0%; Pred. No. 1.09e+00;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 408 qtfvfywftni 417
 :||||: ::
 QY 2 ETVFYWFDV 11

RESULT 11
 ID NF31 NAEFO STANDARD; PRT; 482 AA.
 AC P42661;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE VIRULENCE-RELATED PROTEIN NF314 (EC 3.4.16.-).
 OS NAEGLERIA FOWLERI.
 OC EUKARYOTA; PROTOZOA; SARCOMASTICOPHORA; SARCODINA; RHIZOPODA; LOBOSA;
 OC SCHIZOPYRENIDA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LEE;
 RX MEDLINE; 92267659.
 RA HU W.-N., KOPACHIK W., BAND R.N.;
 RL INFECT. IMMUN. 60:2418-2424(1992).
 CC -|- FUNCTION: MAY BE REQUIRED BUT IS NOT SUFFICIENT FOR INCREASED
 CC VIRULENCE.
 CC -|- INDUCTION: BY GROWTH ON MAMMALIAN CELLS.
 CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10; ALSO KNOWN AS THE
 CC SERINE CARBOXYPEPTIDASE FAMILY.
 DR EMBL; M88397; G159720; -.
 DR PROSITE; PS00131; CARBOXYPEPT_SER_SER.
 DR PROSITE; PS00560; CARBOXYPEPT_SER_HIS.
 KW HYDROLASE; CARBOXYPEPTIDASE.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT ACT_SITE 399 399 BY SIMILARITY.
 FT ACT_SITE 459 459 BY SIMILARITY.
 SQ SEQUENCE 482 AA; 53848 MW; A9865400 CRC32;

Query Match 62.5%; Score 65; DB 6; Length 482;
 Best Local Similarity 57.1%; Pred. No. 1.54e+00;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9
 ID APD RAT STANDARD; PRT; 189 AA.
 AC P23593;
 DT 01-NOV-1991 (REL. 20, CREATED)
 DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE APOLIPOPROTEIN D PRECURSOR.
 GN APD.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H1STAR;
 RX MEDLINE; 90316104.
 RA SPREYER P., SCHAL H., KUHN G., ROTHE T., UNTERBECK A., OLEK K.,
 RA MUELLER H.W.;
 RL EMBL J. 9:2479-2484(1990).
 CC -|- FUNCTION: APD OCCURS IN THE MACROMOLECULAR COMPLEX WITH LECITHIN-
 CC CHOLESTEROL ACYLTRANSFERASE. IT IS PROBABLY INVOLVED IN THE
 CC TRANSPORT AND BINDING OF BILIN.
 CC -|- SUBUNIT: HOMODIMER.
 CC -|- SIMILARITY: THIS PROTEIN BELONGS TO THE FAMILY OF SMALL
 CC HYDROPHOBIC MOLECULES TRANSPORT PROTEINS (LIPOCALINS).
 DR EMBL; X55572; G287650; -.
 DR PIR; S12556; S12556.
 DR HSSP; P05090; ZAPD.
 DR PROSITE; PS00213; LIPOCALIN.
 KW GLYCOPROTEIN; PLASMA; LIPID-BINDING; TRANSPORT; SIGNAL; LIPOCALIN.
 FT SIGNAL 1 20
 FT CHAIN 21 189 APOLIPOPROTEIN D.
 FT CARBOHYD 65 65 POTENTIAL.
 FT CARBOHYD 98 98 POTENTIAL.
 SQ SEQUENCE 189 AA; 21635 MW; A731E791 CRC32;

Query Match 63.5%; Score 66; DB 1; Length 189;
 Best Local Similarity 55.6%; Pred. No. 1.09e+00;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 135 ttfwffhfv 143
 |::|:
 QY 3 TVFYWFDV 11

RESULT 10
 ID PUTX EMENI STANDARD; PRT; 570 AA.
 AC P18696;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE PROLINE-SPECIFIC PERMEASE (PROLINE TRANSPORT PROTEIN).
 GN PRNB.
 OS EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; PLECTOMYCETES; EUROTIALES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89313300.
 RA SOPHIANPOULOU V., SCAZZOFCCHIO C.;
 RL MOL. MICROBIOL. 3:705-714(1989).
 CC -|- FUNCTION: REQUIRED FOR HIGH-AFFINITY PROLINE TRANSPORT.
 CC -|- INDUCTION: BY L-PROLINE.
 CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -|- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID

Db 45 lfyyffe 51
:||||:
Qy 4 VFYWFYD 10

RESULT 12
ID YZOA BACSU STANDARD; PRT; 49 AA.
AC P40769;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL PROTEIN CLONE PSP23 (FRAGMENT).
GN YZOA.
OS BACILLUS SUBTILIS.
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89108019.
RA SMITH H., DE JONG A., BRON S., VENEMA G.;
RL GENE 70:351-361(1988).
DR EMBL; M22914; G143698; -.
DR SUBTILIST; BG11029; YZOA.
KW HYPOTHETICAL PROTEIN.
FT NON TER 49 49
SQ SEQUENCE 49 AA; 5436 MW; 2E63A14A CRC32;

Query Match 61.5%; Score 64; DB 10; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.17e+00;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 fywyf 23
|||||
Qy 5 FYWYF 9

RESULT 13
ID YB9 YEAST STANDARD; PRT; 508 AA.
AC P38109;
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE PUTATIVE SERINE CARBOXYPEPTIDASE IN ESRI-IBR1 INTERGENIC REGION
DE (EC 3.4.16.-).
GN YBR139W OR YBR1015.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-S288C;
RX MEDLINE; 94378717.
RA BECAM A.-M., CULLIN C., GRZYBOWSKA E., LACROUTE F., NASR F.,
RA OZIER-KALOGEROPOULOS O., PALUCHA A., SLONIMSKI P.P., ZAGULSKI M.,
RA HERBERT C.J.;
RL YEAST 10:S1-S11(1994).
RN [2]
RP DISCUSSION OF SEQUENCE.
RX MEDLINE; 95042830.
RA NASR F., BECAM A.-M., GRZYBOWSKA E., ZAGULSKI M., SLONIMSKI P.P.,
RA HERBERT C.J.;
RL CURR. GENET. 26:1-7(1994).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10; ALSO KNOWN AS THE
CC SERINE CARBOXYPEPTIDASE FAMILY.
DR EMBL; X75891; G496869; -.
DR EMBL; Z36008; G536436; -.
RN [1]

DR PIR; S46008; S46008.
DR PIR; S46581; S46581.
DR HSP; P08819; IYSC.
DR PROSITE; PS00131; CARBOXYPEPT SER SER.
DR PROSITE; PS00560; CARBOXYPEPT SER HIS.
KW HYPOTHETICAL PROTEIN; HYDROLASE; CARBOXYPEPTIDASE.
FT ACT SITE 219 219 BY SIMILARITY.
FT ACT SITE 413 413 BY SIMILARITY.
FT ACT SITE 474 474 BY SIMILARITY.
SQ SEQUENCE 508 AA; 57639 MW; 6415CAAB CRC32;

Query Match 61.5%; Score 64; DB 10; Length 508;
Best Local Similarity 66.7%; Pred. No. 2.17e+00;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 107 fywffe 112
||||:
Qy 5 FYWYF 10

RESULT 14
ID ISP4 SCHPO STANDARD; PRT; 776 AA.
AC P40900;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE SEXUAL DIFFERENTIATION PROCESS PROTEIN ISP4.
GN ISP4.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95042833.
RA SATO S., SUZUKI H., WIDYASTUTI U., HOTTA Y., TABATA S.;
RL CURR. GENET. 26:31-37(1994).
CC -1- DEVELOPMENTAL STAGE: TRANSCRIBED SPECIFICALLY DURING SEXUAL
CC DEVELOPMENT.
DR EMBL; D14061; G218543; -.
DR PIR; S43741; S43741.
DR PIR; S45495; S45495.
SQ SEQUENCE 776 AA; 88256 MW; 9D675742 CRC32;

Query Match 61.5%; Score 64; DB 5; Length 776;
Best Local Similarity 60.0%; Pred. No. 2.17e+00;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 460 evpfywyfslv 469
||||:
Qy 2 ETVFYWYFDV 11

RESULT 15
ID SYEP DROME STANDARD; PRT; 1714 AA.
AC P28668;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE (CONTAINS: GLUTAMYL-TRNA
DE SYNTHETASE (EC 6.1.1.17) (GLUTAMATE-TRNA LIGASE), AND PROLYL-TRNA
DE SYNTHETASE (EC 6.1.1.15) (PROLINE-TRNA LIGASE)).
GN AATS-GLUPRO.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN [1]

Mar 18 10:14

US-08-612-929-26.fsp

11

RP SEQUENCE FROM N.A.
 RX MEDLINE: 92097547.
 RA CERINI C., KERJAN P., ASTIER M., GRATECOS D., MIRANDE M., SEMERIVA M.;
 RL EMBO J. 10:4267-4277(1991).
 CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA (GLU) = AMP +
 CC PYROPHOSPHATE + L-GLUTAMYL-TRNA (GLU).
 CC -!- CATALYTIC ACTIVITY: ATP + L-PROLINE + TRNA (PRO) = AMP +
 CC PYROPHOSPHATE + L-PROLYL-TRNA (PRO).
 CC -!- SUBUNIT: COMPONENT OF THE MULTISYNTHETASE COMPLEX WHICH CONTAINS
 CC NINE DIFFERENT AA-TRNA SYNTHETASES.
 CC -!- SIMILARITY: THE N-TERMINAL DOMAIN BELONGS TO CLASS-I AMINOACYL-
 CC TRNA SYNTHETASES.
 CC -!- SIMILARITY: THE N-TERMINAL DOMAIN BELONGS TO CLASS-II AMINOACYL-
 CC TRNA SYNTHETASES.
 CC -!- SIMILARITY: CONTAINS 6 COPIES OF A DOMAIN THAT WE CALL "WHEP-TRS".
 DR EMBL; M74104; G157564; -.
 DR PIR; S18644; S18644.
 DR HSSP; P00962; LGTR.
 DR FLYBASE; FBGN0005674; AATS-GLUPRO.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I.
 DR PROSITE; PS00179; AA_TRNA_LIGASE_II_1.
 DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2.
 DR PROSITE; PS00762; WHEP-TRS.
 KW AMINOACYL-TRNA SYNTHASE; PROTEIN BIOSYNTHESIS; LIGASE; ATP-BINDING;
 KW MULTIFUNCTIONAL ENZYME; REPEAT.
 FT DOMAIN 170 754 GLUTAMYL-TRNA SYNTHETASE.
 FT DOMAIN 755 800 WHEP-TRS 1.
 FT DOMAIN 827 872 WHEP-TRS 2.
 FT DOMAIN 901 946 WHEP-TRS 3.
 FT DOMAIN 980 1025 WHEP-TRS 4.
 FT DOMAIN 1055 1100 WHEP-TRS 5.
 FT DOMAIN 1129 1173 WHEP-TRS 6.
 FT DOMAIN 1174 1180 POLY-GLY.
 FT DOMAIN 1207 1714 PROLYL-TRNA SYNTHETASE.
 FT SIMILAR 209 220 "HIGH" REGION.
 FT SIMILAR 438 442 "KMSKS" REGION.
 FT BINDING 441 441 ATP (BY SIMILARITY).
 SQ SEQUENCE 1714 AA; 189197 MW; 39A9D8E5 CRC32;

Query Match 61.5%; Score 64; DB 8; Length 1714;
 Best Local Similarity 50.0%; Pred. No. 2.17e+00;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 408 rddqfywfid 417
 : |||::|
 Qy 1 RETVFYWFYD 10

Search completed: Tue Mar 18 10:16:11 1997
 Job time : 9 secs.

WVQSEH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 18 10:16:29 1997; MasPar time 2.67 Seconds
Tabular output not generated. 106.055 Million cell updates/sec

Title: >US-08-612-929-26
Description: (1-11) from US08612929.pep
Perfect Score: 104
Sequence: 1 REIVFYWFYDFV 11

Scoring table: PAM 150
Gap 15

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Databases: pir48

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unann
14:unrev

Statistics: Mean 26.397; Variance 58.448; scale 0.452

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.
1	84	80.8	91 5	PH1004 Ig heavy chain V reg	2.03e-02
2	77	74.0	123 5	A30540 Ig heavy chain V reg	1.92e-01
3	73	70.2	31 12	B49038 immunoglobulin lambda	6.68e-01
4	73	70.2	38 12	C49038 immunoglobulin lambda	6.68e-01
5	73	70.2	56 12	E49038 immunoglobulin lambda	6.68e-01
6	73	70.2	58 12	D49038 immunoglobulin lambda	6.68e-01
7	73	70.2	124 5	F30539 Ig heavy chain V reg	6.68e-01
8	73	70.2	124 5	G30539 Ig heavy chain V reg	6.68e-01
9	73	70.2	124 5	H30539 Ig heavy chain V reg	6.68e-01
10	71	68.3	181 4	A28782 cytochrome-c oxidase	1.23e+00
11	71	68.3	284 4	G22848 cytochrome-c oxidase	1.23e+00
12	71	68.3	287 4	A25877 cytochrome-c oxidase	1.23e+00

13	68	65.4	111 12	S13687 Ig heavy chain V reg	3.04e+00
14	67	64.4	107 5	PH0987 Ig heavy chain V reg	4.09e+00
15	67	64.4	108 5	PH1006 Ig heavy chain V reg	4.09e+00
16	67	64.4	123 5	B30540 Ig heavy chain V reg	4.09e+00
17	66	63.5	17 12	S26744 Ig heavy chain J reg	5.50e+00
18	66	63.5	18 12	A25941 Ig heavy chain J-H1	5.50e+00
19	66	63.5	91 12	S13689 Ig heavy chain V reg	5.50e+00
20	66	63.5	101 12	S13692 Ig heavy chain V reg	5.50e+00
21	66	63.5	106 5	PH1002 Ig heavy chain V reg	5.50e+00
22	66	63.5	110 12	S13688 Ig heavy chain V reg	5.50e+00
23	66	63.5	111 5	S26463 Ig heavy chain V reg	5.50e+00
24	66	63.5	111 12	S13693 Ig heavy chain V reg	5.50e+00
25	66	63.5	112 12	S13690 Ig heavy chain V reg	5.50e+00
26	66	63.5	112 12	S13685 Ig heavy chain V reg	5.50e+00
27	66	63.5	112 12	S13686 Ig heavy chain V reg	5.50e+00
28	66	63.5	113 5	PH1018 Ig heavy chain V reg	5.50e+00
29	66	63.5	115 12	S13694 Ig heavy chain V reg	5.50e+00
30	66	63.5	116 12	S13691 Ig heavy chain V reg	5.50e+00
31	66	63.5	117 2	MHMSJ5 Ig heavy chain V reg	5.50e+00
32	66	63.5	121 5	B30539 Ig heavy chain V reg	5.50e+00
33	66	63.5	122 5	B30515 Ig heavy chain V reg	5.50e+00
34	66	63.5	123 5	B30560 Ig heavy chain V reg	5.50e+00
35	66	63.5	123 2	AVMS13 Ig heavy chain V reg	5.50e+00
36	66	63.5	123 2	AVMS75 Ig heavy chain VH1 r	5.50e+00
37	66	63.5	123 5	B30556 Ig heavy chain V reg	5.50e+00
38	66	63.5	123 5	PL0017 Ig heavy chain V-D-J	5.50e+00
39	66	63.5	124 2	AVMS51 Ig heavy chain V reg	5.50e+00
40	66	63.5	137 12	S03326 Ig heavy chain precu	5.50e+00
41	66	63.5	189 6	A60958 apolipoprotein D pre	5.50e+00
42	66	63.5	288 4	S36953 cytochrome-c oxidase	5.50e+00
43	66	63.5	288 4	S36955 cytochrome-c oxidase	5.50e+00
44	66	63.5	288 4	S36954 cytochrome-c oxidase	5.50e+00
45	66	63.5	570 10	S04547 proline transport pr	5.50e+00

ALIGNMENTS

RESULT 1
ENTRY PH1004 #type fragment
TITLE Ig heavy chain V region (clone 165.5) - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Apr-1995

ACCESSIONS PH1004
REFERENCE PH0971
#authors Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
#journal J. Exp. Med. (1992) 176:761-779
#title Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice.

#accession PH1004
#molecule_type mRNA
#residues 1-91 #label TIL
#experimental_source B cell, strain [NZB x NZW]F1
#note nucleotide sequence is not given

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
SUMMARY #length 91 #checksum 5115

Query Match 80.8%; Score 84; DB 5; Length 91;
Best Local Similarity 72.7%; Pred. No. 2.03e-02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 80 regcywyfvdv 90

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QY 1 RETVFWYFDV 11
|| :|||||

RESULT 2
ENTRY A30540 #type fragment
TITLE Ig heavy chain V region (253.1203) - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 12-Apr-1995
ACCESSIONS A30540
REFERENCE A30534
#authors Claflin, J.L.; Berry, J.
#journal J. Immunol. (1988) 141:4012-4019
#title Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae. Germ-line but not mutated T15 antibodies are dominantly selected.
#cross-references MUID:89035545
#accession A30540
#status preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues 1-123 #label CIA
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 123 #checksum 8418

Query Match 74.0%; Score 77; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.92e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 106 fywyfdv 112
:|||||
QY 5 FYWYFDV 11

RESULT 3
ENTRY B49038 #type fragment
TITLE immunoglobulin lambda light chain variable region - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
ACCESSIONS B49038
REFERENCE A49038
#authors Weiss, U.; Zobebelein, R.; Rajewsky, K.
#journal Eur. J. Immunol. (1992) 22:511-517
#title Accumulation of somatic mutants in the B cell compartment after primary immunization with a T cell-dependent antigen.
#cross-references MUID:92164733
#accession B49038
#status preliminary
#molecule_type DNA
#residues 1-31 #label WEI
#cross-references NCBIN:85733; NCBIP:85761
#experimental_source spleen
#note sequence extracted from NCB1 backbone
SUMMARY #length 31 #checksum 9999

Query Match 70.2%; Score 73; DB 12; Length 31;
Best Local Similarity 85.7%; Pred. No. 6.68e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 25 yywyfdv 31
:|||||
QY 5 FYWYFDV 11

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RESULT 4
ENTRY C49038 #type fragment
TITLE immunoglobulin lambda light chain variable region - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
ACCESSIONS C49038
REFERENCE A49038
#authors Weiss, U.; Zobebelein, R.; Rajewsky, K.
#journal Eur. J. Immunol. (1992) 22:511-517
#title Accumulation of somatic mutants in the B cell compartment after primary immunization with a T cell-dependent antigen.
#cross-references MUID:92164733
#accession C49038
#status preliminary
#molecule_type DNA
#residues 1-38 #label WEI
#cross-references NCBIN:85734; NCBIP:85801
#experimental_source spleen
#note sequence extracted from NCB1 backbone
SUMMARY #length 38 #checksum 1027

Query Match 70.2%; Score 73; DB 12; Length 38;
Best Local Similarity 85.7%; Pred. No. 6.68e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 32 yywyfdv 38
:|||||
QY 5 FYWYFDV 11

RESULT 5
ENTRY E49038 #type fragment
TITLE immunoglobulin lambda light chain variable region - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
ACCESSIONS E49038
REFERENCE A49038
#authors Weiss, U.; Zobebelein, R.; Rajewsky, K.
#journal Eur. J. Immunol. (1992) 22:511-517
#title Accumulation of somatic mutants in the B cell compartment after primary immunization with a T cell-dependent antigen.
#cross-references MUID:92164733
#accession E49038
#status preliminary
#molecule_type DNA
#residues 1-56 #label WEI
#cross-references NCBIN:85736; NCBIP:85804
#experimental_source spleen
#note sequence extracted from NCB1 backbone
SUMMARY #length 56 #checksum 7706

Query Match 70.2%; Score 73; DB 12; Length 56;
Best Local Similarity 85.7%; Pred. No. 6.68e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 50 yywyfdv 56
:|||||
QY 5 FYWYFDV 11

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```

RESULT 6
ENTRY D49038 #type fragment
TITLE immunoglobulin lambda light chain variable region - mouse
        (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
        23-Mar-1995
ACCESSIONS D49038
REFERENCE A49038
#authors Weise, U.; Zoebelen, R.; Rajewsky, K.
#journal Eur. J. Immunol. (1992) 22:511-517
#title Accumulation of somatic mutants in the B cell compartment
        after primary immunization with a T cell-dependent antigen.
#cross-references MUID:92164733
#accession D49038
##status preliminary
##molecule_type DNA
##residues 1-58 #label WEI
##cross-references NCBI:85735; NCBI:85802
##experimental_source spleen
##note _sequence extracted from NCBI backbone
SUMMARY #length 58 #checksum 2946

Query Match 70.2%; Score 73; DB 12; Length 58;
Best Local Similarity 85.7%; Pred. No. 6.68e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 52 ywywfdv 58
:|||||
Qy 5 FYWYFDV 11

```

```

RESULT 7
ENTRY F30539 #type fragment
TITLE Ig heavy chain V region (224.4B11) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change
        12-Apr-1995
ACCESSIONS F30539
REFERENCE A30534
#authors Claflin, J.L.; Berry, J.
#journal J. Immunol. (1988) 141:4012-4019
#title Genetics of the phosphocholine-specific antibody response to
        Streptococcus pneumoniae. Germ-line but not mutated T15
        antibodies are dominantly selected.
#cross-references MUID:89035545
#accession F30539
##status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 1-124 #label CIA
##note nucleotide sequence is not given
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 124 #checksum 689

Query Match 70.2%; Score 73; DB 5; Length 124;
Best Local Similarity 85.7%; Pred. No. 6.68e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywywfdv 113
:|||||
Qy 5 FYWYFDV 11

```

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```

RESULT 8
ENTRY G30539 #type fragment
TITLE Ig heavy chain V region (224.7E7) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change
        12-Apr-1995
ACCESSIONS G30539
REFERENCE A30534
#authors Claflin, J.L.; Berry, J.
#journal J. Immunol. (1988) 141:4012-4019
#title Genetics of the phosphocholine-specific antibody response to
        Streptococcus pneumoniae. Germ-line but not mutated T15
        antibodies are dominantly selected.
#cross-references MUID:89035545
#accession G30539
##status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 1-124 #label CIA
##note nucleotide sequence is not given
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 124 #checksum 1542

Query Match 70.2%; Score 73; DB 5; Length 124;
Best Local Similarity 85.7%; Pred. No. 6.68e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywywfdv 113
:|||||
Qy 5 FYWYFDV 11

```

```

RESULT 9
ENTRY H30539 #type fragment
TITLE Ig heavy chain V region (252.5E10) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change
        12-Apr-1995
ACCESSIONS H30539
REFERENCE A30534
#authors Claflin, J.L.; Berry, J.
#journal J. Immunol. (1988) 141:4012-4019
#title Genetics of the phosphocholine-specific antibody response to
        Streptococcus pneumoniae. Germ-line but not mutated T15
        antibodies are dominantly selected.
#cross-references MUID:89035545
#accession H30539
##status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 1-124 #label CIA
##note nucleotide sequence is not given
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 124 #checksum 923

Query Match 70.2%; Score 73; DB 5; Length 124;
Best Local Similarity 85.7%; Pred. No. 6.68e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 107 ywywfdv 113
:|||||
Qy 5 FYWYFDV 11

RESULT 10

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```

ENTRY      A28782      #type fragment
TITLE      cytochrome-c oxidase (EC 1.9.3.1) chain III - Trypanosoma
            brucei mitochondrion (SGC6) (fragment)
ORGANISM   #formal name mitochondrion Trypanosoma brucei
DATE       28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change
            28-Oct-1994
ACCESSIONS A28782
REFERENCE  A28782
            #authors Feagin, J.E.; Abraham, J.M.; Stuart, K.
            #journal Cell (1988) 53:413-422
            #title Extensive editing of the cytochrome c oxidase III transcript
            in Trypanosoma brucei.
            #cross-references MUID:88210456
            #accession A28782
            ##molecule_type mRNA
            ##residues 1-181 ##label FEa
            ##note the authors translated the codon TGT for residues 131
            and 140 as Arg

GENETICS
            #genome mitochondrion
            #genetic_code SGC6
            #classification #superfamily cytochrome-c oxidase chain III
            #keywords electron transfer; membrane-associated complex;
            mitochondrion; oxidoreductase; transmembrane protein
            #summary #length 181 #checksum 1590

Query Match 68.3%; Score 71; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.23e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 32 vfywyf 37
|||||
Qy 4 VFYWF 9

RESULT 11
ENTRY      G22848      #type complete
TITLE      cytochrome-c oxidase (EC 1.9.3.1) chain III - Sauroleishmania
            tarentolae mitochondrion (SGC6)
ORGANISM   #formal name mitochondrion Sauroleishmania tarentolae
DATE       30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
            28-Oct-1994
ACCESSIONS G22848
REFERENCE  A22848
            #authors de la Cruz, V.F.; Neckelmann, N.; Simpson, L.
            #journal J. Biol. Chem. (1984) 259:15136-15147
            #title Sequences of six genes and several open reading frames in the
            kinetoplast maxicircle DNA of Leishmania tarentolae.
            #cross-references MUID:85079995
            #accession G22848
            ##molecule_type DNA
            ##residues 1-284 ##label DEL
            ##cross-references GB:M10126

GENETICS
            #genome mitochondrion
            #genetic_code SGC6
            #classification #superfamily cytochrome-c oxidase chain III
            #keywords electron transfer; membrane-associated complex;
            mitochondrion; oxidoreductase; transmembrane protein
            #summary #length 284 #molecular-weight 34151 #checksum 2764

Query Match 68.3%; Score 71; DB 4; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.23e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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8

```

Db 135 vfywyf 140
|||||
Qy 4 VFYWF 9

RESULT 12
ENTRY      A25877      #type fragment
TITLE      cytochrome-c oxidase (EC 1.9.3.1) chain III - Crithidia
            fasciculata mitochondrion (SGC6) (fragment)
ORGANISM   #formal name mitochondrion Crithidia fasciculata
DATE       19-Jan-1988 #sequence_revision 19-Jan-1988 #text_change
            28-Oct-1994
ACCESSIONS A25877
REFERENCE  A25877
            #authors Sloof, P.; van den Burg, J.; Voogd, A.; Benne, R.
            #journal Nucleic Acids Res. (1987) 15:51-65
            #title The nucleotide sequence of a 3.2 kb segment of mitochondrial
            maxicircle DNA from Crithidia fasciculata containing the
            gene for cytochrome oxidase subunit III, the N-terminal
            part of the apocytochrome b gene and a possible frameshift
            gene; further evidence for the use of unusual initiator
            triplets in trypanosome mitochondria.
            #cross-references MUID:87146364
            #accession A25877
            ##status preliminary; not compared with conceptual translation
            ##molecule_type DNA
            ##residues 1-287 ##label SLO

GENETICS
            #genome mitochondrion
            #genetic_code SGC6
            #classification #superfamily cytochrome-c oxidase chain III
            #keywords electron transfer; membrane-associated complex;
            mitochondrion; oxidoreductase; transmembrane protein
            #summary #length 287 #checksum 9988

Query Match 68.3%; Score 71; DB 4; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.23e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 138 vfywyf 143
|||||
Qy 4 VFYWF 9

RESULT 13
ENTRY      S13687      #type fragment
TITLE      Ig heavy chain V region - mouse (fragment)
ORGANISM   #formal name Mus musculus #common name house mouse
DATE       18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
            10-Nov-1995
ACCESSIONS S13687
REFERENCE  S13685
            #authors Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.;
            Houghton, G.; Clarke, S.H.
            #journal Eur. J. Immunol. (1989) 19:1289-1295
            #title Biased immunoglobulin variable region gene expression by Ly-1
            B cells due to clonal selection.
            #cross-references MUID:89338557
            #accession S13687
            ##molecule_type mRNA
            ##residues 1-111 ##label PEN
            ##cross-references EMBL:X53340
            #summary #length 111 #checksum 5825

```


Mar 18 10:15

US-08-612-929-26 rpr

9

Query Match 65.4%; Score 68; DB 12; Length 111;
Best Local Similarity 60.0%; Pred. No. 3.04e+00;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 98 dslgywyfdv 107
::: |||||
Qy 2 ETVFYWYFDV 11

RESULT 14
ENTRY PH0987 #type fragment
TITLE Ig heavy chain V region (clone 163.47) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Apr-1995
ACCESSIONS PH0987
REFERENCE PH0971
#authors Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
#journal J. Exp. Med. (1992) 176:761-779
#title Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice.
#accession PH0987
#molecule_type mRNA
#residues 1-107 #label TIL
#experimental_source B cell, strain [NZB x NZW]F1
#note nucleotide sequence is not given
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
SUMMARY #length 107 #checksum 8510

Query Match 64.4%; Score 67; DB 5; Length 107;
Best Local Similarity 85.7%; Pred. No. 4.09e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 100 iywyfdv 106
:|||||
Qy 5 FYWYFDV 11

RESULT 15
ENTRY PH1006 #type fragment
TITLE Ig heavy chain V region (clone 202.33) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Apr-1995
ACCESSIONS PH1006
REFERENCE PH0971
#authors Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
#journal J. Exp. Med. (1992) 176:761-779
#title Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice.
#accession PH1006
#molecule_type mRNA
#residues 1-108 #label TIL
#experimental_source B cell, strain [NZB x NZW]F1
#note nucleotide sequence is not given
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
SUMMARY #length 108 #checksum 3884

Query Match 64.4%; Score 67; DB 5; Length 108;

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US-08-612-929-26 rpr

10

Best Local Similarity 87.5%; Pred. No. 4.09e+00;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 100 vgywyfdv 107
:|||||
Qy 4 VFYWYFDV 11

Search completed: Tue Mar 18 10:16:40 1997
Job time : 11 secs.

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